

RESULT 674
ID ACD10523 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-FEB-2003.
RESULT 675
ID ACD12165 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 27-FEB-2003.
RESULT 676
ID ACF42550 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-MAR-2003.
RESULT 677
ID ACF18571 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 27-MAR-2003.
RESULT 678
ID ACF02361 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 13-MAR-2003.
RESULT 679
ID ACF21869 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 13-MAR-2003.
RESULT 680
ID ACF10553 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.
RESULT 681
ID ACF34005 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 03-APR-2003.
RESULT 682
ID ACF4967 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.
RESULT 683
ID ACD90599 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049745-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 13-MAR-2003.
RESULT 684
ID ACD91212 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 13-MAR-2003.
RESULT 685
ID ACF30523 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.
RESULT 686
ID ACD87222 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.
RESULT 687
ID ACF60276 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.
RESULT 688
ID ACF46826 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 08-MAY-2003.
RESULT 689
ID ACF75683 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 22-MAY-2003.
RESULT 690
ID ADA79995 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.
RESULT 691
ID ACF17343 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-MAR-2003.
RESULT 692
ID ACF23097 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 27-MAR-2003.
RESULT 693

ID ACF08097 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 694
ID ACF08404 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 695
ID ACF40708 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 696
ID ACF53887 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 697
ID ACD47151 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US200308693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 698
ID ACF48054 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 699
ID ACF47440 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 700
ID ACF46212 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 701
ID ACD86301 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 702
ID ACF52659 standard; cDNA; 1743 BP.

DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 703
ID ACF52966 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 704
ID ACF64959 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003088737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 705
ID ACF76604 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 706
ID ACF61504 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 707
ID ACF61811 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 708
ID ACD30842 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 709
ID ACD31763 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 710
ID ACD32684 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 711
ID ACF17650 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;

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Best Local Similarity 52.5%; Pred. No. 41;
RESULT 712
ID ACF07483 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 713
ID ACF20641 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 714
ID ACF20948 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 715
ID ACF21255 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 716
ID ACD47765 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 717
ID ACF47747 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 718
ID ACF53580 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 719
ID ACD86915 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 720
ID ACH05163 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 721
ID ACF44660 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 722
ID ADA81722 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 723
ID ACD2315 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 724
ID ACD24662 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 725
ID ACD39865 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 726
ID ACD40172 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 727
ID ACF13480 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 728
ID ACF03282 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 729
ID ACF78753 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 730
ID ACF11474 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
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Best Local Similarity 52.5%; Pred. No. 41;
RESULT 731
ID ACF50817 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 732
ID ACF34312 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 733
ID ACD46537 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 734
ID ACD48379 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 735
ID ACF27760 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 736
ID ACF24632 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 737
ID ACD85687 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 738
ID ACD90292 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 739
ID ACD83845 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 740

ID ACF49282 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US200304540-A1.
PD 05-JUN-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 741
ID ACH07367 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 742
ID ACH07674 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 743
ID ACH08288 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 744
ID ACH11479 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 745
ID ACH11786 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 746
ID ACH10437 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 747
ID ACF01440 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 748
ID ACF41015 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 749
ID ACD24355 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044918-A1.

PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 750
ID ACD31456 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 751
ID ACF17957 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 752
ID ACF32740 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 753
ID ACF40401 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 754
ID ACF48361 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 755
ID ACF38310 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 756
ID ACF25246 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 757
ID ACF27146 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 758
ID ACF29602 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 759
ID ACF19413 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036129-A1.
PD 20-FEB-2003.

PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 760
ID ACF76297 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 761
ID ACF49589 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 762
ID ACF4046 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 763
ID ACH06391 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 764
ID ACH06698 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 765
ID ADA83520 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 766
ID ACC92754 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 767
ID AC93368 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 768
ID ACF19413 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036129-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 769
ID ACD13104 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 770
ID ACF06562 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 771
ID ACC94596 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 772
ID ACC98024 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 773
ID ACC94289 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 774
ID ACF42243 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 775
ID ACD31149 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 776
ID ACD43178 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 777
ID ACD43485 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 778
ID ACF15015 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059879-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 779
ID ACF01747 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 780
ID ACF31819 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 781
ID ACD67496 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 782
ID ACD48686 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 783
ID ACD48993 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 784
ID ACF51431 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 785
ID ACF54194 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 786
ID ACF25918 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 787
ID ACF39231 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 788
ID ACF28988 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 789
ID ACD90905 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 790
ID ACD86608 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 791
ID ACH05470 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 792
ID ACF65266 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 793
ID ADB20563 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 794
ID ACF43739 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 795
ID ACH03209 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 796
ID ACH09516 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 797
ID ACH04508 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.

RESULT 797
ID ADA78915 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 798
ID ACF09939 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 799
ID ACF51124 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 800
ID ACF24018 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 801
ID ACD8450 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 802
ID ACH09823 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 803
ID ACH10744 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 804
ID ACD11551 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 805
ID ACC96601 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 806
ID ACH04508 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.

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PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 807
ID ACC98631 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 808
ID ACF41936 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 809
ID ACF16857 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 810
ID ACD32377 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 811
ID ACD30535 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 812
ID ACD41406 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 813
ID ACF07790 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 814
ID ACF31205 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 815
ID ACF77525 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 816
ID ACF11167 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 817
ID ACF33047 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 818
ID ACF26225 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 819
ID ACD83538 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 820
ID ACP23711 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 821
ID ACF43125 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 822
ID ACF43432 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 823
ID ACH06084 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 824
ID ACH08902 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 825
ID ACC90496 standard; cDNA; 1743 BP.
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DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 826
ID ACF10860 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 827
ID ACF93675 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 828
ID ACC96294 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 829
ID ACD24969 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 830
ID ACF02054 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 831
ID ACF22176 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 832
ID ACF22790 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 833
ID ACF09018 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 834
ID ACF33354 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;

Best Local Similarity 52.5%; Pred. No. 41;
RESULT 835
ID ACF54808 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 836
ID ACF48668 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 837
ID ACD47458 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 838
ID ACD49300 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 839
ID ACF38003 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 840
ID ACF30216 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 841
ID ACD87529 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 842
ID ACF62118 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 843
ID ACHI1051 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 844
ID ACHI1051 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;

ID ACD10216 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036158-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 03-APR-2003.

RESULT 845
ID ACD16941 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003036151-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-FEB-2003.

RESULT 846
ID ACC99238 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040067-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-FEB-2003.

RESULT 847
ID ACF00632 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054456-A1.
PD 20-MAR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-MAR-2003.

RESULT 848
ID ACD41099 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054482-A1.
PD 20-MAR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-MAR-2003.

RESULT 849
ID ACF14708 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054457-A1.
PD 20-MAR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 20-MAR-2003.

RESULT 850
ID ACF22483 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059893-A1.
PD 27-MAR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 27-MAR-2003.

RESULT 851
ID ACF79060 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049764-A1.
PD 13-MAR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 13-MAR-2003.

RESULT 852
ID ACD68052 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.

RESULT 853
ID ACF11781 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073177-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.

RESULT 854
ID ACF51738 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064442-A1.
PD 03-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 03-APR-2003.

RESULT 855
ID ACF33661 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064450-A1.
PD 03-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 03-APR-2003.

RESULT 856
ID ACD49914 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068731-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.

RESULT 857
ID ACF37696 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068683-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.

RESULT 858
ID ACF28681 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068754-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.

RESULT 859
ID ACD88757 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 10-APR-2003.

RESULT 860
ID ACF75376 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003096351-A1.
PD 22-MAY-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 22-MAY-2003.

RESULT 861
ID ACF61197 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003096358-A1.
PD 22-MAY-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 22-MAY-2003.

RESULT 862
ID ACF44353 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104556-A1.
PD 05-JUN-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 05-JUN-2003.

RESULT 863
ID ACF11781 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073177-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
PD 17-APR-2003.

ID ACH08595 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049736-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 864
ID ACC93982 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 865
ID ACD21087 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036121-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 866
ID ACF06869 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 867
ID ACD20780 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 868
ID ACD22929 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 869
ID ACF41629 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 870
ID ACF07176 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 871
ID ACF77832 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 872
ID ACD46230 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 873
ID ACF47133 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 874
ID ACF4501 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 875
ID ACF45905 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 876
ID ACF45598 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 877
ID ACF38617 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 878
ID ACD89678 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 879
ID ACD85380 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 880
ID ACD85994 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 881
ID ACF75990 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;

RESULT 882
ID ACF60890 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 883
ID ACH05777 standard; cDNA: 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 884
ID ADA82886 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 885
ID ACF56036 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 886
ID ACF55422 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 887
ID ADH86194 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 888
ID ACF56343 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 889
ID ACF56650 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 890
ID ACF55729 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 891
ID ACF55115 standard; cDNA: 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 892
ID ADC18104 standard; cDNA: 1743 BP.
DE Human PRO polynucleotide #68.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 893
ID ADD05924 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 894
ID ADD10512 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #112.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 895
ID ADD11472 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #112.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 896
ID ADD70750 standard; cDNA: 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 897
ID ADD39827 standard; cDNA: 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 898
ID ADD70273 standard; cDNA: 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 899
ID ADD37265 standard; cDNA: 1743 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #112.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 900
ID ADD38394 standard; cDNA: 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.

PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 901
ID ADD39350 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 902
ID ADD38873 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 903
ID ADD40304 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 904
ID ADE50525 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 905
ID ADE20137 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 906
ID ADE50048 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 907
ID ADE21606 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 908
ID ADF30031 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 909
ID ADF55924 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003204054-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 910
ID ADG02919 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 911
ID ADG01626 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 912
ID ADF5801 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 913
ID ADG12616 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 914
ID ADH09276 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 915
ID ADH99428 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 916
ID ABX78753 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 917
ID ACA75725 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 918
ID ACA71205 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 10; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 919

ID AC87733 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 920
ID ACF15629 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 931
ID ACA72996 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 932
ID ACD03168 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 933
ID ACD01983 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 934
ID ACA92175 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 935
ID ADL33055 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US20030207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 11; Length 1743;
52.5%; Pred. No. 41;
RESULT 936
ID ADM30591 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 11; Length 1743;
52.5%; Pred. No. 41;
RESULT 937
ID ADE41473 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #112.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
52.5%; Pred. No. 41;
RESULT 938
ID ADE74588 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
52.5%; Pred. No. 41;
RESULT 939
ID ADE75200 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.

ID AC87733 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 920
ID ACF87119 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 921
ID ACD04292 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 922
ID ACF69623 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 923
ID ACA90468 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 924
ID ACC89575 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 925
ID ACA98366 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 926
ID ACA94008 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 927
ID ACD15401 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 928
ID ACD08988 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 10; Length 1743;
52.5%; Pred. No. 41;
RESULT 929
ID ACC96908 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040056-A1.

PN US2003211574-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 940
ID ADE96608 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 941
ID ADF25919 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 942
ID ADF24818 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 943
ID ADF29554 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 944
ID ADE97085 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 945
ID ADF96413 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 946
ID ADG04684 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 947
ID ADG00844 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 948
ID ADG83100 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 949
ID ADH03123 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 950
ID ADH04077 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 951
ID ADH03600 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 952
ID ADH26381 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 953
ID ADH33350 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 954
ID ADH43656 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #112.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 955
ID ADH04554 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 956
ID ADH61555 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1337.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 957
ID ADJ55089 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 12; Length 1743;
Pred. No. 41;
RESULT 958
ID ADJ55089 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.

Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 958
 ID ADK83001 standard; cDNA; 1743 BP.
 DE Human PRO polynucleotide #112.
 PN US2004043927-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 959
 ID ADJ64860 standard; cDNA; 1743 BP.
 DE Human PRO polynucleotide #226.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 960
 ID ADM31756 standard; cDNA; 1743 BP.
 DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 961
 ID ADM36803 standard; cDNA; 1743 BP.
 DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 962
 ID ADM40608 standard; cDNA; 1743 BP.
 DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 963
 ID ADL94754 standard; cDNA; 1743 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1337.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 964
 ID ADN38216 standard; cDNA; 1743 BP.
 DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 12; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 965
 ID AAC46128 standard; DNA; 2016 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49004.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 3; Length 2016;
 Best Local Similarity 57.5%; Pred. No. 42;
 RESULT 966
 ID AAQ27886 standard; DNA; 2418 BP.
 DE P.falciptarum GBP130h.
 PN EP499834-A2.
 PD 26-AUG-1992.
 PA (BEHW) BEHRINGWERKE AG.
 Query Match 5.4%; Score 38.4; DB 2; Length 2418;
 Best Local Similarity 52.5%; Pred. No. 44;
 RESULT 967

ID ADG79359 standard; cDNA; 3337 BP.
 DE Human secreted protein cDNA of the invention SEQ ID NO:165.
 PN WO200268638-A1.
 PD 06-SEP-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.4%; Score 38.4; DB 6; Length 3337;
 Best Local Similarity 50.0%; Pred. No. 47;
 RESULT 968
 ID AAL26509 standard; cDNA; 4010 BP.
 DE Human breast cancer expressed polynucleotide 18966.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 5.4%; Score 38.4; DB 4; Length 4010;
 Best Local Similarity 50.0%; Pred. No. 49;
 RESULT 969
 ID ABL32413 standard; DNA; 6185 BP.
 DE Human immune system associated gene SEQ ID NO: 386.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 6185;
 Best Local Similarity 55.1%; Pred. No. 54;
 RESULT 970
 ID ABK31322 standard; DNA; 6880 BP.
 DE Signal transduction associated gene modified DNA #83.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 6880;
 Best Local Similarity 45.2%; Pred. No. 55;
 RESULT 971
 ID ABL70293 standard; DNA; 6880 BP.
 DE Chemically treated cell signalling DNA sequence#92.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 6880;
 Best Local Similarity 45.2%; Pred. No. 55;
 RESULT 972
 ID AAS61223 standard; DNA; 6880 BP.
 DE Human gene regulation-associated gene oligonucleotide #178.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 6880;
 Best Local Similarity 45.2%; Pred. No. 55;
 RESULT 973
 ID ABK40071 standard; DNA; 9983 BP.
 DE Human chemically pretreated gene sequence #77 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 9983;
 Best Local Similarity 47.5%; Pred. No. 59;
 RESULT 974
 ID ABX11085 standard; DNA; 22118 BP.
 DE Mouse ribosomal RNA (rRNA) gene.
 PN US2002160410-A1.
 PD 31-OCT-2002.
 PA (HADL/) HADLACZYK G.
 PA (SZAL/) SZALAY A A.
 Query Match 5.4%; Score 38.4; DB 8; Length 22118;
 Best Local Similarity 58.3%; Pred. No. 70;
 RESULT 975
 ID ABQ66997 standard; DNA; 37515 BP.
 DE Human angiogenesis associated polynucleotide SEQ ID NO 27.
 PN WO200246454-A2.
 PD 13-JUN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.4%; Score 38.4; DB 6; Length 37515;
 Best Local Similarity 45.6%; Pred. No. 78;
 RESULT 976

RESULT 977
ID AAV21210 standard; DNA; 58407 BP.
DE Methanococcus jannaschii large circular extrachromosomal element.
PN WO9807830-A2.
PD 26-FEB-1998.
PA (GENO-) INST GENOMIC RES.
PA (UNII) UNIV ILLINOIS FOUND.
PA (UJYO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match
Best Local Similarity 47.5%; Pred. No. 86; Length 58407;
RESULT 978
ID AAL57272 standard; DNA; 177851 BP.
DE bA38B23-1 'human modifier of p53 pathway' DNA.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 177851;
RESULT 979
ID ADL43989 standard; DNA; 324 BP.
DE Human ovarian cancer DNA marker #17879.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 5; Length 324;
RESULT 980
ID ABS05479 standard; DNA; 456 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 5470.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 456;
RESULT 981
ID AHA34164 standard; cDNA; 511 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1246.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 4; Length 511;
RESULT 982
ID AAV70954 standard; DNA; 1141 BP.
DE Zea mays 10 kDa zein gene portion used as a promoter in plasmids.
PN WO9844780-A1.
PD 15-OCT-1998.
PA (EXSE-) EXSEED GENETICS LLC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 2; Length 1141;
RESULT 983
ID ABQ41663 standard; DNA; 1164 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28254.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 1164;
RESULT 984
ID ABAQ41662 standard; DNA; 1164 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28253.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 1164;
RESULT 985
ID ABN80239 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 256.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 15121;
RESULT 986
ID AAV70953 standard; DNA; 2562 BP.
DE Zea mays 10 kDa zein gene DNA sequence.
PN WO9844780-A1.
PD 15-OCT-1998.
PA (EXSE-) EXSEED GENETICS LLC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 2; Length 2562;
RESULT 987
ID ADP13500 standard; DNA; 2623 BP.
DE Renal cell carcinoma differentially expressed gene #236.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN) TWINE N C.
PA (BURC) BURCZYNSKI M E.
PA (TREP) TREPICCHIO W L.
PA (DORN) DORNER A.
PA (STOV) STOVER J A.
PA (SLON) SLOMI D K.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 12; Length 2623;
RESULT 988
ID ADC30694 standard; cDNA; 4414 BP.
DE Human novel cDNA sequence, SEQ ID NO:776.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 10; Length 4414;
RESULT 989
ID ABK52611 standard; DNA; 4755 BP.
DE DNA encoding human Claspain protein.
PN WO200233115-A2.
PD 25-APR-2002.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 4755;
RESULT 990
ID ABV30199 standard; cDNA; 4804 BP.
DE Human prostate expression marker cDNA 30190.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 5; Length 4804;
RESULT 991
ID ABL33760 standard; DNA; 7851 BP.
DE Human immune system associated gene SEQ ID NO: 1733.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 7851;
RESULT 992
ID ABN80239 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 256.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 15121;
RESULT 993
ID ABL32672 standard; DNA; 16287 BP.
DE Human immune system associated gene SEQ ID NO: 645.

RESULT 985
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 8.4%; Pred. No. 47; Length 2000;
RESULT 986
ID AAV70953 standard; DNA; 2562 BP.
DE Zea mays 10 kDa zein gene DNA sequence.
PN WO9844780-A1.
PD 15-OCT-1998.
PA (EXSE-) EXSEED GENETICS LLC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 2; Length 2562;
RESULT 987
ID ADP13500 standard; DNA; 2623 BP.
DE Renal cell carcinoma differentially expressed gene #236.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN) TWINE N C.
PA (BURC) BURCZYNSKI M E.
PA (TREP) TREPICCHIO W L.
PA (DORN) DORNER A.
PA (STOV) STOVER J A.
PA (SLON) SLOMI D K.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 12; Length 2623;
RESULT 988
ID ADC30694 standard; cDNA; 4414 BP.
DE Human novel cDNA sequence, SEQ ID NO:776.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 10; Length 4414;
RESULT 989
ID ABK52611 standard; DNA; 4755 BP.
DE DNA encoding human Claspain protein.
PN WO200233115-A2.
PD 25-APR-2002.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 4755;
RESULT 990
ID ABV30199 standard; cDNA; 4804 BP.
DE Human prostate expression marker cDNA 30190.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 5; Length 4804;
RESULT 991
ID ABL33760 standard; DNA; 7851 BP.
DE Human immune system associated gene SEQ ID NO: 1733.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 7851;
RESULT 992
ID ABN80239 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 256.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 15121;
RESULT 993
ID ABL32672 standard; DNA; 16287 BP.
DE Human immune system associated gene SEQ ID NO: 645.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 16287;
RESULT 994
ID ABX52612 standard; DNA; 58837 BP.
DE Human Claspin genomic sequence.
PN WO200233115-A2.
PD 25-APR-2002.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 6; Length 58837;
RESULT 995
ID AAX90201 standard; DNA; 119950 BP.
DE Human Yes1 gene.
PN WO9335290-A1.
PD 15-JUL-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 2; Length 119950;
RESULT 996
ID ADL1309 standard; DNA; 129588 BP.
DE Osteoarthritis-associated polymorphic nucleotide #441.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 10; Length 129588;
RESULT 997
ID AD056277 standard; DNA; 200620 BP.
DE Human presynaptic cytomatrix protein, REPS2, genomic sequence.
PN WO2004044164-A2.
PD 27-MAY-2004.
PA (SEQU-) SEQUENOM INC.
Query Match
Best Local Similarity 5.4%; Score 38.2; DB 12; Length 200620;
RESULT 998
ID AAT42808 standard; DNA; 486 BP.
DE Human polymorphic locus Q900 sequence.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 4; Length 447;
RESULT 999
ID AAT42808 standard; DNA; 486 BP.
DE Polymorphic locus Q900 sequence.
PN WO9634979-A2.
PD 07-NOV-1996.
PA (REHO-) CENT RECH HOPITAL SAINTE-JUSTINE.
Query Match
Best Local Similarity 5.3%; Score 38; DB 2; Length 486;
RESULT 1000
ID AAS62239 standard; cDNA; 681 BP.
DE cDNA sequence #26 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GENY) GENETICS INST INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 681;
RESULT 1001
ID ADB51912 standard; DNA; 905 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2454.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 10; Length 905;
RESULT 1002
ID ADG33178 standard; DNA; 1381 BP.
DE Human DNA differentially expressed in patients with SLE SeqID502.
PN WO2003090694-A2.

PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 10; Length 1381;
RESULT 1003
ID ADP28980 standard; DNA; 1755 BP.
DE Human secreted protein encoding sequence SEQ ID #978.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 12; Length 1755;
RESULT 1004
ID ADG79262 standard; cDNA; 3067 BP.
DE Human secreted protein cDNA of the invention SEQ ID NO:68.
PN WO200268638-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 3067;
RESULT 1005
ID ABL32998 standard; DNA; 5461 BP.
DE Human immune system associated gene SEQ ID NO: 971.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 5461;
RESULT 1006
ID ABQ66977 standard; DNA; 5461 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 7.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 5461;
RESULT 1007
ID ABL70346 standard; DNA; 6754 BP.
DE Chemically treated cell signalling DNA sequence complementary to#118.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 6754;
RESULT 1008
ID AAS61305 standard; DNA; 6754 BP.
DE Human gene regulation-associated gene oligonucleotide #260.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 6754;
RESULT 1009
ID ABK39972 standard; DNA; 7615 BP.
DE Human chemically pretreated gene sequence #27 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 7615;
RESULT 1010
ID ABL32426 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 399.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.3%; Score 38; DB 6; Length 9810;
RESULT 1011
ID ADJ81645 standard; DNA; 10427 BP.
DE Human tyrosine phosphatase SHP1 bisulphited genomic DNA SeqID 5.
PN JP2004000128-A.
PD 08-JAN-2004.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.3%; Score 38; DB 12; Length 10427;
Best Local Similarity 51.1%; Pred. No. 74;
RESULT 1012
ID ABL34155 standard; DNA; 15548 BP.
DE Human immune system associated gene SEQ ID NO: 2128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 38; DB 6; Length 15548;
Best Local Similarity 47.2%; Pred. No. 80;
RESULT 1013
ID ABL30294 standard; DNA; 18396 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42355.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 5.3%; Score 38; DB 4; Length 18396;
Best Local Similarity 51.8%; Pred. No. 83;
RESULT 1014
ID ABL49345 standard; DNA; 19233 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 45.
PN WO20017377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 38; DB 6; Length 19233;
Best Local Similarity 53.6%; Pred. No. 84;
RESULT 1015
ID AHA4800 standard; DNA; 80578 BP.
DE Human GPCR protein KAT06734L DNA containing exons 1 and 2 SEQ ID NO:15.
PN JP200124566-A.
PD 11-SEP-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.3%; Score 38; DB 4; Length 80578;
Best Local Similarity 55.2%; Pred. No. 1.1e+02;
RESULT 1016
ID ADE87477 standard; DNA; 266145 BP.
DE Fowlpox virus genome DNA.
PN WO2003047617-A2.
PD 12-JUN-2003.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 5.3%; Score 38; DB 10; Length 266145;
Best Local Similarity 46.0%; Pred. No. 1.5e+02;
RESULT 1017
ID AAI10792 standard; DNA; 470 BP.
DE Probe #725 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1018
ID ABA52442 standard; DNA; 470 BP.
DE Human foetal liver single exon nucleic acid probe #747.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1019
ID AAI32050 standard; DNA; 470 BP.
DE Probe #736 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1020
ID ABA42021 standard; DNA; 470 BP.
DE Human breast cell single exon nucleic acid probe #716.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1021
ID ABA22235 standard; DNA; 470 BP.
DE Probe #701 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1022
ID AAK26162 standard; DNA; 470 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 719.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1023
ID AAK00710 standard; DNA; 470 BP.
DE Human brain expressed single exon probe SEQ ID NO: 701.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1024
ID ABS25751 standard; DNA; 470 BP.
DE Human liver single exon probe, SEQ ID No 741.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 4; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1025
ID AAI00717 standard; DNA; 470 BP.
DE Probe #708 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 5; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1026
ID ABS00747 standard; DNA; 470 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 738.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 37.8; DB 6; Length 470;
Best Local Similarity 53.8%; Pred. No. 43;
RESULT 1027
ID ABQ46793 standard; DNA; 538 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33384.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 538;
Best Local Similarity 52.9%; Pred. No. 44;
RESULT 1028
ID ABQ46792 standard; DNA; 538 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33383.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 538;
Best Local Similarity 52.9%; Pred. No. 44;
RESULT 1029
ID AAL26474 standard; cDNA; 1160 BP.
DE Human breast cancer expressed polynucleotide 18931.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.3%; Score 37.8; DB 4; Length 1160;

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Best Local Similarity 49.8%; Pred. No. 52;
RESULT 1030
ID AAF58662 standard; DNA; 1537 BP.
DE Porcine myostatin gene promoter.
PN EPI072680-A1.
PD 31-JAN-2001.
PA (PFIZ ) PFIZER PROD INC.
Query Match 5.3%; Score 37.8; DB 4; Length 1537;
Best Local Similarity 45.0%; Pred. No. 55;
RESULT 1031
ID AAG21090 standard; cDNA; 1811 BP.
DE cDNA encoding human ubiquitin-conjugating enzyme 10_01.
PN WO200194407-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 5.3%; Score 37.8; DB 6; Length 1811;
Best Local Similarity 64.0%; Pred. No. 57;
RESULT 1032
ID ADJ41453 standard; cDNA; 2000 BP.
DE Plant cDNA #2453.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICK D.
PA (ZHUT/) ZHU T.
Query Match 5.3%; Score 37.8; DB 12; Length 2000;
Best Local Similarity 45.9%; Pred. No. 58;
RESULT 1033
ID ABZ11664 standard; cDNA; 3953 BP.
DE Human polynucleotide SEQ ID NO 546.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HVSE-) HVSEQ INC.
Query Match 5.3%; Score 37.8; DB 6; Length 3953;
Best Local Similarity 49.8%; Pred. No. 67;
RESULT 1034
ID ADM44182 standard; cDNA; 3953 BP.
DE Novel human arginine-rich protein cDNA #546.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRNA/) DRMANAC R T.
Query Match 5.3%; Score 37.8; DB 12; Length 3953;
Best Local Similarity 49.8%; Pred. No. 67;
RESULT 1035
ID ABL34148 standard; DNA; 6242 BP.
DE Human immune system associated gene SEQ ID NO: 2121.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 6242;
Best Local Similarity 50.2%; Pred. No. 74;
RESULT 1036
ID ABK39963 standard; DNA; 6731 BP.
DE Human chemically pretreated gene sequence #22 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 6731;
Best Local Similarity 48.4%; Pred. No. 75;
RESULT 1037
ID ABK31471 standard; DNA; 7072 BP.
DE Signal transduction associated gene modified complementary DNA #157.
PN WO200200926-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 7072;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 1038
ID ABL70566 standard; DNA; 7072 BP.
DE Chemically treated cell signalling DNA sequence complementary to#228.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 7072;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 1039
ID AAS61385 standard; DNA; 7072 BP.
DE Human gene regulation-associated gene oligonucleotide #340.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 7072;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 1040
ID ACF62786 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:35.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1041
ID ACF62753 standard; DNA; 7369 BP.
DE Human p21 genomic DNA SEQ ID NO:2.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1042
ID ACF62808 standard; DNA; 7369 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:57.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1043
ID ABZ09879 standard; DNA; 7369 BP.
DE Human 5' and/or regulatory region of CDKN1A DNA SEQ ID NO:19.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1044
ID ABZ09992 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #132.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1045
ID ABZ10138 standard; DNA; 7369 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #278.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 8; Length 7369;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 1046
ID ABK28407 standard; DNA; 9504 BP.
DE DNA transcription associated genomic DNA #141.
PN WO200192565-A2.
PD 06-DEC-2001.
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PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 9504;
Best Local Similarity 57.0%; Pred. No. 81;
RESULT 1047
ID AAS46304 standard; DNA; 10369 BP.
DE tumour suppressor gene derived chemically modified sequence #26.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 4; Length 10369;
Best Local Similarity 51.5%; Pred. No. 82;
RESULT 1048
ID ABL32393 standard; DNA; 10369 BP.
DE Human immune system associated gene SEQ ID NO: 366.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 10369;
Best Local Similarity 51.5%; Pred. No. 82;
RESULT 1049
ID ABK31249 standard; DNA; 10543 BP.
DE Signal transduction associated gene modified complementary DNA #46.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 10543;
Best Local Similarity 45.8%; Pred. No. 82;
RESULT 1050
ID ABL70206 standard; DNA; 10543 BP.
DE Chemically treated cell signalling DNA sequence complementary to#48.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 10543;
Best Local Similarity 45.8%; Pred. No. 82;
RESULT 1051
ID AAS61161 standard; DNA; 10543 BP.
DE Human gene regulation-associated gene oligonucleotide #116.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 14920;
Best Local Similarity 45.8%; Pred. No. 82;
RESULT 1052
ID ABN80146 standard; DNA; 14920 BP.
DE Human chemically modified disease associated gene SEQ ID NO 163.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 14920;
Best Local Similarity 47.6%; Pred. No. 89;
RESULT 1053
ID ABL33617 standard; DNA; 16918 BP.
DE Human immune system associated gene SEQ ID NO: 1590.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 16918;
Best Local Similarity 44.0%; Pred. No. 91;
RESULT 1054
ID ABL32766 standard; DNA; 19659 BP.
DE Human immune system associated gene SEQ ID NO: 739.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 19659;
Best Local Similarity 48.8%; Pred. No. 94;
RESULT 1055
ID ADA02963 standard; DNA; 29956 BP.
DE Mouse Lck carcinoma associated gene, SEQ ID NO:1481.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 5.3%; Score 37.8; DB 9; Length 29956;
Best Local Similarity 58.4%; Pred. No. 1e+02;
RESULT 1056
ID ADB72701 standard; DNA; 29956 BP.
DE Mouse Lck gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.3%; Score 37.8; DB 10; Length 29956;
Best Local Similarity 58.4%; Pred. No. 1e+02;
RESULT 1057
ID ADC85443 standard; DNA; 29956 BP.
DE Mouse Lck genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.3%; Score 37.8; DB 10; Length 29956;
Best Local Similarity 58.4%; Pred. No. 1e+02;
RESULT 1058
ID ADM74558 standard; DNA; 29956 BP.
DE Murine carcinoma associated (CA) nucleic acid #115.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 5.3%; Score 37.8; DB 12; Length 29956;
Best Local Similarity 58.4%; Pred. No. 1e+02;
RESULT 1059
ID ABL70604 standard; DNA; 34548 BP.
DE Chemically treated cell signalling DNA sequence complementary to#247.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.8; DB 6; Length 34548;
Best Local Similarity 46.4%; Pred. No. 1.1e+02;
RESULT 1060
Query Match 5.3%; Score 37.8; DB 6; Length 110000;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
RESULT 1061
Query Match 5.3%; Score 37.8; DB 6; Length 110000;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
RESULT 1062
ID ABS52506 standard; DNA; 202001 BP.
DE Human transporter protein genomic DNA.
Query Match 5.3%; Score 37.8; DB 6; Length 202001;
Best Local Similarity 51.5%; Pred. No. 1.5e+02;
RESULT 1063
ID ADG46742 standard; DNA; 202001 BP.
DE Human transporter genomic DNA.
Query Match 5.3%; Score 37.8; DB 10; Length 202001;
Best Local Similarity 51.5%; Pred. No. 1.5e+02;
RESULT 1064
ID ABV48259 standard; cDNA; 306 BP.
DE Human prostate expression marker cDNA 48250.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.3%; Score 37.6; DB 5; Length 306;
Best Local Similarity 52.6%; Pred. No. 44;
RESULT 1065
ID ADF82256 standard; DNA; 983 BP.
DE Leukaemia-related DNA sequence #2812.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 5.3%; Score 37.6; DB 10; Length 983;
Best Local Similarity 51.5%; Pred. No. 56;
RESULT 1066
ID AAN90224 standard; DNA; 1052 BP.

DE Malaria-specific DNA insert of clone 41-2.
PN EP322712-A.
PD 05-JUL-1989.
PA (BEHW) BEHRINGWERKE AG.
Query Match 5.3%; Score 37.6; DB 1; Length 1052;
Best Local Similarity 44.3%; Pred. No. 57;
RESULT 1067
ID ADQ23230 standard; DNA; 1140 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6050.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.3%; Score 37.6; DB 12; Length 1140;
Best Local Similarity 55.3%; Pred. No. 58;
RESULT 1068
ID ADF01165 standard; DNA; 1335 BP.
DE Bacterial polynucleotide #1450.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.3%; Score 37.6; DB 10; Length 1335;
Best Local Similarity 49.5%; Pred. No. 59;
RESULT 1069
ID AAA70123 standard; DNA; 1452 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:256.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 5.3%; Score 37.6; DB 3; Length 1452;
Best Local Similarity 56.2%; Pred. No. 60;
RESULT 1070
ID ADB54303 standard; DNA; 1984 BP.
DE Pretreated genomic DNA region 227.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 10; Length 1984;
Best Local Similarity 51.2%; Pred. No. 65;
RESULT 1071
ID ADE37776 standard; DNA; 1984 BP.
DE Human chemically treated calcitonin nucleotide sequence SEQ ID NO:22.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 10; Length 1984;
Best Local Similarity 51.2%; Pred. No. 65;
RESULT 1072
ID ABL33266 standard; DNA; 5218 BP.
DE Human immune system associated gene SEQ ID NO: 1239.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 5218;
Best Local Similarity 49.5%; Pred. No. 79;
RESULT 1073
ID AAS63306 standard; DNA; 6149 BP.
DE Chemically pretreated metabolism associated gene #1.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 6149;
Best Local Similarity 56.5%; Pred. No. 82;
RESULT 1074
ID ABL32049 standard; DNA; 6240 BP.
DE Human immune system associated gene SEQ ID NO: 22.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 6240;
Best Local Similarity 48.2%; Pred. No. 82;

RESULT 1075
ID ABK39923 standard; DNA; 6247 BP.
DE Human chemically pretreated gene sequence #2 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 6247;
Best Local Similarity 45.8%; Pred. No. 82;
RESULT 1076
ID ADB54279 standard; DNA; 8085 BP.
DE Pretreated genomic DNA region 203.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 10; Length 8085;
Best Local Similarity 47.1%; Pred. No. 87;
RESULT 1077
ID ABL34427 standard; DNA; 9209 BP.
DE Human immune system associated gene SEQ ID NO: 2400.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 9209;
Best Local Similarity 44.0%; Pred. No. 89;
RESULT 1078
ID AAS46808 standard; DNA; 9219 BP.
DE Tumour suppressor gene derived chemically modified sequence #534.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 4; Length 9219;
Best Local Similarity 44.0%; Pred. No. 89;
RESULT 1079
ID ABL32343 standard; DNA; 11534 BP.
DE Human immune system associated gene SEQ ID NO: 316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 11534;
Best Local Similarity 55.3%; Pred. No. 93;
RESULT 1080
ID ABL33227 standard; DNA; 13125 BP.
DE Human immune system associated gene SEQ ID NO: 1200.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 13125;
Best Local Similarity 49.5%; Pred. No. 96;
RESULT 1081
ID ABL34557 standard; DNA; 13125 BP.
DE Human metastasis associated gene SEQ ID NO: 110.
PN WO20017376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 13125;
Best Local Similarity 49.5%; Pred. No. 96;
RESULT 1082
ID ABL70284 standard; DNA; 13125 BP.
DE Chemically treated cell signalling DNA sequence complementary to #87.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 13125;
Best Local Similarity 49.5%; Pred. No. 96;
RESULT 1083
ID ABL33032 standard; DNA; 14798 BP.
DE Human immune system associated gene SEQ ID NO: 1005.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 14798;
Best Local Similarity 48.2%; Pred. No. 98;
RESULT 1084

ID ABL32601 standard; DNA; 17528 BP.
DE Human immune system associated gene SEQ ID NO: 574.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 17528;
Best Local Similarity 44.0%; Pred. No. 1e+02;
RESULT 1085
ID ABL33450 standard; DNA; 19787 BP.
DE Human immune system associated gene SEQ ID NO: 1423.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 19787;
Best Local Similarity 47.5%; Pred. No. 1e+02;
RESULT 1086
ID ABL34125 standard; DNA; 73334 BP.
DE Human immune system associated gene SEQ ID NO: 2098.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 73334;
Best Local Similarity 51.2%; Pred. No. 1.4e+02;
RESULT 1087
ID ABL92319 standard; DNA; 73334 BP.
DE Chemically treated DNA repair gene fragment complementary to #64.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.3%; Score 37.6; DB 6; Length 73334;
Best Local Similarity 51.2%; Pred. No. 1.4e+02;
RESULT 1088
ID AA227709 standard; DNA; 361 BP.
DE Human DNA marker clone G025.
PN WO9940194-A1.
PD 12-AUG-1999.
PA (PROM-) PROMEGA CORP.
Query Match 5.2%; Score 37.4; DB 2; Length 361;
Best Local Similarity 62.1%; Pred. No. 50;
RESULT 1089
ID ADL44915 standard; DNA; 510 BP.
DE Human ovarian cancer DNA marker #18805.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.4; DB 5; Length 510;
Best Local Similarity 48.8%; Pred. No. 54;
RESULT 1090
ID ADL37966 standard; DNA; 579 BP.
DE Human ovarian cancer DNA marker #11856.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.4; DB 5; Length 579;
Best Local Similarity 43.3%; Pred. No. 55;
RESULT 1091
ID ADI72827 standard; DNA; 579 BP.
DE Human ovarian cancer DNA marker #5569.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.4; DB 5; Length 579;
Best Local Similarity 43.3%; Pred. No. 55;
RESULT 1092
ID AAS64805 standard; cDNA; 1767 BP.
DE DNA encoding novel human diagnostic protein #609.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 37.4; DB 5; Length 1767;
Best Local Similarity 58.6%; Pred. No. 70;
RESULT 1093
ID AAS75105 standard; cDNA; 1767 BP.

DE DNA encoding novel human diagnostic protein #10909.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 37.4; DB 5; Length 1767;
Best Local Similarity 58.6%; Pred. No. 70;
RESULT 1094
ID ADO35574 standard; DNA; 2310 BP.
DE Novel mouse gene sequence #247.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.2%; Score 37.4; DB 12; Length 2310;
Best Local Similarity 60.2%; Pred. No. 74;
RESULT 1095
ID AAQ11711 standard; DNA; 2422 BP.
DE Shuttle vector pMW1530.
PN WO9106644-A.
PD 16-MAY-1991.
PA (UYMA-) UNIV MACQUARIE.
Query Match 5.2%; Score 37.4; DB 2; Length 2422;
Best Local Similarity 48.7%; Pred. No. 75;
RESULT 1096
ID ADM01479 standard; cDNA; 2778 BP.
DE Human cDNA of the invention SEQ ID NO:164.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.2%; Score 37.4; DB 11; Length 2778;
Best Local Similarity 62.1%; Pred. No. 77;
RESULT 1097
ID RAQ11710 standard; DNA; 5852 BP.
DE Dictyostelium plasmid Ddp2 containing Rep gene.
PN WO9106644-A.
PD 16-MAY-1991.
PA (UYMA-) UNIV MACQUARIE.
Query Match 5.2%; Score 37.4; DB 2; Length 5852;
Best Local Similarity 48.7%; Pred. No. 90;
RESULT 1098
ID ABQ66993 standard; DNA; 5984 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 23.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 5984;
Best Local Similarity 53.8%; Pred. No. 91;
RESULT 1099
ID ABK31367 standard; DNA; 6181 BP.
DE Signal transduction associated gene modified complementary DNA #105.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6181;
Best Local Similarity 48.8%; Pred. No. 91;
RESULT 1100
ID ABL70324 standard; DNA; 6181 BP.
DE Chemically treated cell signalling DNA sequence complementary to #107.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6181;
Best Local Similarity 48.8%; Pred. No. 91;
RESULT 1101
ID AAS61271 standard; DNA; 6181 BP.
DE Human gene regulation-associated gene oligonucleotide #236.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6181;
Best Local Similarity 48.8%; Pred. No. 91;
RESULT 1102
ID ABL33776 standard; DNA; 6239 BP.
DE Human immune system associated gene SEQ ID NO: 1749.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6239;
Best Local Similarity 50.3%; Pred. No. 91;
RESULT 1103
ID ABK28297 standard; DNA; 6239 BP.
DE DNA transcription associated genomic DNA #86.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6239;
Best Local Similarity 50.3%; Pred. No. 91;
RESULT 1104
ID ARN80215 standard; DNA; 6250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 232.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6250;
Best Local Similarity 51.5%; Pred. No. 91;
RESULT 1105
ID AAS46417 standard; DNA; 6668 BP.
DE Tumour suppressor gene derived chemically modified sequence #139.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 4; Length 6668;
Best Local Similarity 53.8%; Pred. No. 93;
RESULT 1106
ID ABL33218 standard; DNA; 6668 BP.
DE Human immune system associated gene SEQ ID NO: 1191.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6668;
Best Local Similarity 53.8%; Pred. No. 93;
RESULT 1107
ID ARN80162 standard; DNA; 6668 BP.
DE Human chemically modified disease associated gene SEQ ID NO 179.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6668;
Best Local Similarity 53.8%; Pred. No. 93;
RESULT 1108
ID ABL34235 standard; DNA; 6917 BP.
DE Human immune system associated gene SEQ ID NO: 2208.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 6917;
Best Local Similarity 46.4%; Pred. No. 93;
RESULT 1109
ID ABL54323 standard; DNA; 7231 BP.
DE Chemically treated apoptosis gene #12.
PN WO20017164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 7231;
Best Local Similarity 47.6%; Pred. No. 94;
RESULT 1110
ID ABL33568 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1541.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 8305;
Best Local Similarity 48.4%; Pred. No. 97;
RESULT 1111
ID ADO59810 standard; cDNA; 10591 BP.
DE Novel human cDNA sequence SeqID1.
PN JP2004097206-A.

PD 02-APR-2004.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 5.2%; Score 37.4; DB 12; Length 10591;
Best Local Similarity 48.0%; Pred. No. 1e+02;
RESULT 1112
ID AAS46665 standard; DNA; 17144 BP.
DE Tumour suppressor gene derived chemically modified sequence #387.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 4; Length 17144;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
RESULT 1113
ID ADP72698 standard; DNA; 19080 BP.
DE Renal toxin progression gene marker #1287.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 5.2%; Score 37.4; DB 12; Length 19080;
Best Local Similarity 52.2%; Pred. No. 1.2e+02;
RESULT 1114
ID AAK73166 standard; DNA; 19965 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.4; DB 4; Length 19965;
Best Local Similarity 47.3%; Pred. No. 1.2e+02;
RESULT 1115
ID ABK69932 standard; DNA; 19965 BP.
DE Human secreted protein gene 68 genomic DNA fragment #20.
PN WO20026931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.4; DB 6; Length 19965;
Best Local Similarity 47.3%; Pred. No. 1.2e+02;
RESULT 1116
ID AAK68939 standard; DNA; 28180 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23751.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.4; DB 4; Length 28180;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 1117
ID ABL34197 standard; DNA; 37973 BP.
DE Human immune system associated gene SEQ ID NO: 2170.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 37973;
Best Local Similarity 60.2%; Pred. No. 1.3e+02;
RESULT 1118
ID AAD36834 standard; DNA; 59215 BP.
DE Human transporter protein genomic DNA.
PN WO200058509-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 5.2%; Score 37.4; DB 8; Length 59215;
Best Local Similarity 70.4%; Pred. No. 1.5e+02;
RESULT 1119
ID AAC89888 standard; DNA; 78925 BP.
DE Human FN gene.
PN WO200058509-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 5.2%; Score 37.4; DB 3; Length 78925;
Best Local Similarity 62.1%; Pred. No. 1.6e+02;
RESULT 1120
ID ABL33568 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1541.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.4; DB 6; Length 8305;
Best Local Similarity 48.4%; Pred. No. 97;
RESULT 1121
ID ADO59810 standard; cDNA; 10591 BP.
DE Novel human cDNA sequence SeqID1.
PN JP2004097206-A.

Query Match 5.2%; Score 37.4; DB 10; Length 110000;
Best Local Similarity 48.0%; Pred. No. 1.7e+02;
RESULT 1123
Query Match 5.2%; Score 37.4; DB 12; Length 110000;
Best Local Similarity 62.1%; Pred. No. 1.7e+02;
RESULT 1124
Query Match 5.2%; Score 37.4; DB 12; Length 110000;
Best Local Similarity 62.1%; Pred. No. 1.7e+02;
RESULT 1125
Query Match 5.2%; Score 37.4; DB 12; Length 110000;
Best Local Similarity 62.1%; Pred. No. 1.7e+02;
RESULT 1126
ID ADB12769 standard; DNA; 139308 BP.
DE Human PRKR DNA.
PN DE10128838-A1.
PD 02-JAN-2003
PA (GENP-) GENPROFILE AG.
Query Match 5.2%; Score 37.4; DB 8; Length 139308;
Best Local Similarity 47.3%; Pred. No. 1.8e+02;
RESULT 1127
ID ADL13648 standard; DNA; 143391 BP.
DE Osteoarthritis-associated polymorphic nucleotide #180.
PN WO2003054166-A2.
PD 03-JUL-2003
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.2%; Score 37.4; DB 10; Length 143391;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
RESULT 1128
ID ABQ88179 standard; cDNA; 160771 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 86.
PN WO200250301-A2.
PD 27-JUN-2002
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 5.2%; Score 37.4; DB 6; Length 160771;
Best Local Similarity 58.6%; Pred. No. 1.8e+02;
RESULT 1129
ID ADI72102 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #4844.
PN WO200170979-A2.
PD 27-SEP-2001
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.2; DB 5; Length 299;
Best Local Similarity 42.9%; Pred. No. 54;
RESULT 1130
ID ADL37251 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #11141.
PN WO200170979-A2.
PD 27-SEP-2001
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.2; DB 5; Length 299;
Best Local Similarity 42.9%; Pred. No. 54;
RESULT 1131
ID AAH35985 standard; cDNA; 540 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:3067.
PN WO200122920-A2.
PD 05-APR-2001
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 4; Length 540;
Best Local Similarity 46.6%; Pred. No. 61;
RESULT 1132
ID AAH11276 standard; cDNA; 581 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:8111.
PN EP1074617-A2.
PD 07-FEB-2001
PA (HELI-) HELIX RES INST.
Query Match 5.2%; Score 37.2; DB 4; Length 581;
Best Local Similarity 49.4%; Pred. No. 62;
RESULT 1133
ID ABQ68320 standard; DNA; 692 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1086.
PN WO200228891-A2.
PD 11-APR-2002

PA (INSP) INST PASTEUR.
Query Match 5.2%; Score 37.2; DB 6; Length 692;
Best Local Similarity 49.0%; Pred. No. 64;
RESULT 1134
ID ABV16074 standard; cDNA; 843 BP.
DE Human prostate expression marker cDNA 16065.
PN WO200160860-A2.
PD 23-AUG-2001
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 37.2; DB 5; Length 843;
Best Local Similarity 49.7%; Pred. No. 67;
RESULT 1135
ID AAC59297 standard; cDNA; 887 BP.
DE Human secreted protein cDNA #21.
PN WO2000056753-A1.
PD 28-SEP-2000
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 3; Length 887;
Best Local Similarity 46.8%; Pred. No. 68;
RESULT 1136
ID AAH34404 standard; cDNA; 891 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1486.
PN WO200122920-A2.
PD 05-APR-2001
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 4; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1137
ID AAH19205 standard; cDNA; 891 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HPWAY46, SEQ ID NO:46.
PN WO200132910-A2.
PD 10-MAY-2001
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 4; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1138
ID ADA40469 standard; cDNA; 891 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 8; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1139
ID ADC73918 standard; DNA; 891 BP.
DE Human secreted protein-related DNA - SEQ ID 551.
PN WO2003038063-A2.
PD 08-MAY-2003
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 10; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1140
ID ADD37784 standard; cDNA; 891 BP.
DE Human secreted protein encoding sequence #266.
PN WO200290526-A2.
PD 14-NOV-2002
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 10; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1141
ID ADA56629 standard; DNA; 891 BP.
DE Gene encoding human secreted protein #445.
PN WO2002102994-A2.
PD 27-DEC-2002
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 10; Length 891;
Best Local Similarity 49.0%; Pred. No. 68;
RESULT 1142
ID ABQ70593 standard; DNA; 1657 BP.
DE Listeria monocytogenes 4b contig DNA sequence #535.
PN WO200228891-A2.
PD 11-APR-2002

PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.2%; Score 37.2; DB 6; Length 1657;
Best Local Similarity 49.0%; Pred. No. 77;
RESULT 1143
ID AB216061 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3866.
PN W0200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 2000;
Best Local Similarity 46.0%; Pred. No. 80;
RESULT 1144
ID ADA71517 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 4840.
PN W02003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 37.2; DB 8; Length 2000;
Best Local Similarity 50.0%; Pred. No. 80;
RESULT 1145
ID ABX77542 standard; cDNA; 2602 BP.
DE Differentially expressed breast cancer associated cDNA #37.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN) CHEN H.
Query Match 5.2%; Score 37.2; DB 8; Length 2602;
Best Local Similarity 51.2%; Pred. No. 85;
RESULT 1146
ID AB235963 standard; cDNA; 2695 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 127.
PN W0200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.2%; Score 37.2; DB 8; Length 2695;
Best Local Similarity 56.6%; Pred. No. 85;
RESULT 1147
ID ACA29559 standard; DNA; 3096 BP.
DE Prokaryotic essential gene #11216.
PN W020027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 37.2; DB 8; Length 3096;
Best Local Similarity 49.0%; Pred. No. 88;
RESULT 1148
ID ABK42990 standard; DNA; 4149 BP.
DE Genomic sequence #889 encoding novel human connective tissue polypeptide.
PN W0200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 4; Length 4149;
Best Local Similarity 56.6%; Pred. No. 93;
RESULT 1149
ID AAK78680 standard; DNA; 4149 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33492.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 4; Length 4149;
Best Local Similarity 56.6%; Pred. No. 93;
RESULT 1150
ID ADB61146 standard; DNA; 4149 BP.
DE Connective tissue related genomic DNA #889.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 9; Length 4149;
Best Local Similarity 56.6%; Pred. No. 93;
RESULT 1151
ID ABL32900 standard; DNA; 5204 BP.
DE Human immune system associated gene SEQ ID NO: 873.
PN W0200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 5204;
Best Local Similarity 45.6%; Pred. No. 98;
RESULT 1152
ID ABZ10144 standard; DNA; 5660 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #284.
PN W020027727-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 8; Length 5660;
Best Local Similarity 50.6%; Pred. No. 1e+02;
RESULT 1153
ID ACF62812 standard; DNA; 5666 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:61.
PN W02003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 8; Length 5666;
Best Local Similarity 50.6%; Pred. No. 1e+02;
RESULT 1154
ID ABL32182 standard; DNA; 5763 BP.
DE Human immune system associated gene SEQ ID NO: 155.
PN W0200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 5763;
Best Local Similarity 50.0%; Pred. No. 1e+02;
RESULT 1155
ID ABL32972 standard; DNA; 6145 BP.
DE Human immune system associated gene SEQ ID NO: 945.
PN W0200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 6145;
Best Local Similarity 54.3%; Pred. No. 1e+02;
RESULT 1156
ID ABQ67049 standard; DNA; 6486 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 79.
PN W0200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 6486;
Best Local Similarity 46.5%; Pred. No. 1e+02;
RESULT 1157
ID AAL60047 standard; cDNA; 7096 BP.
DE Human Pc0219 cDNA.
PN W02003040331-A2.
PD 15-MAY-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 5.2%; Score 37.2; DB 10; Length 7096;
Best Local Similarity 56.6%; Pred. No. 1e+02;
RESULT 1158
ID ABL92234 standard; DNA; 7145 BP.
DE Chemically treated DNA repair gene fragment#22.
PN W0200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 7145;
Best Local Similarity 47.1%; Pred. No. 1e+02;
RESULT 1159
ID AAD22321 standard; DNA; 7145 BP.
DE Chemically treated human genomic DNA #11 associated with DNA adducts.
PN W0200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 7145;
Best Local Similarity 47.1%; Pred. No. 1e+02;
RESULT 1160
ID ABL32401 standard; DNA; 7167 BP.
DE Human immune system associated gene SEQ ID NO: 374.
PN W0200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 7167;
Best Local Similarity 51.9%; Pred. No. 1e+02;
RESULT 1161
ID ADB54240 standard; DNA; 8666 BP.
DE Pretreated genomic DNA region 164.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 10; Length 8666;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 1162
ID ADE84178 standard; DNA; 8666 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #114.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 10; Length 8666;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 1163
ID AAS46699 standard; DNA; 8711 BP.
DE Tumour suppressor gene derived chemically modified sequence #422.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 4; Length 8711;
Best Local Similarity 45.1%; Pred. No. 1.1e+02;
RESULT 1164
ID RAV52150 standard; DNA; 9064 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:17.
PN WO9818931-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 37.2; DB 2; Length 9064;
Best Local Similarity 49.8%; Pred. No. 1.1e+02;
RESULT 1165
ID ABL33901 standard; DNA; 11662 BP.
DE Human immune system associated gene SEQ ID NO: 1874.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 11662;
Best Local Similarity 48.6%; Pred. No. 1.2e+02;
RESULT 1166
ID ABK31231 standard; DNA; 13133 BP.
DE Signal transduction associated gene modified complementary DNA #37.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 13133;
Best Local Similarity 47.4%; Pred. No. 1.2e+02;
RESULT 1167
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 13511;
Best Local Similarity 45.7%; Pred. No. 1.2e+02;
RESULT 1168
ID AAS46771 standard; DNA; 17280 BP.
DE Tumour suppressor gene derived chemically modified sequence #495.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 4; Length 17280;
Best Local Similarity 50.6%; Pred. No. 1.3e+02;
RESULT 1169
ID ABL32570 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 543.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 5.2%; Score 37.2; DB 6; Length 18997;
Best Local Similarity 55.4%; Pred. No. 1.3e+02;
RESULT 1170
ID ABK33948 standard; DNA; 18997 BP.
DE Human DNA for staging of Astrocytomas #16.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 18997;
Best Local Similarity 55.4%; Pred. No. 1.3e+02;
RESULT 1171
ID ADA20352 standard; DNA; 18997 BP.
DE Prostate tumour related genomic DNA sample #9.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 8; Length 18997;
Best Local Similarity 55.4%; Pred. No. 1.3e+02;
RESULT 1172
ID ADA84159 standard; DNA; 18997 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:17.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 8; Length 18997;
Best Local Similarity 55.4%; Pred. No. 1.3e+02;
RESULT 1173
ID AAS46787 standard; DNA; 61020 BP.
DE Tumour suppressor gene derived chemically modified sequence #513.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 4; Length 61020;
Best Local Similarity 51.2%; Pred. No. 1.6e+02;
RESULT 1174
ID ADA2609 standard; DNA; 96598 BP.
DE Mouse Nfkb1 carcinoma associated gene, SEQ ID NO:1127.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 37.2; DB 9; Length 96598;
Best Local Similarity 65.9%; Pred. No. 1.8e+02;
RESULT 1175
ID ADB72347 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 37.2; DB 10; Length 96598;
Best Local Similarity 65.9%; Pred. No. 1.8e+02;
RESULT 1176
ID ADE82941 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene genomic DNA sequence.
PN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 37.2; DB 10; Length 96598;
Best Local Similarity 65.9%; Pred. No. 1.8e+02;
RESULT 1177
ID ADE95857 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 37.2; DB 10; Length 96598;
Best Local Similarity 65.9%; Pred. No. 1.8e+02;
RESULT 1178
ID ADE95857 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 37.2; DB 10; Length 96598;
Best Local Similarity 65.9%; Pred. No. 1.8e+02;
RESULT 1179
ID ABL32570 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 543.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

ID ABL34174 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2147.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37.2; DB 6; Length 113515;
Best Local Similarity 44.2%; Pred. No. 1.9e+02;
RESULT 1181
ID AAK33570 standard; DNA; 453 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 8127.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 453;
Best Local Similarity 52.2%; Pred. No. 65;
RESULT 1182
ID AAK07727 standard; DNA; 453 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7718.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 453;
Best Local Similarity 52.2%; Pred. No. 65;
RESULT 1183
ID ABS33358 standard; DNA; 453 BP.
DE Human liver single exon probe, SEQ ID NO 8348.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 453;
Best Local Similarity 52.2%; Pred. No. 65;
RESULT 1184
ID ABS08446 standard; DNA; 453 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 8437.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 6; Length 453;
Best Local Similarity 52.2%; Pred. No. 65;
RESULT 1185
ID ABA59751 standard; DNA; 599 BP.
DE Human foetal liver single exon nucleic acid probe #8056.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 599;
Best Local Similarity 52.2%; Pred. No. 69;
RESULT 1186
ID AAI39617 standard; DNA; 599 BP.
DE Probe #8303 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 599;
Best Local Similarity 52.2%; Pred. No. 69;
RESULT 1187
ID AAK33892 standard; DNA; 599 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 8449.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 599;
Best Local Similarity 52.2%; Pred. No. 69;
RESULT 1188
ID AAK08020 standard; DNA; 599 BP.
DE Human brain expressed single exon probe SEQ ID NO: 8011.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 599;
Best Local Similarity 52.2%; Pred. No. 69;
RESULT 1189
ID ABS33700 standard; DNA; 599 BP.

DE Human liver single exon probe, SEQ ID NO 8690.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.2%; Score 37; DB 4; Length 599;
Best Local Similarity 52.2%; Pred. No. 69;
RESULT 1190
ID ABO42518 standard; DNA; 1030 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29109.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 1030;
Best Local Similarity 46.4%; Pred. No. 77;
RESULT 1191
ID ABO42519 standard; DNA; 1030 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29110.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 1030;
Best Local Similarity 46.4%; Pred. No. 77;
RESULT 1192
ID AAH16077 standard; cDNA; 1385 BP.
DE Human cDNA sequence SEQ ID NO:14774.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.2%; Score 37; DB 4; Length 1385;
Best Local Similarity 49.8%; Pred. No. 82;
RESULT 1193
ID ABS76410 standard; cDNA; 1385 BP.
DE cDNA encoding human ovarian cancer marker OV28.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.2%; Score 37; DB 6; Length 1385;
Best Local Similarity 49.8%; Pred. No. 82;
RESULT 1194
ID AAF83292 standard; cDNA; 2110 BP.
DE P. rhizinflata egla protein encoding partial cDNA.
PN US622028-B1.
PD 24-APR-2001.
PA (SINI-) ACAD SINICA.
Query Match 5.2%; Score 37; DB 4; Length 2110;
Best Local Similarity 50.2%; Pred. No. 90;
RESULT 1195
ID AAH17775 standard; cDNA; 2545 BP.
DE Human cDNA sequence SEQ ID NO:17414.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.2%; Score 37; DB 4; Length 2545;
Best Local Similarity 49.8%; Pred. No. 94;
RESULT 1196
ID ACC69470 standard; cDNA; 3078 BP.
DE Human malignant neoplasm related protein encoding cDNA SEQ ID NO:11.
PN WO2003025135-A2.
PD 27-MAR-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 5.2%; Score 37; DB 8; Length 3078;
Best Local Similarity 53.9%; Pred. No. 97;
RESULT 1197
ID AAX25612 standard; DNA; 3559 BP.
DE Banana ripening fruit Gluc. DNA.
PN WO9915668-A2.
PD 01-APR-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.2%; Score 37; DB 2; Length 3559;
Best Local Similarity 50.7%; Pred. No. 1e+02;
RESULT 1198
ID ABL70349 standard; DNA; 5504 BP.
DE Chemically treated cell signalling DNA sequence#120.

PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 5504;
RESULT 1199
ID AAS61308 standard; DNA; 5504 BP.
DE Human gene regulation-associated gene oligonucleotide #263.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 5504;
RESULT 1200
ID ABL33679 standard; DNA; 6070 BP.
DE Human immune system associated gene SEQ ID NO: 1652.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6070;
RESULT 1201
ID ABL34579 standard; DNA; 6070 BP.
DE Human metastasis associated gene SEQ ID NO: 132.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6070;
RESULT 1202
ID ABL70372 standard; DNA; 6070 BP.
DE Chemically treated cell signalling DNA sequence complementary to#131.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6070;
RESULT 1203
ID ABQ67130 standard; DNA; 6070 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6070;
RESULT 1204
ID AAS46663 standard; DNA; 6076 BP.
DE Tumour suppressor gene derived chemically modified sequence #385.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 4; Length 6076;
RESULT 1205
ID ABL34219 standard; DNA; 6077 BP.
DE Human immune system associated gene SEQ ID NO: 2192.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6077;
RESULT 1206
ID ABL33046 standard; DNA; 6290 BP.
DE Human immune system associated gene SEQ ID NO: 1019.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6290;
RESULT 1207
ID ADE97422 standard; DNA; 6602 BP.
DE DNA derived from between T-DNA borders of plasmid pGPTV-kan-ocs-ATR-Iga2.
PN WO2003064992-A2.

PD 07-AUG-2003.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR-) LARRICK J W.
PA (WYCO-) WYCOFF K L.
Query Match
Best Local Similarity 5.2%; Score 37; DB 10; Length 6602;
RESULT 1208
ID ABQ67153 standard; DNA; 6729 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 183.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 6729;
RESULT 1209
ID ABK28328 standard; DNA; 8346 BP.
DE DNA transcription associated complementary genomic DNA #101.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 8346;
RESULT 1210
ID AAV63723 standard; DNA; 10160 BP.
DE Vector plasmid pDAB406.
PN WO9856921-A1.
PD 17-DEC-1998.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match
Best Local Similarity 5.2%; Score 37; DB 2; Length 10160;
RESULT 1211
ID AAX90954 standard; DNA; 10323 BP.
DE Plant transformation binary vector, plasmid pDAB1542.
PN WO9950430-A2.
PD 07-OCT-1999.
Query Match
Best Local Similarity 5.2%; Score 37; DB 2; Length 10323;
RESULT 1212
ID AAV63724 standard; DNA; 11784 BP.
DE Vector plasmid pDAB411.
PN WO9856921-A1.
PD 17-DEC-1998.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match
Best Local Similarity 5.2%; Score 37; DB 2; Length 11784;
RESULT 1213
ID ABK31321 standard; DNA; 11907 BP.
DE Signal transduction associated gene modified complementary DNA #82.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 11907;
RESULT 1214
ID AAV63725 standard; DNA; 11991 BP.
DE Vector plasmid pDAB419.
PN WO9856921-A1.
PD 17-DEC-1998.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match
Best Local Similarity 5.2%; Score 37; DB 2; Length 11991;
RESULT 1215
ID AAS63313 standard; DNA; 12409 BP.
DE Chemically pretreated metabolism associated gene #8.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 37; DB 6; Length 12409;
RESULT 1216
ID AAS46355 standard; DNA; 14537 BP.
DE Tumour suppressor gene derived chemically modified sequence #77.
PN WO200168912-A2.

PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 4; Length 14537;
Best Local Similarity 45.2%; Pred. No. 1.3e+02;
RESULT 1217
ID ABL34173 standard; DNA; 15518 BP.
DE Human immune system associated gene SEQ ID NO: 2146.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 15518;
Best Local Similarity 45.6%; Pred. No. 1.4e+02;
RESULT 1218
ID ABJ34625 standard; DNA; 15518 BP.
DE Human metastasis associated gene SEQ ID NO: 178.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 15518;
Best Local Similarity 45.6%; Pred. No. 1.4e+02;
RESULT 1219
ID ABL70608 standard; DNA; 15518 BP.
DE Chemically treated cell signalling DNA sequence complementary to#249.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 15518;
Best Local Similarity 45.6%; Pred. No. 1.4e+02;
RESULT 1220
ID AAD01288 standard; DNA; 15676 BP.
DE Arabidopsis transformation binary vector, pAct2-bin.
PN WO200032800-A1.
PD 08-JUN-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 5.2%; Score 37; DB 3; Length 15676;
Best Local Similarity 53.0%; Pred. No. 1.4e+02;
RESULT 1221
ID AAD01289 standard; DNA; 17111 BP.
DE Arabidopsis transformation binary vector, pAct2Af-bin.
PN WO200032800-A1.
PD 08-JUN-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 5.2%; Score 37; DB 3; Length 17111;
Best Local Similarity 53.0%; Pred. No. 1.4e+02;
RESULT 1222
ID AAD01290 standard; DNA; 17116 BP.
DE Arabidopsis transformation binary vector, pAct2Af-bin.
PN WO200032800-A1.
PD 08-JUN-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 5.2%; Score 37; DB 3; Length 17116;
Best Local Similarity 53.0%; Pred. No. 1.4e+02;
RESULT 1223
ID AAS45323 standard; DNA; 17848 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #14.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 4; Length 17848;
Best Local Similarity 44.0%; Pred. No. 1.4e+02;
RESULT 1224
ID ABK39976 standard; DNA; 17848 BP.
DE Human chemically pretreated gene sequence #29 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 17848;
Best Local Similarity 44.0%; Pred. No. 1.4e+02;
RESULT 1225
ID ABK28164 standard; DNA; 17848 BP.
DE DNA transcription associated complementary genomic DNA #19.
PN WO200192565-A2.
PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 17848;
Best Local Similarity 44.0%; Pred. No. 1.4e+02;
RESULT 1226
ID AAN50226 standard; DNA; 24593 BP.
DE Sequence of opine synthase gene.
PN EPI40556-A.
PD 08-MAY-1985.
PA (AGRK) AGRIGENETICS RES ASSOC LTD.
PA (LUBR) LUBRIZOL GENETICS INC.
Query Match 5.2%; Score 37; DB 1; Length 24593;
Best Local Similarity 53.0%; Pred. No. 1.5e+02;
RESULT 1227
ID AAN50182 standard; DNA; 24596 BP.
DE Complete nucleotide sequence of the T-DNA region of the octopine Ti
DE plasmid pTi15955.
PN EPI45338-A.
PD 19-JUN-1985.
PA (AGRK) AGRIGENETICS RES ASSOC LTD.
PA (LUBR) LUBRIZOL GENETICS INC.
Query Match 5.2%; Score 37; DB 1; Length 24596;
Best Local Similarity 53.0%; Pred. No. 1.5e+02;
RESULT 1228
ID ADB37660 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:2.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 10; Length 29993;
Best Local Similarity 50.9%; Pred. No. 1.6e+02;
RESULT 1229
ID AAS46745 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #469.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 4; Length 38342;
Best Local Similarity 50.9%; Pred. No. 1.7e+02;
RESULT 1230
ID ABK31506 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 37; DB 6; Length 38342;
Best Local Similarity 50.9%; Pred. No. 1.7e+02;
RESULT 1231
ID ADL44350 standard; DNA; 350 BP.
DE Human ovarian cancer DNA marker #18240.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 36.8; DB 5; Length 350;
Best Local Similarity 52.6%; Pred. No. 69;
RESULT 1232
ID AAL07623 standard; cDNA; 391 BP.
DE Human breast cancer expressed polynucleotide 80.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 36.8; DB 4; Length 391;
Best Local Similarity 49.4%; Pred. No. 70;
RESULT 1233
ID AAI81705 standard; cDNA; 403 BP.
DE Human polynucleotide SEQ ID NO 1765.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 36.8; DB 4; Length 403;
Best Local Similarity 58.0%; Pred. No. 71;
RESULT 1234
ID ABX36056 standard; cDNA; 408 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1221.

PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 8; Length 408;
RESULT 1235
ID ACH27023 standard; cDNA; 416 BP.
DE Human adult ovary cDNA #5403.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 9; Length 416;
RESULT 1236
ID ABL56232 standard; DNA; 453 BP.
DE AnEPV apoptosis associated protein (AMV193) encoding sequence.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 6; Length 453;
RESULT 1237
ID ASX46983 standard; cDNA; 453 BP.
DE Bovine ESR associated with lactation/muscle/fat deposition #12148.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 8; Length 453;
RESULT 1238
ID ABV57839 standard; cDNA; 507 BP.
DE Human prostate expression marker cDNA 57830.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 5; Length 507;
RESULT 1239
ID ABV58219 standard; cDNA; 567 BP.
DE Human prostate expression marker cDNA 58210.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 5; Length 567;
RESULT 1240
ID AAA02542 standard; cDNA; 1199 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2533.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 3; Length 1199;
RESULT 1241
ID ABZ23586 standard; DNA; 1269 BP.
DE Candida albicans essential gene SEQ ID NO 6873.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 6; Length 1269;
RESULT 1242

ID ADJ75071 standard; DNA; 1331 BP.
DE Marker gene SEQ ID NO:323.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 12; Length 1331;
RESULT 1243
ID AAS29132 standard; cDNA; 1387 BP.
DE cDNA encoding for human DNA-binding protein #103.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 5; Length 1387;
RESULT 1244
ID ABS68272 standard; cDNA; 1387 BP.
DE cDNA encoding human DNA-binding protein #103.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 6; Length 1387;
RESULT 1245
ID ADC25266 standard; cDNA; 1387 BP.
DE Human cDNA from extracellular matrix gene 103.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 10; Length 1387;
RESULT 1246
ID ADO35573 standard; DNA; 1520 BP.
DE Novel mouse gene sequence #246.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 12; Length 1520;
RESULT 1247
ID ADB58887 standard; DNA; 1967 BP.
DE Toxicity-related gene, SEQ ID 3913.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 10; Length 1967;
RESULT 1248
ID AAF22346 standard; cDNA; 2058 BP.
DE Human secreted protein gene 31 SEQ ID NO:41.
PN WO200061748-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 3; Length 2058;
RESULT 1249
ID ADM67057 standard; DNA; 2388 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 192.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HME-) HMGNE INC.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 12; Length 2388;
RESULT 1250
ID ABL92207 standard; DNA; 5826 BP.
DE Chemically treated DNA repair gene fragment complementary to #8.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.2%; Score 36.8; DB 6; Length 5826;
RESULT 1251

RESULT 1251
ID ABL31425 standard; DNA; 7321 BP.
DE Signal transduction associated gene modified complementary DNA #134.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7321;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1252
ID ABL70386 standard; DNA; 7321 BP.
DE Chemically treated cell signalling DNA sequence complementary to#138.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7321;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1253
ID AAS61338 standard; DNA; 7321 BP.
DE Human gene regulation-associated gene oligonucleotide #293.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7321;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1254
ID AAS61394 standard; DNA; 7341 BP.
DE Human gene regulation-associated gene oligonucleotide #349.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7341;
Best Local Similarity 48.1%; Pred. No. 1.3e+02;
RESULT 1255
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7346;
Best Local Similarity 46.0%; Pred. No. 1.3e+02;
RESULT 1256
ID ABL33784 standard; DNA; 7461 BP.
DE Human immune system associated gene SEQ ID NO: 1757.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7461;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 1257
ID ABL70435 standard; DNA; 7749 BP.
DE Chemically treated cell signalling DNA sequence#163.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 7749;
Best Local Similarity 44.9%; Pred. No. 1.3e+02;
RESULT 1258
ID ABZ10246 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 8; Length 8056;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
RESULT 1259
ID ABZ10100 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 8; Length 8056;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
RESULT 1260
ID ABL49302 standard; DNA; 10467 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 2.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 10467;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
RESULT 1261
ID ABL32119 standard; DNA; 11416 BP.
DE Human immune system associated gene SEQ ID NO: 92.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 11416;
Best Local Similarity 47.4%; Pred. No. 1.4e+02;
RESULT 1262
ID ABL70136 standard; DNA; 11416 BP.
DE Chemically treated cell signalling DNA sequence complementary to#13.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 11416;
Best Local Similarity 47.4%; Pred. No. 1.4e+02;
RESULT 1263
ID AAS61064 standard; DNA; 11416 BP.
DE Human gene regulation-associated gene oligonucleotide #19.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 36.8; DB 6; Length 11416;
Best Local Similarity 47.4%; Pred. No. 1.4e+02;
RESULT 1264
ID AAT72882 standard; cDNA; 19124 BP.
DE Plasmodium var-7 gene.
PN WO9640766-A2.
PD 19-DEC-1996.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.2%; Score 36.8; DB 2; Length 19124;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
RESULT 1265
ID AAZ38287 standard; DNA; 19124 BP.
DE Plasmodium var-7 polypeptide encoding DNA.
PN US5993827-A.
PD 30-NOV-1999.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.2%; Score 36.8; DB 3; Length 19124;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
RESULT 1266
ID AAL05628 standard; DNA; 32176 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8316.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 4; Length 32176;
Best Local Similarity 46.5%; Pred. No. 1.8e+02;
RESULT 1267
ID ADC87242 standard; DNA; 38918 BP.
DE Human GPCR gene SEQ ID NO:1695.
PN EP12070724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 5.2%; Score 36.8; DB 10; Length 38918;
Best Local Similarity 51.2%; Pred. No. 1.8e+02;
RESULT 1268
ID ABL56202 standard; DNA; 50000 BP.
DE AmEPV genome fragment#4.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 5.2%; Score 36.8; DB 6; Length 50000;
Best Local Similarity 50.6%; Pred. No. 1.9e+02;
RESULT 1269

ID AAK86025 standard; DNA; 54863 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40837.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 4; Length 54863;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1270
ID AAK86026 standard; DNA; 54877 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40838.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 4; Length 54877;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1271
ID ABZ74225 standard; DNA; 54877 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1372.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 8; Length 54877;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1272
ID ADA98754 standard; DNA; 54877 BP.
DE Human secreted protein-related DNA sequence #347.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 8; Length 54877;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1273
ID ABZ67791 standard; DNA; 54877 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1314.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 36.8; DB 10; Length 54877;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1274
ID ABX08336 standard; DNA; 1691080 BP.
DE Human phosphodiesterase 4D (PDE4D) gene.
Query Match 5.2%; Score 36.8; DB 6; Length 110000;
Best Local Similarity 45.3%; Pred. No. 2.3e+02;
RESULT 1275
ID ADJ25985 standard; DNA; 1691139 BP.
DE Human phosphodiesterase 4D (PDE4D) genomic DNA.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.2%; Score 36.8; DB 12; Length 110000;
Best Local Similarity 45.3%; Pred. No. 2.3e+02;
RESULT 1276
ID ADN97989 standard; DNA; 1691138 BP.
DE Human phosphodiesterase 4D genomic sequence.
PN WO2004028341-A2.
PD 08-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.2%; Score 36.8; DB 12; Length 110000;
Best Local Similarity 45.3%; Pred. No. 2.3e+02;
RESULT 1277
ID ADOS0281 standard; DNA; 1691134 BP.
DE Human phosphodiesterase 4D (PDE4D) gene.
PN US2004091865-A1.
PD 13-MAY-2004.
Query Match 5.2%; Score 36.8; DB 12; Length 110000;
Best Local Similarity 45.3%; Pred. No. 2.3e+02;
RESULT 1278
ID ABL85806 standard; cDNA; 200 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:8784.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.

Query Match 5.1%; Score 36.6; DB 6; Length 200;
Best Local Similarity 62.6%; Pred. No. 68;
RESULT 1279
ID ABX40612 standard; cDNA; 241 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5777.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARF/) WARREN W C.
Query Match 5.1%; Score 36.6; DB 8; Length 241;
Best Local Similarity 50.9%; Pred. No. 71;
RESULT 1280
ID ADL43653 standard; DNA; 392 BP.
DE Human ovarian cancer DNA marker #17543.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.6; DB 5; Length 392;
Best Local Similarity 41.1%; Pred. No. 78;
RESULT 1281
ID AAI83622 standard; cDNA; 456 BP.
DE Human polynucleotide SEQ ID NO 3682.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 36.6; DB 4; Length 456;
Best Local Similarity 49.2%; Pred. No. 81;
RESULT 1282
ID ABV52764 standard; cDNA; 456 BP.
DE Human prostate expression marker cDNA 52755.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.6; DB 5; Length 456;
Best Local Similarity 48.8%; Pred. No. 81;
RESULT 1283
ID ABV56478 standard; cDNA; 559 BP.
DE Human prostate expression marker cDNA 56469.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.6; DB 5; Length 559;
Best Local Similarity 58.9%; Pred. No. 84;
RESULT 1284
ID ADF74262 standard; DNA; 1239 BP.
DE Enterocaggregative E_coli aata DNA.
PN US2003180315-A1.
PD 25-SEP-2003.
PA (NATA/) NATARO J.
Query Match 5.1%; Score 36.6; DB 10; Length 1239;
Best Local Similarity 49.2%; Pred. No. 1e+02;
RESULT 1285
ID AAH48299 standard; cDNA; 2863 BP.
DE Human phosphoenol pyruvate carboxylase 81 coding sequence.
PN WO200155412-A1.
PD 02-AUG-2001.
PA (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
Query Match 5.1%; Score 36.6; DB 4; Length 2863;
Best Local Similarity 49.8%; Pred. No. 1.2e+02;
RESULT 1286
ID AAC93445 standard; cDNA; 2904 BP.
DE Human secreted protein gene 24 SEQ ID NO:34.
PN WO200061625-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.1%; Score 36.6; DB 3; Length 2904;
Best Local Similarity 49.2%; Pred. No. 1.2e+02;
RESULT 1287
ID ADI35832 standard; DNA; 4018 BP.
DE Mouse proopiomelanocortin (POMC) regulatory region.

PN US2004003422-A1.
PD 01-JAN-2004.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.1%; Score 36.6; DB 12; Length 4018;
Best Local Similarity 57.4%; Pred. No. 1.3e+02;
RESULT 1288
ID ADB54224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 10; Length 4316;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 1289
ID ABL01896 standard; cDNA; 4755 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 170.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 36.6; DB 4; Length 4755;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 1290
ID ADF74255 standard; DNA; 7000 BP.
DE Genomic DNA sequence of the pAA plasmid of EAEC strain 042.
PN US2003180315-A1.
PD 25-SEP-2003.
PA (NATA/) NATARO J.
Query Match 5.1%; Score 36.6; DB 10; Length 7000;
Best Local Similarity 49.2%; Pred. No. 1.4e+02;
RESULT 1291
ID ABL40060 standard; DNA; 7025 BP.
DE Human chemically pretreated gene sequence #71 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 7025;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
RESULT 1292
ID AAS63351 standard; DNA; 7025 BP.
DE Chemically pretreated metabolism associated gene #46.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 7025;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
RESULT 1293
ID ABL32983 standard; DNA; 7143 BP.
DE Human immune system associated gene SEQ ID NO: 956.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 7143;
Best Local Similarity 55.0%; Pred. No. 1.4e+02;
RESULT 1294
ID AAS45477 standard; DNA; 7657 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #91.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 4; Length 7657;
Best Local Similarity 54.0%; Pred. No. 1.5e+02;
RESULT 1295
ID ABL34022 standard; DNA; 7657 BP.
DE Human immune system associated gene SEQ ID NO: 1995.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 7657;
Best Local Similarity 54.0%; Pred. No. 1.5e+02;
RESULT 1296
ID ABL33897 standard; DNA; 8143 BP.
DE Human immune system associated gene SEQ ID NO: 1870.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 8143;
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
RESULT 1297
ID ABL08220 standard; cDNA; 8242 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19142.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 36.6; DB 4; Length 8242;
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
RESULT 1298
ID AAS45452 standard; DNA; 9515 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #79.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 4; Length 9515;
Best Local Similarity 52.3%; Pred. No. 1.5e+02;
RESULT 1299
ID ABL28307 standard; DNA; 9515 BP.
DE DNA transcription associated genomic DNA #91.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 9515;
Best Local Similarity 52.3%; Pred. No. 1.5e+02;
RESULT 1300
ID ABL80244 standard; DNA; 9515 BP.
DE Human chemically modified disease associated gene SEQ ID NO 261.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 9515;
Best Local Similarity 52.3%; Pred. No. 1.5e+02;
RESULT 1301
ID AAD03729 standard; DNA; 10640 BP.
DE P. falciparum telomerase reverse transcriptase (TERT) full length gene.
PN WO200127287-A2.
PD 19-APR-2001.
PA (RERE-) RES & DEV INST INC.
Query Match 5.1%; Score 36.6; DB 4; Length 10640;
Best Local Similarity 46.3%; Pred. No. 1.6e+02;
RESULT 1302
ID ABL32752 standard; DNA; 11131 BP.
DE Human immune system associated gene SEQ ID NO: 725.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 11131;
Best Local Similarity 58.9%; Pred. No. 1.6e+02;
RESULT 1303
ID ABL92226 standard; DNA; 11131 BP.
DE Chemically treated DNA repair gene fragment#18.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 11131;
Best Local Similarity 58.9%; Pred. No. 1.6e+02;
RESULT 1304
ID ABL49327 standard; DNA; 11131 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 27.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.6; DB 6; Length 11131;
Best Local Similarity 58.9%; Pred. No. 1.6e+02;
RESULT 1305
ID AAS45314 standard; DNA; 11260 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #10.
PN WO200168911-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 4; Length 11260;
 Best Local Similarity 44.8%; Pred. No. 1.6e+02;
 RESULT 1306
 ID ABK28153 standard; DNA; 11260 BP.
 DE DNA transcription associated genomic DNA #14.
 PN WO200192565-A2.
 PD 06-DEC-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 6; Length 11260;
 Best Local Similarity 44.8%; Pred. No. 1.6e+02;
 RESULT 1307
 ID AEN80038 standard; DNA; 11260 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 55.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 6; Length 11260;
 Best Local Similarity 44.8%; Pred. No. 1.6e+02;
 RESULT 1308
 ID ABL34493 standard; DNA; 11996 BP.
 DE Human metastasis associated gene SEQ ID NO: 46.
 PN WO200177376-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 6; Length 11996;
 Best Local Similarity 48.0%; Pred. No. 1.6e+02;
 RESULT 1309
 ID AAS02354 standard; DNA; 27048 BP.
 DE Porcine Gal alpha(1,3) galactosyl transferase gene introns 3-8.
 PN WO200123541-A2.
 PD 05-APR-2001.
 PA (ALEX-) ALEXION PHARM INC.
 Query Match 5.1%; Score 36.6; DB 4; Length 27048;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 RESULT 1310
 ID ABL19792 standard; DNA; 33472 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10849.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PERE) PE CORP NY.
 Query Match 5.1%; Score 36.6; DB 4; Length 33472;
 Best Local Similarity 56.1%; Pred. No. 2e+02;
 RESULT 1311
 ID ABK31511 standard; DNA; 47108 BP.
 DE Signal transduction associated gene modified complementary DNA #177.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 6; Length 47108;
 Best Local Similarity 48.4%; Pred. No. 2.1e+02;
 RESULT 1312
 ID AAV26084 standard; cDNA; 51952 BP.
 DE Tomato pest resistance Mi gene (copy 1).
 PN WO9815171-A1.
 PD 16-APR-1998.
 PA (REG) UNIV CALIFORNIA.
 Query Match 5.1%; Score 36.6; DB 2; Length 51952;
 Best Local Similarity 52.9%; Pred. No. 2.2e+02;
 RESULT 1313
 ID ADA02666 standard; DNA; 52242 BP.
 DE Human MDM2 carcinoma associated gene, SEQ ID NO:1184.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 5.1%; Score 36.6; DB 9; Length 52242;
 Best Local Similarity 52.3%; Pred. No. 2.2e+02;
 RESULT 1314
 ID ADB72404 standard; DNA; 52242 BP.
 DE Human MDM2 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 5.1%; Score 36.6; DB 10; Length 52242;
 Best Local Similarity 52.3%; Pred. No. 2.2e+02;
 RESULT 1315
 ID ADE95914 standard; DNA; 52242 BP.
 DE Human MDM2 gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 5.1%; Score 36.6; DB 10; Length 52242;
 Best Local Similarity 52.3%; Pred. No. 2.2e+02;
 RESULT 1316
 ID AAS46788 standard; DNA; 61020 BP.
 DE Tumour suppressor gene derived chemically modified sequence #514.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 4; Length 61020;
 Best Local Similarity 48.8%; Pred. No. 2.3e+02;
 RESULT 1317
 ID ABL34175 standard; DNA; 113515 BP.
 DE Human immune system associated gene SEQ ID NO: 2148.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 5.1%; Score 36.6; DB 6; Length 113515;
 Best Local Similarity 45.2%; Pred. No. 2.6e+02;
 RESULT 1318
 ID ABZ80818 standard; DNA; 159095 BP.
 DE Human PAI-2 polymorphism PAI2u1.
 PN WO2003007801-A2.
 PD 30-JAN-2003.
 PA (VITI-) VITIVITY INC.
 Query Match 5.1%; Score 36.6; DB 8; Length 159095;
 Best Local Similarity 68.0%; Pred. No. 2.8e+02;
 RESULT 1319
 ID AAH88704 standard; DNA; 160755 BP.
 DE Human DNA sequence SEQ ID 544.
 PN WO200151659-A2.
 PD 19-JUL-2001.
 PA (GEST) GENSET.
 Query Match 5.1%; Score 36.6; DB 4; Length 160755;
 Best Local Similarity 56.1%; Pred. No. 2.8e+02;
 RESULT 1320
 ID ADL08126 standard; DNA; 191395 BP.
 DE Human gene associated with low HDL-C PAI2.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 5.1%; Score 36.6; DB 12; Length 191395;
 Best Local Similarity 68.0%; Pred. No. 2.9e+02;
 RESULT 1321
 ID ADI73160 standard; DNA; 318 BP.
 DE Human ovarian cancer DNA marker #5902.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 5.1%; Score 36.4; DB 5; Length 318;
 Best Local Similarity 45.6%; Pred. No. 83;
 RESULT 1322
 ID ADL38293 standard; DNA; 318 BP.
 DE Human ovarian cancer DNA marker #12183.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 5.1%; Score 36.4; DB 5; Length 318;
 Best Local Similarity 45.6%; Pred. No. 83;
 RESULT 1323
 ID AAH53278 standard; DNA; 342 BP.
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:1949.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 5.1%; Score 36.4; DB 4; Length 342;

Best Local Similarity 56.8%; Pred. No. 85;
RESULT 1324
ID ABX47837 standard; cDNA; 344 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13002.
US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.1%; Score 36.4; DB 8; Length 344;
Best Local Similarity 52.7%; Pred. No. 85;
RESULT 1325
ID ABN92001 standard; DNA; 408 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1464.
FN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.1%; Score 36.4; DB 6; Length 408;
Best Local Similarity 56.8%; Pred. No. 88;
RESULT 1326
ID AA191807 standard; cDNA; 435 BP.
DE Human polynucleotide SEQ ID NO 11867.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 36.4; DB 4; Length 435;
Best Local Similarity 51.2%; Pred. No. 89;
RESULT 1327
ID ABN93640 standard; DNA; 462 BP.
DE Gene #138 used to diagnose liver cancer.
FN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.1%; Score 36.4; DB 6; Length 462;
Best Local Similarity 44.2%; Pred. No. 90;
RESULT 1328
ID ABT40613 standard; DNA; 479 BP.
DE Toxicity modelling related rat gene SEQ ID No 315.
FN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.1%; Score 36.4; DB 10; Length 479;
Best Local Similarity 47.7%; Pred. No. 91;
RESULT 1329
ID ARL35041 standard; cDNA; 926 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 570.
FN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 5.1%; Score 36.4; DB 6; Length 926;
Best Local Similarity 53.5%; Pred. No. 1e+02;
RESULT 1330
ID AE277144 standard; cDNA; 1230 BP.
DE Human protein kinase encoding cDNA SEQ ID NO:37.
FN WO200300901-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.1%; Score 36.4; DB 10; Length 1230;
Best Local Similarity 61.7%; Pred. No. 1.1e+02;
RESULT 1331
ID ABN81046 standard; DNA; 1256 BP.
DE Shrimp polynucleotide SEQ ID NO 50.
FN WO20034476-A2.
PD 15-JUN-2000.
PA (TUFT) TUFTS COLLEGE.
Query Match 5.1%; Score 36.4; DB 3; Length 1256;
Best Local Similarity 58.2%; Pred. No. 1.1e+02;
RESULT 1332
ID ADO20394 standard; DNA; 1506 BP.
DE Human PRO polynucleotide #760.
FN WO200404361-A2.
PD 27-MAY-2004.

PA (GETH) GENENTECH INC.
Query Match 5.1%; Score 36.4; DB 12; Length 1506;
Best Local Similarity 56.8%; Pred. No. 1.2e+02;
RESULT 1333
ID AQ025453 standard; DNA; 1559 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8273.
FN WO2004049938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.1%; Score 36.4; DB 12; Length 1559;
Best Local Similarity 56.8%; Pred. No. 1.2e+02;
RESULT 1334
ID ADM91294 standard; DNA; 1902 BP.
DE DNA homologue of a human DNA sequence encoding a protein seqID 628.
FN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 5.1%; Score 36.4; DB 12; Length 1902;
Best Local Similarity 61.7%; Pred. No. 1.2e+02;
RESULT 1335
ID ADA72008 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5333.
FN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.1%; Score 36.4; DB 8; Length 2000;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
RESULT 1336
ID AAH16252 standard; cDNA; 2308 BP.
DE Human cDNA sequence SEQ ID NO:15093.
FN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.1%; Score 36.4; DB 4; Length 2308;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 1337
ID ACC72733 standard; cDNA; 2308 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:72.
FN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.1%; Score 36.4; DB 10; Length 2308;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 1338
ID ADJ91782 standard; cDNA; 2308 BP.
DE Human PRO69889 encoding cDNA SEQ ID NO:3.
FN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.1%; Score 36.4; DB 12; Length 2308;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 1339
ID ADO35529 standard; DNA; 2506 BP.
DE Novel mouse gene sequence #202.
FN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.1%; Score 36.4; DB 12; Length 2506;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
RESULT 1340
ID AAH54088 standard; DNA; 3005 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3452.
FN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.1%; Score 36.4; DB 4; Length 3005;
Best Local Similarity 56.8%; Pred. No. 1.3e+02;
RESULT 1341
ID AAX25320 standard; cDNA; 3331 BP.
DE Mouse TNF receptor TRL cDNA.
FN WO9915663-A1.

PD 01-APR-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 5.1%; Score 36.4; DB 2; Length 3331;
Best Local Similarity 59.8%; Pred. No. 1.4e+02;
RESULT 1342
ID ADQ24604 standard; DNA; 3655 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7424.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.1%; Score 36.4; DB 12; Length 3655;
Best Local Similarity 51.2%; Pred. No. 1.4e+02;
RESULT 1343
ID ABL32957 standard; DNA; 5182 BP.
DE Human immune system associated gene SEQ ID NO: 930.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 5182;
Best Local Similarity 56.8%; Pred. No. 1.5e+02;
RESULT 1344
ID RAN50530 standard; DNA; 5760 BP.
DE Sequence encoding the P195 protein of Plasmodium falciparum.
PN EP154454-A.
PD 11-SEP-1985.
PA (WELL) WELLCOME FOUND LTD.
Query Match 5.1%; Score 36.4; DB 1; Length 5760;
Best Local Similarity 45.9%; Pred. No. 1.5e+02;
RESULT 1345
ID AAD46980 standard; DNA; 5917 BP.
DE Plasmodium falciparum merozoite surface protein-1 (MSP-1) DNA.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELL-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 5.1%; Score 36.4; DB 6; Length 5917;
Best Local Similarity 45.9%; Pred. No. 1.5e+02;
RESULT 1346
ID ABK31498 standard; DNA; 5986 BP.
DE Signal transduction associated gene modified DNA #171.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 5986;
Best Local Similarity 49.5%; Pred. No. 1.5e+02;
RESULT 1347
ID AAS61432 standard; DNA; 5986 BP.
DE Human gene regulation-associated gene oligonucleotide #387.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 5986;
Best Local Similarity 49.5%; Pred. No. 1.5e+02;
RESULT 1348
ID ABK28370 standard; DNA; 6167 BP.
DE DNA transcription associated complementary genomic DNA #122.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 6167;
Best Local Similarity 52.7%; Pred. No. 1.6e+02;
RESULT 1349
ID ABL92263 standard; DNA; 6935 BP.
DE Chemically treated DNA repair gene fragment complementary to #36.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 6935;
Best Local Similarity 50.6%; Pred. No. 1.6e+02;
RESULT 1350
ID ABL32784 standard; DNA; 8979 BP.
DE Human immune system associated gene SEQ ID NO: 757.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 8979;
Best Local Similarity 51.9%; Pred. No. 1.7e+02;
RESULT 1351
ID ABK31270 standard; DNA; 8979 BP.
DE Signal transduction associated gene modified DNA #57.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 8979;
Best Local Similarity 51.9%; Pred. No. 1.7e+02;
RESULT 1352
ID ABL70231 standard; DNA; 8979 BP.
DE Chemically treated cell signalling DNA sequence #61.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 8979;
Best Local Similarity 51.9%; Pred. No. 1.7e+02;
RESULT 1353
ID AAS61178 standard; DNA; 9293 BP.
DE Human gene regulation-associated gene oligonucleotide #133.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 8979;
Best Local Similarity 51.9%; Pred. No. 1.7e+02;
RESULT 1354
ID AAS45321 standard; DNA; 9293 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #13.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 4; Length 9293;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
RESULT 1355
ID ABK39974 standard; DNA; 9293 BP.
DE Human chemically pretreated gene sequence #28 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 9293;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
RESULT 1356
ID ABK28160 standard; DNA; 9293 BP.
DE DNA transcription associated complementary genomic DNA #17.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 9293;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
RESULT 1357
ID ACF57521 standard; DNA; 10907 BP.
DE Human p21 DNA SEQ ID NO: 22.
PN WO2003093303-A1.
PD 13-NOV-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 5.1%; Score 36.4; DB 12; Length 10907;
Best Local Similarity 61.7%; Pred. No. 1.7e+02;
RESULT 1358
ID ADJ62879 standard; DNA; 10907 BP.
DE Human p21 WAF-1 gene related to cancer treatment.
PN US2003228285-A1.
PD 11-DEC-2003.
PA (HUNG/) HUNG M.
PA (KWON/) KWONG K Y.
PA (ZOUY/) ZOU Y.
Query Match 5.1%; Score 36.4; DB 12; Length 10907;
Best Local Similarity 61.7%; Pred. No. 1.7e+02;
RESULT 1359
ID AAH48024 standard; DNA; 14041 BP.
DE Internal control B19c #1.
PN WO200146463-A2.

PD 28-JUN-2001.
PA (BAXT) BAXTER AG.
Query Match 5.1%; Score 36.4; DB 4; Length 14041;
Best Local Similarity 16.0%; Pred. No. 1.8e+02;
RESULT 1360
ID ABL34585 standard; DNA; 14551 BP.
DE Human metastasis associated gene SEQ ID NO: 138.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 14551;
Best Local Similarity 43.7%; Pred. No. 1.9e+02;
RESULT 1361
ID ABL62905 standard; DNA; 15000 BP.
DE Breast cancer related gene sequence SEQ ID NO:1242.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 5.1%; Score 36.4; DB 6; Length 15000;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
RESULT 1362
ID ABL32363 standard; DNA; 15674 BP.
DE Human immune system associated gene SEQ ID NO: 336.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15674;
Best Local Similarity 47.4%; Pred. No. 1.9e+02;
RESULT 1363
ID ABL34477 standard; DNA; 15674 BP.
DE Human metastasis associated gene SEQ ID NO: 30.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15674;
Best Local Similarity 47.4%; Pred. No. 1.9e+02;
RESULT 1364
ID ABL70514 standard; DNA; 15674 BP.
DE Chemically treated cell signalling DNA sequence complementary to#202.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15674;
Best Local Similarity 47.4%; Pred. No. 1.9e+02;
RESULT 1365
ID ABL33681 standard; DNA; 15951 BP.
DE Human immune system associated gene SEQ ID NO: 1654.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15951;
Best Local Similarity 47.3%; Pred. No. 1.9e+02;
RESULT 1366
ID ABL34581 standard; DNA; 15951 BP.
DE Human metastasis associated gene SEQ ID NO: 134.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15951;
Best Local Similarity 47.3%; Pred. No. 1.9e+02;
RESULT 1367
ID ABL70374 standard; DNA; 15951 BP.
DE Chemically treated cell signalling DNA sequence complementary to#132.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 15951;
Best Local Similarity 47.3%; Pred. No. 1.9e+02;
RESULT 1368
ID ABL2654 standard; DNA; 17211 BP.
DE Human immune system associated gene SEQ ID NO: 627.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 17211;
Best Local Similarity 48.1%; Pred. No. 1.9e+02;
RESULT 1369
ID ABL33933 standard; DNA; 19734 BP.
DE Human immune system associated gene SEQ ID NO: 1906.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 19734;
Best Local Similarity 45.7%; Pred. No. 2e+02;
RESULT 1370
ID AAK70623 standard; DNA; 26410 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25435.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 36.4; DB 4; Length 26410;
Best Local Similarity 61.7%; Pred. No. 2.1e+02;
RESULT 1371
ID AAL05121 standard; DNA; 29163 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7809.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 36.4; DB 4; Length 29163;
Best Local Similarity 61.7%; Pred. No. 2.1e+02;
RESULT 1372
ID ABL98013 standard; DNA; 29163 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2665.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 36.4; DB 4; Length 29163;
Best Local Similarity 61.7%; Pred. No. 2.1e+02;
RESULT 1373
ID ADB37660 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:2.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 10; Length 29993;
Best Local Similarity 49.0%; Pred. No. 2.2e+02;
RESULT 1374
ID AAS46745 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #469.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 4; Length 38342;
Best Local Similarity 49.0%; Pred. No. 2.3e+02;
RESULT 1375
ID ABK31506 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.4; DB 6; Length 38342;
Best Local Similarity 49.0%; Pred. No. 2.3e+02;
RESULT 1376
ID ADA14747 standard; DNA; 42998 BP.
DE Human ribosomal DNA complete repeating unit.
PN US2002160970-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZYK G.
PA (SZAL/) SZALAY A. A.
Query Match 5.1%; Score 36.4; DB 8; Length 42998;
Best Local Similarity 61.7%; Pred. No. 2.3e+02;
RESULT 1377
ID ABS65032 standard; DNA; 42999 BP.
DE Invertebrate foraging behaviour associated human DNA sequence #12.
PN WO200259370-A2.
PD 01-AUG-2002.

PA (NEUR-) NEUROSCIENCES RES FOUND INC.
Query Match 5.1%; Score 36.4; DB 6; Length 42999;
Best Local Similarity 61.7%; Pred. No. 2.3e+02;
RESULT 1378
ID AAD61411 standard; DNA; 42999 BP.
DE Human ribosomal DNA (rDNA) repeat region.
PN US2003101480-A1.
PD 29-MAY-2003.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 5.1%; Score 36.4; DB 10; Length 42999;
Best Local Similarity 61.7%; Pred. No. 2.3e+02;
RESULT 1379
ID ADA02705 standard; DNA; 54786 BP.
DE Mouse Zfx1b carcinoma associated gene, SEQ ID NO:1223.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 9; Length 54786;
Best Local Similarity 61.7%; Pred. No. 2.5e+02;
RESULT 1380
ID ADB72443 standard; DNA; 54786 BP.
DE Mouse Zfx1b gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 10; Length 54786;
Best Local Similarity 61.7%; Pred. No. 2.5e+02;
RESULT 1381
ID ADE95953 standard; DNA; 54786 BP.
DE Mouse Zfx1b gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 10; Length 54786;
Best Local Similarity 61.7%; Pred. No. 2.5e+02;
RESULT 1382
ID ABL03438 standard; cDNA; 76574 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4796.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 36.4; DB 4; Length 76574;
Best Local Similarity 53.5%; Pred. No. 2.6e+02;
RESULT 1383
ID AAL61326 standard; DNA; 91000 BP.
DE Human farnesoid X receptor (FXR) DNA #2.
PN WO2003044167-A2.
PD 30-MAY-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 5.1%; Score 36.4; DB 9; Length 91000;
Best Local Similarity 61.7%; Pred. No. 2.7e+02;
RESULT 1384
ID ADP08388 standard; DNA; 95400 BP.
DE Human laminin alpha 4 (LAMA4) genomic DNA.
PN WO2003045230-A2.
Query Match 5.1%; Score 36.4; DB 12; Length 95400;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
RESULT 1385
ID ADC85392 standard; DNA; 96587 BP.
DE Human Jak2 genomic sequence.
PN WO2003057146-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 10; Length 96587;
Best Local Similarity 45.7%; Pred. No. 2.8e+02;
RESULT 1386
ID ADA02912 standard; DNA; 96589 BP.
DE Human Jak2 carcinoma associated gene, SEQ ID NO:1430.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 9; Length 96589;
Best Local Similarity 45.7%; Pred. No. 2.8e+02;

RESULT 1387
ID ADB72650 standard; DNA; 96589 BP.
DE Human Jak2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.1%; Score 36.4; DB 10; Length 96589;
Best Local Similarity 45.7%; Pred. No. 2.8e+02;
RESULT 1388
ID ADM74507 standard; DNA; 96589 BP.
DE Human carcinoma associated (CA) nucleic acid #88.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 5.1%; Score 36.4; DB 12; Length 96589;
Best Local Similarity 45.7%; Pred. No. 2.8e+02;
RESULT 1389
ID ABL18718 standard; DNA; 106416 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7627.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 36.4; DB 4; Length 106416;
Best Local Similarity 47.7%; Pred. No. 2.8e+02;
RESULT 1390
ID ABA90521 standard; DNA; 2365589 BP.
DE Genomic sequence of Lactococcus lactis IL1403.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.1%; Score 36.4; DB 6; Length 110000;
Best Local Similarity 53.5%; Pred. No. 2.8e+02;
RESULT 1391
ID ADF13118 standard; DNA; 161652 BP.
DE Hypermethylation site in human breast cancer CpG island locus HBC-48.
PN US2003129602-A1.
PD 10-JUL-2003.
PA (HUANG/) HUANG T H.
Query Match 5.1%; Score 36.4; DB 12; Length 161652;
Best Local Similarity 47.4%; Pred. No. 3.1e+02;
RESULT 1392
ID ADI37264 standard; DNA; 161652 BP.
DE Hypermethylation in cancer (HBC) locus-48.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR) UNIV MISSOURI.
Query Match 5.1%; Score 36.4; DB 12; Length 161652;
Best Local Similarity 47.4%; Pred. No. 3.1e+02;
RESULT 1393
ID ABX94407 standard; cDNA; 251 BP.
DE Rice endosperm-associated EST cDNA SEQ ID 7.
PN CN1364918-A.
PD 21-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 5.1%; Score 36.2; DB 10; Length 251;
Best Local Similarity 51.6%; Pred. No. 88;
RESULT 1394
ID ABX48177 standard; cDNA; 286 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13342.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.1%; Score 36.2; DB 8; Length 286;
Best Local Similarity 52.3%; Pred. No. 91;
RESULT 1395
ID AAL14832 standard; cDNA; 287 BP.
DE Human breast cancer expressed polynucleotide 7289.
PN WO200151628-A2.
PD 19-JUL-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 4; Length 287;
Best Local Similarity 40.9%; Pred. No. 91;
RESULT 1396
ID ABV59017 standard; cDNA; 325 BP.
DE Human prostate expression marker cDNA 59008.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 325;
Best Local Similarity 47.9%; Pred. No. 93;
RESULT 1397
ID AAL25369 standard; cDNA; 367 BP.
DE Human breast cancer expressed polynucleotide 17826.
FN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 538;
Best Local Similarity 51.4%; Pred. No. 96;
RESULT 1398
ID AAH69544 standard; cDNA; 369 BP.
DE Human cervical cancer marker nucleic acid 818.
FN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 4; Length 367;
Best Local Similarity 49.4%; Pred. No. 96;
RESULT 1399
ID AAL11189 standard; cDNA; 393 BP.
DE Human breast cancer expressed polynucleotide 3646.
FN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 4; Length 393;
Best Local Similarity 51.0%; Pred. No. 97;
RESULT 1400
ID AAI87163 standard; cDNA; 394 BP.
DE Human polynucleotide SEQ ID NO 7223.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 36.2; DB 4; Length 394;
Best Local Similarity 49.2%; Pred. No. 97;
RESULT 1401
ID ABV08266 standard; cDNA; 461 BP.
DE Human prostate expression marker cDNA 8257.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 461;
Best Local Similarity 49.6%; Pred. No. 1e+02;
RESULT 1402
ID ABV55326 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 55317.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 464;
Best Local Similarity 50.9%; Pred. No. 1e+02;
RESULT 1403
ID ABV55197 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 55188.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 469;
Best Local Similarity 50.9%; Pred. No. 1e+02;
RESULT 1404
ID ABV09921 standard; cDNA; 473 BP.
DE Human prostate expression marker cDNA 9912.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 473;
Best Local Similarity 50.2%; Pred. No. 1e+02;
RESULT 1405
ID AAL16526 standard; cDNA; 496 BP.
DE Human breast cancer expressed polynucleotide 8983.
FN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 4; Length 496;
Best Local Similarity 49.4%; Pred. No. 1e+02;
RESULT 1406
ID ADL37492 standard; DNA; 538 BP.
DE Human ovarian cancer DNA marker #11382.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 538;
Best Local Similarity 51.4%; Pred. No. 1e+02;
RESULT 1407
ID ADI72348 standard; DNA; 538 BP.
DE Human ovarian cancer DNA marker #5090.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.1%; Score 36.2; DB 5; Length 538;
Best Local Similarity 51.4%; Pred. No. 1e+02;
RESULT 1408
ID AAX37532 standard; cDNA; 725 BP.
DE Human secreted protein cDNA fragment containing gene 82.
FN WO9918208-A1.
PD 15-APR-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 36.2; DB 2; Length 725;
Best Local Similarity 52.3%; Pred. No. 1.1e+02;
RESULT 1409
ID ADC86904 standard; DNA; 919 BP.
DE Human GPCR gene SEQ ID NO:1357.
FN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 5.1%; Score 36.2; DB 10; Length 919;
Best Local Similarity 62.9%; Pred. No. 1.2e+02;
RESULT 1410
ID ADK16276 standard; DNA; 1062 BP.
DE Nanoarchaeum equitans cancer-associated (CA) gene #114.
FN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.1%; Score 36.2; DB 12; Length 1062;
Best Local Similarity 48.4%; Pred. No. 1.2e+02;
RESULT 1411
ID ACA23122 standard; DNA; 1587 BP.
DE Prokaryotic essential gene #4779.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 36.2; DB 8; Length 1587;
Best Local Similarity 45.8%; Pred. No. 1.3e+02;
RESULT 1412
ID ABZ17397 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 5202.
FN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
Query Match 5.1%; Score 36.2; DB 6; Length 2000;
Best Local Similarity 53.6%; Pred. No. 1.4e+02;
RESULT 1413
ID AAD37062 standard; cDNA; 2396 BP.
DE Influenza B virus/vienna/1/99/ca PB2 mutant cDNA.
FN WO200224876-A2.
PD 28-MAR-2002.

PA (POLY-) POLYUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
Query Match 5.1%; Score 36.2; DB 6; Length 2396;
Best Local Similarity 51.6%; Pred. No. 1.4e+02;
RESULT 1414
ID ABL17264 standard; DNA; 3296 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 36.2; DB 4; Length 3296;
Best Local Similarity 45.5%; Pred. No. 1.5e+02;
RESULT 1415
ID ABL34627 standard; DNA; 5539 BP.
DE Human metastasis associated gene SEQ ID NO: 180.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 5539;
Best Local Similarity 55.0%; Pred. No. 1.7e+02;
RESULT 1416
ID ABL33566 standard; DNA; 5647 BP.
DE Human immune system associated gene SEQ ID NO: 1539.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 5647;
Best Local Similarity 50.3%; Pred. No. 1.7e+02;
RESULT 1417
ID ABL70355 standard; DNA; 5647 BP.
DE Chemically treated cell signalling DNA sequence#123.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 5647;
Best Local Similarity 50.3%; Pred. No. 1.7e+02;
RESULT 1418
ID AAS61320 standard; DNA; 5647 BP.
DE Human gene regulation-associated gene oligonucleotide #275.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 5647;
Best Local Similarity 50.3%; Pred. No. 1.7e+02;
RESULT 1419
ID ABL33662 standard; DNA; 5845 BP.
DE Human immune system associated gene SEQ ID NO: 1635.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 5845;
Best Local Similarity 45.6%; Pred. No. 1.7e+02;
RESULT 1420
ID AAQ11710 standard; DNA; 5852 BP.
DE Dictyostelium plasmid Ddp2 containing Rep gene.
PN WO9106644-A.
PD 16-MAY-1991.
PA (UYNA-) UNIV MACQUARIE.
Query Match 5.1%; Score 36.2; DB 2; Length 5852;
Best Local Similarity 53.1%; Pred. No. 1.7e+02;
RESULT 1421
ID ABL32431 standard; DNA; 6113 BP.
DE Human immune system associated gene SEQ ID NO: 404.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6113;
Best Local Similarity 54.0%; Pred. No. 1.7e+02;
RESULT 1422
ID ABL92205 standard; DNA; 6113 BP.
DE Chemically treated DNA repair gene fragment complementary to#7.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 5.1%; Score 36.2; DB 6; Length 6113;
Best Local Similarity 54.0%; Pred. No. 1.7e+02;
RESULT 1423
ID ABL49314 standard; DNA; 6113 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 14.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6113;
Best Local Similarity 54.0%; Pred. No. 1.7e+02;
RESULT 1424
ID ABL33974 standard; DNA; 6121 BP.
DE Human immune system associated gene SEQ ID NO: 1947.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6121;
Best Local Similarity 56.2%; Pred. No. 1.7e+02;
RESULT 1425
ID ABK31200 standard; DNA; 6154 BP.
DE Signal transduction associated gene modified DNA #22.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6154;
Best Local Similarity 44.5%; Pred. No. 1.7e+02;
RESULT 1426
ID ABL70167 standard; DNA; 6154 BP.
DE Chemically treated cell signalling DNA sequence#29.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6154;
Best Local Similarity 44.5%; Pred. No. 1.7e+02;
RESULT 1427
ID AAS61112 standard; DNA; 6154 BP.
DE Human gene regulation-associated gene oligonucleotide #67.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6154;
Best Local Similarity 44.5%; Pred. No. 1.7e+02;
RESULT 1428
ID ABL32693 standard; DNA; 6222 BP.
DE Human immune system associated gene SEQ ID NO: 666.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6222;
Best Local Similarity 44.9%; Pred. No. 1.7e+02;
RESULT 1429
ID ABL32484 standard; DNA; 6244 BP.
DE Human immune system associated gene SEQ ID NO: 457.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 6244;
Best Local Similarity 46.9%; Pred. No. 1.7e+02;
RESULT 1430
ID ABK40057 standard; DNA; 7441 BP.
DE Human chemically pretreated gene sequence #70 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 7441;
Best Local Similarity 54.0%; Pred. No. 1.8e+02;
RESULT 1431
ID AAS63344 standard; DNA; 7479 BP.
DE Chemically pretreated metabolism associated gene #39.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 7479;

Best Local Similarity 54.0%; Pred. No. 1.8e+02;
RESULT 1432
ID ABU32948 standard; DNA; 7589 BP.
DE Human immune system associated gene SEQ ID NO: 921.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 7589;
Best Local Similarity 54.0%; Pred. No. 1.8e+02;
RESULT 1433
ID AAS46760 standard; DNA; 7900 BP.
DE Tumour suppressor gene derived chemically modified sequence #484.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 4; Length 7900;
Best Local Similarity 46.9%; Pred. No. 1.8e+02;
RESULT 1434
ID ABU32063 standard; DNA; 9905 BP.
DE Human immune system associated gene SEQ ID NO: 36.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 9905;
Best Local Similarity 54.0%; Pred. No. 1.9e+02;
RESULT 1435
ID ABU32880 standard; DNA; 10197 BP.
DE Human immune system associated gene SEQ ID NO: 853.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 10197;
Best Local Similarity 59.0%; Pred. No. 1.9e+02;
RESULT 1436
ID ABK31248 standard; DNA; 10543 BP.
DE Signal transduction associated gene modified DNA #46.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 10543;
Best Local Similarity 55.0%; Pred. No. 1.9e+02;
RESULT 1437
ID ABU70205 standard; DNA; 10543 BP.
DE Chemically treated cell signalling DNA sequence#48.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 10543;
Best Local Similarity 55.0%; Pred. No. 1.9e+02;
RESULT 1438
ID AAS61160 standard; DNA; 10543 BP.
DE Human gene regulation-associated gene oligonucleotide #115.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 10543;
Best Local Similarity 55.0%; Pred. No. 1.9e+02;
RESULT 1439
ID ABU34187 standard; DNA; 11944 BP.
DE Human immune system associated gene SEQ ID NO: 2160.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 11944;
Best Local Similarity 55.0%; Pred. No. 2e+02;
RESULT 1440
ID AAS46509 standard; DNA; 12356 BP.
DE Tumour suppressor gene derived chemically modified sequence #231.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 4; Length 12356;
Best Local Similarity 48.8%; Pred. No. 2e+02;

RESULT 1441
ID AAS46554 standard; DNA; 12986 BP.
DE Tumour suppressor gene derived chemically modified sequence #276.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 4; Length 12986;
Best Local Similarity 48.3%; Pred. No. 2e+02;
RESULT 1442
ID AAS46704 standard; DNA; 14615 BP.
DE Tumour suppressor gene derived chemically modified sequence #427.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 4; Length 14615;
Best Local Similarity 50.3%; Pred. No. 2.1e+02;
RESULT 1443
ID ABK31221 standard; DNA; 15923 BP.
DE Signal transduction associated gene modified complementary DNA #32.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 15923;
Best Local Similarity 54.0%; Pred. No. 2.1e+02;
RESULT 1444
ID ABU70180 standard; DNA; 15923 BP.
DE Chemically treated cell signalling DNA sequence complementary to#35.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 15923;
Best Local Similarity 54.0%; Pred. No. 2.1e+02;
RESULT 1445
ID AAS61133 standard; DNA; 15923 BP.
DE Human gene regulation-associated gene oligonucleotide #88.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 15923;
Best Local Similarity 54.0%; Pred. No. 2.1e+02;
RESULT 1446
ID ABU33344 standard; DNA; 17674 BP.
DE Human immune system associated gene SEQ ID NO: 1317.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 17674;
Best Local Similarity 49.2%; Pred. No. 2.2e+02;
RESULT 1447
ID ABN80226 standard; DNA; 19236 BP.
DE Human chemically modified disease associated gene SEQ ID NO 243.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 19236;
Best Local Similarity 51.7%; Pred. No. 2.2e+02;
RESULT 1448
ID ABU33933 standard; DNA; 19734 BP.
DE Human immune system associated gene SEQ ID NO: 1906.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 19734;
Best Local Similarity 48.8%; Pred. No. 2.2e+02;
RESULT 1449
ID ABQ66981 standard; DNA; 23695 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 11.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 23695;
Best Local Similarity 53.1%; Pred. No. 2.3e+02;
RESULT 1450

ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 36.2; DB 6; Length 47108;
Best Local Similarity 48.3%; Pred. No. 2.6e+02;
RESULT 1451
ID AAS13655 standard; DNA; 53552 BP.
DE Genomic DNA sequence encoding human hspG15.
PN WO200166752-A2.
PD 13-SEP-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 5.1%; Score 36.2; DB 5; Length 53552;
Best Local Similarity 51.6%; Pred. No. 2.7e+02;
RESULT 1452
ID ADG86768 standard; DNA; 104245 BP.
DE Human clone RPI-109F14 from chromosome 6p21.2-21.3.
PN US2003224514-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 5.1%; Score 36.2; DB 12; Length 104245;
Best Local Similarity 56.2%; Pred. No. 3.1e+02;
RESULT 1453
ID ADL34706 standard; DNA; 104245 BP.
DE Human PPAR-delta DNA fragment SEQ ID 4.
PN US2004063129-A1.
PD 01-APR-2004.
PA (GAAR/) GAARDE W.
PA (FREI/) FREIER S M.
PA (WATT/) WATT A T.
Query Match 5.1%; Score 36.2; DB 12; Length 104245;
Best Local Similarity 56.2%; Pred. No. 3.1e+02;
RESULT 1454
Query Match 5.1%; Score 36.2; DB 2; Length 110000;
Best Local Similarity 45.8%; Pred. No. 3.2e+02;
RESULT 1455
Query Match 5.1%; Score 36.2; DB 6; Length 110000;
Best Local Similarity 50.3%; Pred. No. 3.2e+02;
RESULT 1456
ID ADK16049 standard; DNA; 490885 BP.
DE Nancarchaeum equitans genome.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.1%; Score 36.2; DB 12; Length 110000;
Best Local Similarity 48.4%; Pred. No. 3.2e+02;
RESULT 1457
Query Match 5.1%; Score 36.2; DB 12; Length 110000;
Best Local Similarity 48.4%; Pred. No. 3.2e+02;
RESULT 1458
Query Match 5.1%; Score 36.2; DB 12; Length 110000;
Best Local Similarity 50.3%; Pred. No. 3.2e+02;
RESULT 1459
Query Match 5.1%; Score 36.2; DB 12; Length 110000;
Best Local Similarity 50.3%; Pred. No. 3.2e+02;
RESULT 1460
Query Match 5.1%; Score 36.2; DB 12; Length 110000;
Best Local Similarity 50.3%; Pred. No. 3.2e+02;
RESULT 1461
ID ADP13586 standard; DNA; 170245 BP.
DE Renal cell carcinoma differentially expressed gene #322.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLOW/) SLOWI D K.
Query Match 5.1%; Score 36.2; DB 12; Length 170245;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;

RESULT 1462
ID ACF62741 standard; DNA; 189013 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:669.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.1%; Score 36.2; DB 8; Length 189013;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 1463
ID ADB20856 standard; DNA; 189013 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:669.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.1%; Score 36.2; DB 8; Length 189013;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 1464
ID ADB87945 standard; DNA; 189013 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:669.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.1%; Score 36.2; DB 10; Length 189013;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 1465
ID ADB96928 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.1%; Score 36.2; DB 10; Length 189013;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 1466
ID ADB92119 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.1%; Score 36.2; DB 10; Length 189013;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 1467
ID ABX49849 standard; cDNA; 375 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #15014.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.0%; Score 36; DB 8; Length 375;
Best Local Similarity 45.2%; Pred. No. 1.1e+02;
RESULT 1468
ID ABX46053 standard; cDNA; 424 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11218.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.0%; Score 36; DB 8; Length 424;
Best Local Similarity 49.0%; Pred. No. 1.1e+02;
RESULT 1469
ID ABX47746 standard; cDNA; 442 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12911.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.0%; Score 36; DB 8; Length 442;
Best Local Similarity 53.6%; Pred. No. 1.1e+02;

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RESULT 1470
ID ADL44075 standard; DNA; 469 BP.
DE Human ovarian cancer DNA marker #17965.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.0%; Score 36; DB 5; Length 469;
Best Local Similarity 55.2%; Pred. No. 1.1e+02;
RESULT 1471
ID ARN64010 standard; cDNA; 480 BP.
DE Human cancer related polynucleotide SEQ ID NO 3977.
FN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 36; DB 6; Length 480;
Best Local Similarity 49.0%; Pred. No. 1.1e+02;
RESULT 1472
ID ABL34634 standard; DNA; 1984 BP.
DE Human metastasis associated gene SEQ ID NO: 187.
FN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 1984;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1473
ID ABL70613 standard; DNA; 1984 BP.
DE Chemically treated cell signalling DNA sequence#252.
FN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 1984;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1474
ID ADB54175 standard; DNA; 1984 BP.
DE Pretreated genomic DNA region 99.
FN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 10; Length 1984;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1475
ID ADE37766 standard; DNA; 1984 BP.
DE Human chemically treated calcitonin nucleotide sequence SEQ ID NO:12.
FN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 10; Length 1984;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1476
ID AA252560 standard; cDNA; 2262 BP.
DE Human secreted protein clone yer7_1 nucleotide sequence SEQ ID NO:171.
FN WO9958642-A2.
PD 18-NOV-1999.
PA (GEMY) GENETICS INST INC.
Query Match 5.0%; Score 36; DB 3; Length 2262;
Best Local Similarity 47.4%; Pred. No. 1.6e+02;
RESULT 1477
ID AAS31262 standard; cDNA; 2645 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.
FN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 36; DB 4; Length 2645;
Best Local Similarity 52.7%; Pred. No. 1.6e+02;
RESULT 1478
ID ABQ66586 standard; cDNA; 2645 BP.
DE Human polynucleotide SEQ ID NO 76.
FN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.0%; Score 36; DB 8; Length 3664;
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
RESULT 1479
ID ADL44075 standard; cDNA; 2645 BP.
DE Human CDNA from extracellular matrix gene 66.
FN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 36; DB 10; Length 2645;
Best Local Similarity 52.7%; Pred. No. 1.6e+02;
RESULT 1480
ID AAH17823 standard; cDNA; 2729 BP.
DE Human CDNA sequence SEQ ID NO:17494.
FN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.0%; Score 36; DB 4; Length 2729;
Best Local Similarity 49.5%; Pred. No. 1.6e+02;
RESULT 1481
ID ADO20361 standard; cDNA; 2729 BP.
DE Human PRO polynucleotide #628.
FN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 36; DB 12; Length 2729;
Best Local Similarity 49.5%; Pred. No. 1.6e+02;
RESULT 1482
ID AAS46319 standard; DNA; 2865 BP.
DE Tumour suppressor gene derived chemically modified sequence #41.
FN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 4; Length 2865;
Best Local Similarity 49.0%; Pred. No. 1.6e+02;
RESULT 1483
ID ABN80050 standard; DNA; 2865 BP.
DE Human chemically modified disease associated gene SEQ ID NO 67.
FN WO20020927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 2865;
Best Local Similarity 49.0%; Pred. No. 1.6e+02;
RESULT 1484
ID ABZ36285 standard; cDNA; 3196 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 449.
FN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 36; DB 8; Length 3196;
Best Local Similarity 49.5%; Pred. No. 1.7e+02;
RESULT 1485
ID AAH54139 standard; DNA; 3335 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3503.
FN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.0%; Score 36; DB 4; Length 3335;
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
RESULT 1486
ID AAH54890 standard; DNA; 3465 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4254.
FN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.0%; Score 36; DB 4; Length 3465;
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
RESULT 1487
ID ACF62820 standard; DNA; 3664 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:69.
FN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 8; Length 3664;
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Best Local Similarity 43.1%; Pred. No. 1.7e+02;
RESULT 1488
ID ABL210128 standard; DNA; 3664 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #268.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 8; Length 3664;
Best Local Similarity 43.1%; Pred. No. 1.7e+02;
RESULT 1489
ID ABV27603 standard; cDNA; 4085 BP.
DE Human prostate expression marker cDNA 27594.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.0%; Score 36; DB 5; Length 4085;
Best Local Similarity 49.5%; Pred. No. 1.8e+02;
RESULT 1490
ID ABV21780 standard; cDNA; 4085 BP.
DE Human prostate expression marker cDNA 21771.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.0%; Score 36; DB 5; Length 4085;
Best Local Similarity 49.5%; Pred. No. 1.8e+02;
RESULT 1491
ID ABQ75107 standard; cDNA; 4985 BP.
DE Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.
PN WO200259274-A2.
PD 01-AUG-2002.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.0%; Score 36; DB 6; Length 4985;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
RESULT 1492
ID ACF79720 standard; DNA; 4985 BP.
DE Mosquito odorant receptor 2 genomic DNA.
PN WO2003076590-A2.
PD 18-SEP-2003.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.0%; Score 36; DB 10; Length 4985;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
RESULT 1493
ID ABL32901 standard; DNA; 5204 BP.
DE Human immune system associated gene SEQ ID NO: 874.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 5204;
Best Local Similarity 51.2%; Pred. No. 1.9e+02;
RESULT 1494
ID ABL33772 standard; DNA; 5666 BP.
DE Human immune system associated gene SEQ ID NO: 1745.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 5666;
Best Local Similarity 48.2%; Pred. No. 1.9e+02;
RESULT 1495
ID ABL33520 standard; DNA; 5754 BP.
DE Human immune system associated gene SEQ ID NO: 1493.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 5754;
Best Local Similarity 45.9%; Pred. No. 1.9e+02;
RESULT 1496
ID ABL33565 standard; DNA; 6061 BP.
DE Human immune system associated gene SEQ ID NO: 1538.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 6061;
Best Local Similarity 50.6%; Pred. No. 1.9e+02;

RESULT 1497
ID ABL70594 standard; DNA; 6061 BP.
DE Chemically treated cell signalling DNA sequence complementary to#242.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 6061;
Best Local Similarity 50.6%; Pred. No. 1.9e+02;
RESULT 1498
ID AAS61311 standard; DNA; 6061 BP.
DE Human gene regulation-associated gene oligonucleotide #266.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 6061;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 1499
ID AEN80089 standard; DNA; 6067 BP.
DE Human chemically modified disease associated gene SEQ ID NO 106.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 6067;
Best Local Similarity 51.2%; Pred. No. 1.9e+02;
RESULT 1500
ID ABL32820 standard; DNA; 6123 BP.
DE Human immune system associated gene SEQ ID NO: 793.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 36; DB 6; Length 6123;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;

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OM nucleic - nucleic search, using sw model

Run on: December 1, 2004, 21:05:55 ; Search time 100.514 Seconds
(without alignments)
5041.999 Million cell updates/sec

Perfect score: 713
Sequence: 1 aaatatcatctattatca.....tggtccaaggaaaaaaa 713

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	83	11.6	85	4	US-09-513-999C-28212
3	77.6	10.9	2298	3	US-08-772-440-1
4	75.2	10.5	528	3	US-08-772-440-7
5	46.6	6.5	7218	1	US-08-232-463-14
6	45.2	6.3	832	4	US-09-621-976-2813
7	45.2	6.3	1141	4	US-09-806-708B-22
8	45.2	6.3	1141	4	US-09-806-708B-22
9	44	6.2	640681	4	US-09-790-988-1
10	42.8	6.0	1055	4	US-09-806-708B-23
11	40.4	5.7	5847	4	US-09-920-672-10
12	39.6	5.6	20674	4	US-09-641-638-651
13	39.6	5.6	20674	4	US-10-170-097-651
14	39.2	5.5	8920	2	US-08-446-855A-1
15	39.2	5.5	8920	3	US-09-150-741-1
16	38.6	5.4	4526	1	US-07-855-412B-4
17	38.6	5.4	4526	2	US-08-308-887A-4
18	38.6	5.4	4526	3	US-08-881-094-4
19	38.4	5.4	58407	4	US-08-916-421B-2
20	38.4	5.4	58407	4	US-09-602-708-2
21	38	5.3	19233	4	US-10-204-708-11
22	37.8	5.3	1537	4	US-09-626-959D-2
23	37.8	5.3	3953	4	US-09-799-451-546
24	37.8	5.3	202001	4	US-09-734-674-3
25	37.6	5.3	1335	4	US-09-543-681A-1450
26	37.4	5.2	275	4	US-08-585-593A-42
27	37.4	5.2	361	3	US-09-018-584A-9
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Sequence 3, Appl
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Sequence 17, Appl
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Sequence 8, Appl
Sequence 11, Appl
Sequence 9, Appl
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Sequence 10369, A
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Sequence 13, Appl
Sequence 5, Appl
Sequence 27, Appl
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Sequence 1949, Ap
Sequence 1464, Ap
Sequence 83, Appl
Sequence 3452, Ap
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Sequence 40, Appl
Sequence 14, Appl
Sequence 171, App
Sequence 3503, Ap
Sequence 4254, Ap
Sequence 11, Appl
Sequence 86, Appl
Sequence 3, Appl
Sequence 12468, A
Sequence 111, App
Sequence 2, Appl
Sequence 110, App
Sequence 110, App
Sequence 110, App
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Sequence 110, App
Sequence 110, App
Sequence 2, Appl
Sequence 360, App
Sequence 64, Appl
Sequence 69, Appl
Sequence 7, Appl
Sequence 1, Appl
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Sequence 1, Appl
Sequence 595, App
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2459, Ap
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 2293, Ap
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Sequence 11, Appl
Sequence 11, Appl

c 102	35	4.9	6317	4	US-10-204-708-11	Sequence 11, Appl	c 175	33.8	4.7	7452	5	PCT-US94-07644A-1	Sequence 1, Appl
c 103	35	4.9	72604	3	US-09-268-992-7	Sequence 7, Appl	176	33.8	4.7	7664	4	US-10-204-708-84	Sequence 84, Appl
c 104	35	4.9	72604	3	US-09-657-474-7	Sequence 7, Appl	c 177	33.8	4.7	12047	2	US-09-022-461-1	Sequence 1, Appl
c 105	35	4.9	90541	4	US-09-759-359A-3	Sequence 3, Appl	c 178	33.8	4.7	12047	4	US-09-033-556-3	Sequence 3, Appl
c 106	35	4.9	90541	4	US-10-207-973-3	Sequence 3, Appl	c 179	33.8	4.7	12047	4	US-09-474-899-11	Sequence 11, Appl
c 107	34.8	4.9	334	2	US-08-623-906A-9	Sequence 9, Appl	c 180	33.8	4.7	12047	4	US-09-151-376-3	Sequence 3, Appl
c 108	34.8	4.9	348	2	US-08-623-906A-14	Sequence 14, Appl	c 181	33.8	4.7	12047	4	US-09-814-351-11	Sequence 11, Appl
c 109	34.8	4.9	1291	4	US-09-685-232-6	Sequence 6, Appl	c 182	33.8	4.7	45546	3	US-09-146-053-6	Sequence 6, Appl
c 110	34.8	4.9	1442	4	US-09-270-767-6007	Sequence 6007, Ap	c 183	33.6	4.7	333	3	US-09-018-584A-27	Sequence 27, Appl
c 111	34.8	4.9	1442	4	US-09-270-767-21289	Sequence 21289, A	c 184	33.6	4.7	333	3	US-08-784-423-27	Sequence 27, Appl
c 112	34.8	4.9	3005	4	US-09-710-279-4096	Sequence 4096, Ap	c 185	33.6	4.7	615	3	US-08-998-416-186	Sequence 186, App
c 113	34.8	4.9	5690	4	US-09-773-416-13	Sequence 13, Appl	c 186	33.6	4.7	1000	3	US-09-018-584A-33	Sequence 33, Appl
c 114	34.8	4.9	1664976	4	US-09-916-4218-1	Sequence 1, Appl	c 187	33.6	4.7	1000	4	US-09-784-423-33	Sequence 33, Appl
c 115	34.8	4.9	1664976	4	US-08-632-570-1	Sequence 1, Appl	c 188	33.6	4.7	1707	4	US-08-311-021-51	Sequence 51, Appl
c 116	34.6	4.9	396	4	US-09-640-173-16	Sequence 16, Appl	c 189	33.6	4.7	2447	2	US-09-014-969-14	Sequence 14, Appl
c 117	34.6	4.9	396	4	US-09-713-550-16	Sequence 16, Appl	c 190	33.6	4.7	5501	4	US-10-204-708-37	Sequence 37, Appl
c 118	34.6	4.9	396	4	US-09-825-294-16	Sequence 16, Appl	c 191	33.6	4.7	6306	4	US-10-204-708-50	Sequence 50, Appl
c 119	34.6	4.9	396	4	US-09-970-966-16	Sequence 16, Appl	c 192	33.6	4.7	6583	4	US-10-204-708-26	Sequence 26, Appl
c 120	34.6	4.9	454	2	US-08-623-906A-6	Sequence 6, Appl	c 193	33.6	4.7	6656	4	US-10-204-708-75	Sequence 75, Appl
c 121	34.6	4.9	1083	4	US-09-540-236-109	Sequence 109, App	c 194	33.6	4.7	44453	3	US-09-146-053-5	Sequence 5, Appl
c 122	34.6	4.9	5562	4	US-10-204-708-63	Sequence 63, Appl	c 195	33.6	4.7	64467	4	US-09-803-671B-3	Sequence 3, Appl
c 123	34.6	4.9	5852	1	US-07-867-106-2	Sequence 2, Appl	c 196	33.6	4.7	202001	4	US-09-734-674-3	Sequence 3, Appl
c 124	34.6	4.9	31147	4	US-09-596-002-25	Sequence 25, Appl	c 197	33.4	4.7	362	3	US-09-018-584A-11	Sequence 11, Appl
c 125	34.6	4.9	319608	4	US-09-539-333D-1	Sequence 1, Appl	c 198	33.4	4.7	362	4	US-09-784-423-11	Sequence 11, Appl
c 126	34.6	4.9	319608	4	US-09-679-409-1	Sequence 1, Appl	c 199	33.4	4.7	459	4	US-09-270-767-8010	Sequence 8010, Ap
c 127	34.4	4.8	1228	6	5187133-5	Patent No. 5187133	c 200	33.4	4.7	459	4	US-09-270-767-23292	Sequence 23292, A
c 128	34.4	4.8	1228	6	5220013-5	Patent No. 5220013	c 201	33.4	4.7	507	4	US-09-621-976-2506	Sequence 2506, Ap
c 129	34.4	4.8	1228	6	5223482-5	Patent No. 5223482	c 202	33.4	4.7	1111	4	US-08-956-171E-756	Sequence 756, App
c 130	34.4	4.8	4673	5	PCT-US92-00018-1	Sequence 1, Appl	c 203	33.4	4.7	1111	4	US-08-781-986A-756	Sequence 756, App
c 131	34.4	4.8	4673	5	PCT-US92-00018-1	Sequence 1, Appl	c 204	33.4	4.7	1559	3	US-09-013-095A-7	Sequence 7, Appl
c 132	34.4	4.8	20966	4	US-09-776-976-7	Sequence 7, Appl	c 205	33.4	4.7	1719	3	US-09-543-681A-2653	Sequence 2653, Ap
c 133	34.4	4.8	20966	4	US-09-909-547-7	Sequence 7, Appl	c 206	33.4	4.7	1826	3	US-09-286-691-11	Sequence 11, Appl
c 134	34.4	4.8	20966	4	US-09-569-852B-1	Sequence 1, Appl	c 207	33.4	4.7	1826	3	US-07-715-751B-2	Sequence 2, Appl
c 135	34.4	4.8	580073	4	US-08-545-528D-1	Sequence 1, Appl	c 208	33.4	4.7	1939	1	US-09-248-796A-6178	Sequence 6178, Ap
c 136	34.4	4.8	640681	4	US-09-790-988-1	Sequence 1, Appl	c 209	33.4	4.7	2433	4	US-09-248-796A-2886	Sequence 2886, Ap
c 137	34.2	4.8	696	4	US-09-107-532A-1647	Sequence 1647, Ap	c 210	33.4	4.7	2454	4	US-09-710-279-3482	Sequence 3482, Ap
c 138	34.2	4.8	756	4	US-09-248-796A-10621	Sequence 10621, A	c 211	33.4	4.7	3116	4	US-09-710-279-3721	Sequence 3721, Ap
c 139	34.2	4.8	1321	4	US-09-461-325-104	Sequence 104, App	c 212	33.4	4.7	3228	4	US-09-579-664B-5	Sequence 5, Appl
c 140	34.2	4.8	1321	4	US-10-012-542-104	Sequence 104, App	c 213	33.4	4.7	3228	4	US-10-355-975A-5	Sequence 5, Appl
c 141	34.2	4.8	1321	4	US-10-115-123-104	Sequence 104, App	c 214	33.4	4.7	3228	4	US-09-823-038A-58	Sequence 58, Appl
c 142	34.2	4.8	1551	4	US-09-248-796A-549	Sequence 549, App	c 215	33.4	4.7	3503	4	US-08-961-527-208	Sequence 208, App
c 143	34.2	4.8	2311	4	US-09-800-729-66	Sequence 66, Appl	c 216	33.4	4.7	3503	4	US-08-961-527-208	Sequence 208, App
c 144	34.2	4.8	2394	4	US-09-800-729-33	Sequence 33, Appl	c 217	33.2	4.7	251	4	US-08-621-976-14639	Sequence 14639, A
c 145	34.2	4.8	2791	3	US-09-570-367C-1	Sequence 1, Appl	c 218	33.2	4.7	251	4	US-08-621-976-14639	Sequence 8, Appl
c 146	34.2	4.8	2791	3	US-09-515-524-1	Sequence 1, Appl	c 219	33.2	4.7	516	3	US-09-018-584A-24	Sequence 24, Appl
c 147	34.2	4.8	2791	3	US-09-934-634-1	Sequence 1, Appl	c 220	33.2	4.7	516	3	US-09-784-423-24	Sequence 24, Appl
c 148	34.2	4.8	3095	6	5231168-1	Patent No. 5231168	c 221	33.2	4.7	2373	3	US-08-975-762-45	Sequence 45, Appl
c 149	34.2	4.8	168174	4	US-10-071-411A-63	Sequence 63, Appl	c 222	33.2	4.7	2373	3	US-09-295-028-45	Sequence 45, Appl
c 150	34.2	4.8	168273	4	US-10-071-411A-2	Sequence 2, Appl	c 223	33.2	4.7	2373	3	US-09-106-582-45	Sequence 45, Appl
c 151	34.2	4.8	168575	4	US-09-426-290-1	Sequence 1, Appl	c 224	33.2	4.7	2373	3	US-09-159-469-45	Sequence 45, Appl
c 152	34.2	4.8	392000	4	US-10-027-983-11	Sequence 11, Appl	c 225	33.2	4.7	2373	4	US-09-693-542-45	Sequence 45, Appl
c 153	34	4.8	192	4	US-09-248-796A-7389	Sequence 7389, Ap	c 226	33.2	4.7	3709	4	US-09-270-767-26056	Sequence 26056, A
c 154	34	4.8	640	3	US-08-961-083-33	Sequence 33, Appl	c 227	33.2	4.7	4663	4	US-09-270-767-10617	Sequence 10617, A
c 155	34	4.8	640	3	US-09-536-784-33	Sequence 33, Appl	c 228	33.2	4.7	5360	4	US-10-204-708-66	Sequence 66, Appl
c 156	34	4.8	1359	4	US-09-248-796A-1541	Sequence 1541, Ap	c 229	33.2	4.7	6182	4	US-10-204-708-87	Sequence 87, Appl
c 157	34	4.8	1422	1	US-08-319-704-5	Sequence 5, Appl	c 230	33.2	4.7	90050	3	US-09-245-041-5	Sequence 5, Appl
c 158	34	4.8	1641	4	US-09-270-767-5483	Sequence 5483, Ap	c 231	33.2	4.7	90050	4	US-09-358-055B-5	Sequence 5, Appl
c 159	34	4.8	1641	4	US-09-270-767-20765	Sequence 20765, A	c 232	33.2	4.7	100848	4	US-09-893-238-5	Sequence 38, Appl
c 160	34	4.8	1911	4	US-09-248-796A-763	Sequence 763, App	c 233	33.2	4.7	100848	4	US-09-596-002-39	Sequence 17, Appl
c 161	34	4.8	2539	3	US-08-749-522-3	Sequence 3, Appl	c 234	33.2	4.7	176373	3	US-09-128-155-17	Sequence 758, App
c 162	34	4.8	3129	4	US-09-904-615-18	Sequence 18, Appl	c 235	33	4.6	402	4	US-08-956-171E-758	Sequence 758, App
c 163	34	4.8	4315	4	US-09-444-905-1	Sequence 1, Appl	c 236	33	4.6	402	4	US-08-781-986A-758	Sequence 12075, A
c 164	34	4.8	6583	4	US-10-204-708-26	Sequence 26, Appl	c 237	33	4.6	553	4	US-09-270-767-12075	Sequence 12075, A
c 165	34	4.8	11309	4	US-08-961-527-108	Sequence 108, App	c 238	33	4.6	884	4	US-09-270-767-27131	Sequence 27131, A
c 166	34	4.8	19124	2	US-08-487-826B-13	Sequence 13, Appl	c 239	33	4.6	911	4	US-09-270-767-11534	Sequence 11534, A
c 167	33.8	4.7	320	4	US-09-513-999C-34601	Sequence 34601, A	c 240	33	4.6	1566	3	US-09-134-001C-1453	Sequence 1453, Ap
c 168	33.8	4.7	443	4	US-09-513-999C-9917	Sequence 9917, Ap	c 241	33	4.6	1578	4	US-08-956-171E-216	Sequence 216, App
c 169	33.8	4.7	1179	1	US-08-336-778-3	Sequence 3, Appl	c 242	33	4.6	1578	4	US-08-781-986A-216	Sequence 216, App
c 170	33.8	4.7	3275	4	US-09-370-838-151	Sequence 151, App	c 243	33	4.6	1582	3	US-08-545-196B-12	Sequence 12, Appl
c 171	33.8	4.7	3275	4	US-09-854-133-151	Sequence 151, App	c 244	33	4.6	1582	3	US-08-545-196B-12	Sequence 12, Appl
c 172	33.8	4.7	5144	4	US-09-824-735-1	Sequence 1, Appl	c 245	33	4.6	1694	4	US-09-023-655-218	Sequence 218, App
c 173	33.8	4.7	7452	3	US-08-592-500-1	Sequence 1, Appl	c 246	33	4.6	4015	4	US-09-774-528-201	Sequence 201, App
c 174	33.8	4.7	7452	3	US-08-195-006-1	Sequence 1, Appl	c 247	33	4.6	6156	4	US-10-204-708-59	Sequence 59, Appl

248	33	4.6	6306	4	US-10-204-708-50	Sequence 50, Appl	321	32.4	4.5	450	3	US-09-020-818-4	Sequence 4, Appl
249	33	4.6	6669	4	US-10-204-708-6	Sequence 6, Appl	322	32.4	4.5	450	3	US-08-307-740-4	Sequence 4, Appl
C 250	33	4.6	9844	3	US-08-462-437-30	Sequence 30, Appl	323	32.4	4.5	450	4	US-08-397-467-4	Sequence 4, Appl
C 251	33	4.6	13104	3	US-08-256-799-4	Sequence 4, Appl	324	32.4	4.5	450	4	US-08-399-023-28	Sequence 28, Appl
C 252	33	4.6	13104	3	US-08-462-437-4	Sequence 4, Appl	325	32.4	4.5	450	5	PCT-US94-07072-2	Sequence 2, Appl
C 253	33	4.6	51259	3	US-08-781-891-209	Sequence 209, App	326	32.4	4.5	475	2	US-08-623-906A-20	Sequence 20, Appl
C 254	33	4.6	51259	4	US-09-618-166-209	Sequence 209, App	327	32.4	4.5	717	4	US-09-496-445-3	Sequence 3, Appl
C 255	33	4.6	51952	3	US-08-947-823-1	Sequence 1, Appl	C 327	32.4	4.5	736	4	US-09-861-451A-73	Sequence 73, Appl
C 256	33	4.6	128779	4	US-09-437-855A-38	Sequence 38, Appl	C 328	32.4	4.5	883	4	US-09-714-767A-5	Sequence 5, Appl
257	32.8	4.6	556	4	US-09-270-767-9809	Sequence 9809, App	C 329	32.4	4.5	885	4	US-09-248-796A-1714	Sequence 130, App
258	32.8	4.6	556	4	US-09-270-767-25091	Sequence 25091, A	C 330	32.4	4.5	1020	4	US-09-248-796A-5496	Sequence 1714, App
259	32.8	4.6	912	4	US-09-495-406-16	Sequence 16, Appl	C 331	32.4	4.5	1020	4	US-09-248-796A-817	Sequence 5496, App
260	32.8	4.6	912	4	US-09-816-028A-28	Sequence 28, Appl	C 332	32.4	4.5	1119	4	US-09-270-767-31484	Sequence 817, App
C 261	32.8	4.6	1014	4	US-09-303-162-28	Sequence 28, Appl	C 333	32.4	4.5	1259	4	US-09-270-767-31484	Sequence 31484, A
C 262	32.8	4.6	1014	4	US-09-248-796A-9456	Sequence 9456, App	C 334	32.4	4.5	1732	4	US-09-270-767-15462	Sequence 15162, A
C 263	32.8	4.6	1631	3	US-09-118-319-1	Sequence 1, Appl	C 335	32.4	4.5	1937	3	US-09-276-531-130	Sequence 130, App
C 264	32.8	4.6	2185	4	US-09-270-767-11027	Sequence 11027, A	C 336	32.4	4.5	2479	3	US-09-050-863-4	Sequence 4, Appl
C 265	32.8	4.6	2328	4	US-09-601-198-49	Sequence 49, Appl	C 337	32.4	4.5	2479	3	US-09-359-081-4	Sequence 4, Appl
C 266	32.8	4.6	2476	4	US-10-140-002-489	Sequence 489, App	C 338	32.4	4.5	2695	4	US-09-706-197-3	Sequence 3, Appl
C 267	32.8	4.6	2559	4	US-09-569-098A-109	Sequence 109, App	C 339	32.4	4.5	2712	4	US-09-976-594-374	Sequence 374, App
C 268	32.8	4.6	2632	4	US-09-774-528-279	Sequence 279, App	C 340	32.4	4.5	2732	4	US-08-394-689C-8	Sequence 8, Appl
C 269	32.8	4.6	2913	4	US-09-248-796A-2088	Sequence 2088, App	C 341	32.4	4.5	3218	4	US-09-496-445-4	Sequence 4, Appl
C 270	32.8	4.6	4866	1	US-08-110-158-5	Sequence 5, Appl	C 342	32.4	4.5	3318	4	US-08-169-613A-1	Sequence 1, Appl
C 271	32.8	4.6	5501	4	US-10-204-708-38	Sequence 38, Appl	C 343	32.4	4.5	3944	1	US-07-678-408A-1	Sequence 1, Appl
C 272	32.8	4.6	5666	4	US-10-204-708-29	Sequence 29, Appl	C 344	32.4	4.5	4059	5	PCT-US94-06069-2	Sequence 2, Appl
C 273	32.8	4.6	6326	4	US-10-204-708-57	Sequence 57, Appl	C 345	32.4	4.5	4059	5	US-08-564-313-2	Sequence 2, Appl
C 274	32.8	4.6	6769	1	US-08-480-784-20	Sequence 20, Appl	C 346	32.4	4.5	4069	4	US-09-170-496B-287	Sequence 287, App
C 275	32.8	4.6	6769	1	US-08-483-553-20	Sequence 20, Appl	C 347	32.4	4.5	4069	4	US-09-170-496B-288	Sequence 288, App
C 276	32.8	4.6	6769	1	US-08-487-002-20	Sequence 20, Appl	C 348	32.4	4.5	4069	4	US-09-364-425B-52	Sequence 52, Appl
C 277	32.8	4.6	6769	1	US-08-483-554B-20	Sequence 20, Appl	C 349	32.4	4.5	4069	4	US-09-364-425B-53	Sequence 53, Appl
C 278	32.8	4.6	6769	1	US-08-488-011B-20	Sequence 20, Appl	C 350	32.4	4.5	4273	3	US-08-795-430-3	Sequence 3, Appl
C 279	32.8	4.6	6769	1	US-08-850-727-20	Sequence 20, Appl	C 351	32.4	4.5	4273	3	US-09-355-700-3	Sequence 3, Appl
C 280	32.8	4.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 352	32.4	4.5	4273	4	US-08-601-132-37	Sequence 37, Appl
C 281	32.8	4.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 353	32.4	4.5	4273	4	US-08-671-573B-37	Sequence 37, Appl
C 282	32.8	4.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 354	32.4	4.5	4273	4	US-09-631-092B-37	Sequence 37, Appl
C 283	32.8	4.6	11049	4	US-10-204-708-24	Sequence 24, Appl	C 355	32.4	4.5	4503	3	US-08-675-566-7	Sequence 7, Appl
C 284	32.8	4.6	11131	4	US-10-204-708-27	Sequence 27, Appl	C 356	32.4	4.5	4810	1	US-08-188-281B-3	Sequence 3, Appl
C 285	32.8	4.6	19233	3	US-10-204-708-46	Sequence 46, Appl	C 357	32.4	4.5	4810	2	US-08-453-552-7	Sequence 7, Appl
C 286	32.8	4.6	50000	3	US-09-146-053-4	Sequence 4, Appl	C 358	32.4	4.5	4810	2	US-08-710-637-7	Sequence 7, Appl
C 287	32.8	4.6	279	2	US-08-623-906A-3	Sequence 3, Appl	C 359	32.4	4.5	4810	5	PCT-US93-00907-7	Sequence 7, Appl
C 288	32.6	4.6	303	4	US-09-248-796A-12862	Sequence 12862, A	C 360	32.4	4.5	4810	5	PCT-US94-07280-3	Sequence 3, Appl
C 289	32.6	4.6	376	2	US-08-623-906A-18	Sequence 18, Appl	C 361	32.4	4.5	4810	5	PCT-US95-01087-3	Sequence 3, Appl
C 290	32.6	4.6	783	4	US-09-248-796A-2644	Sequence 2644, App	C 362	32.4	4.5	5125	1	US-08-453-552-11	Sequence 11, Appl
C 291	32.6	4.6	851	4	US-09-270-767-8286	Sequence 8286, App	C 363	32.4	4.5	5125	2	US-08-710-637-11	Sequence 11, Appl
C 292	32.6	4.6	881	4	US-09-270-767-23568	Sequence 23568, App	C 364	32.4	4.5	5125	5	PCT-US93-00907-11	Sequence 11, Appl
C 293	32.6	4.6	903	4	US-09-270-767-23568	Sequence 23568, A	C 365	32.4	4.5	5157	2	US-08-474-169-7	Sequence 7, Appl
C 294	32.6	4.6	1107	4	US-09-513-999C-12345	Sequence 12345, A	C 366	32.4	4.5	5178	2	US-08-474-169-2	Sequence 2, Appl
C 295	32.6	4.6	1117	3	US-09-247-373B-33	Sequence 33, Appl	C 367	32.4	4.5	5183	3	US-09-039-555B-18	Sequence 18, Appl
C 296	32.6	4.6	1197	4	US-09-248-796A-1264	Sequence 1264, App	C 368	32.4	4.5	5215	4	US-09-173-053-8	Sequence 8, Appl
C 297	32.6	4.6	1848	4	US-09-248-796A-503	Sequence 503, App	C 369	32.4	4.5	5243	2	US-08-414-335-2	Sequence 2, Appl
C 298	32.6	4.6	2175	4	US-09-710-279-967	Sequence 967, App	C 370	32.4	4.5	5276	4	US-08-994-689C-9	Sequence 9, Appl
C 299	32.6	4.6	2304	4	US-08-356-171B-432	Sequence 432, App	C 371	32.4	4.5	5323	1	US-08-453-552-9	Sequence 9, Appl
C 300	32.6	4.6	2304	4	US-08-781-986A-432	Sequence 432, App	C 372	32.4	4.5	5323	5	PCT-US93-00907-9	Sequence 9, Appl
C 301	32.6	4.6	3001	4	US-09-539-333D-198	Sequence 198, App	C 373	32.4	4.5	5337	5	US-08-784-512-4	Sequence 4, Appl
C 302	32.6	4.6	3073	4	US-09-710-279-3606	Sequence 3606, App	C 374	32.4	4.5	5337	3	US-08-862-431-29	Sequence 29, Appl
C 303	32.6	4.6	3124	4	US-09-710-279-4336	Sequence 4336, App	C 375	32.4	4.5	5337	3	US-08-536-559A-2	Sequence 2, Appl
C 304	32.6	4.6	3138	1	US-07-867-106-4	Sequence 4, Appl	C 376	32.4	4.5	5789	3	US-08-862-431-27	Sequence 27, Appl
C 305	32.6	4.6	4136	4	US-09-688-188B-19	Sequence 19, Appl	C 377	32.4	4.5	5791	3	US-08-862-431-31	Sequence 31, Appl
C 306	32.6	4.6	4196	4	US-09-291-417D-19	Sequence 19, Appl	C 378	32.4	4.5	5793	3	US-08-862-431-29	Sequence 29, Appl
C 307	32.6	4.6	4216	4	US-09-710-279-3544	Sequence 3544, App	C 379	32.4	4.5	5793	3	US-08-862-431-30	Sequence 30, Appl
C 308	32.6	4.6	11049	4	US-10-204-708-23	Sequence 23, Appl	C 380	32.4	4.5	5818	2	US-08-536-559A-3	Sequence 3, Appl
C 309	32.6	4.6	13011	2	US-08-791-849A-14	Sequence 14, Appl	C 381	32.4	4.5	5819	2	US-08-536-559A-2	Sequence 2, Appl
C 310	32.6	4.6	16595	3	US-09-146-053-7	Sequence 7, Appl	C 382	32.4	4.5	5819	3	US-08-862-431-27	Sequence 27, Appl
C 311	32.6	4.6	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 383	32.4	4.5	5819	3	US-08-862-431-31	Sequence 31, Appl
C 312	32.6	4.6	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 384	32.4	4.5	5825	4	US-08-809-513A-7	Sequence 7, Appl
C 313	32.6	4.6	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 385	32.4	4.5	5916	4	US-09-826-630-9	Sequence 9, Appl
C 314	32.6	4.6	1830121	4	US-09-557-884-1	Sequence 1, Appl	C 386	32.4	4.5	5938	2	US-08-536-559A-4	Sequence 4, Appl
C 315	32.6	4.6	1830121	4	US-09-557-884-1	Sequence 1, Appl	C 387	32.4	4.5	6092	2	US-08-536-559A-1	Sequence 1, Appl
C 316	32.6	4.6	1830121	4	US-10-329-960-1	Sequence 1, Appl	C 388	32.4	4.5	6092	3	US-08-862-431-26	Sequence 26, Appl
C 317	32.4	4.5	450	1	US-08-090-523-28	Sequence 28, Appl	C 389	32.4	4.5	6107	4	US-09-482-273-47	Sequence 47, Appl
C 318	32.4	4.5	450	1	US-08-398-627-28	Sequence 28, Appl	C 390	32.4	4.5	6151	5	PCT-US91-02954-12	Sequence 12, Appl
C 319	32.4	4.5	450	1	US-08-406-857-2	Sequence 2, Appl	C 391	32.4	4.5	6206	3	US-08-474-169-3	Sequence 3, Appl
C 320	32.4	4.5	450	1	US-08-596-024-4	Sequence 4, Appl	C 392	32.4	4.5	6420	2	US-08-374-483-1	Sequence 1, Appl
							C 393	32.4	4.5	6601	1	US-08-232-463-15	Sequence 15, Appl

C 394	32.4	4.5	6623	2	US-08-244-434-36	Sequence 36, Appl	C 467	32.2	4.5	1423	4	US-09-461-325-51	Sequence 51, Appl
C 395	32.4	4.5	6630	2	US-08-244-434-37	Sequence 37, Appl	C 468	32.2	4.5	1423	4	US-10-042-542-51	Sequence 51, Appl
C 396	32.4	4.5	6671	1	US-08-280-443-1	Sequence 1, Appl	C 469	32.2	4.5	1423	4	US-10-115-123-51	Sequence 51, Appl
C 397	32.4	4.5	6671	1	US-08-457-459-1	Sequence 1, Appl	C 470	32.2	4.5	1767	4	US-09-248-736A-6736	Sequence 6736, Ap
C 398	32.4	4.5	6671	1	US-08-555-678-1	Sequence 1, Appl	C 471	32.2	4.5	1978	1	US-07-753-520B-2	Sequence 2, Appl
C 399	32.4	4.5	6671	5	PCT-US95-02275-1	Sequence 1, Appl	C 472	32.2	4.5	2536	2	US-09-027-013-2	Sequence 2, Appl
C 400	32.4	4.5	7463	2	US-08-715-808-13	Sequence 13, Appl	C 473	32.2	4.5	2536	3	US-09-244-233-2	Sequence 2, Appl
C 401	32.4	4.5	7731	4	US-09-301-593-29	Sequence 29, Appl	C 474	32.2	4.5	3709	4	US-09-270-767-26056	Sequence 26056, A
C 402	32.4	4.5	7731	4	US-09-301-593-42	Sequence 42, Appl	C 475	32.2	4.5	4064	4	US-09-873-737A-3	Sequence 3, Appl
C 403	32.4	4.5	7892	2	US-07-916-098A-40	Sequence 40, Appl	C 476	32.2	4.5	4663	4	US-09-270-767-10617	Sequence 10617, A
C 404	32.4	4.5	7892	2	US-07-916-098A-40	Sequence 40, Appl	C 477	32.2	4.5	4663	3	US-09-392-184-1	Sequence 1, Appl
C 405	32.4	4.5	8068	4	US-09-301-593-27	Sequence 27, Appl	C 478	32.2	4.5	4858	3	US-08-956-171E-1	Sequence 1, Appl
C 406	32.4	4.5	8068	4	US-09-301-593-35	Sequence 35, Appl	C 479	32.2	4.5	5895	4	US-08-781-986A-1	Sequence 1, Appl
C 407	32.4	4.5	8225	3	US-08-793-618-1	Sequence 1, Appl	C 480	32.2	4.5	5895	4	US-09-636-215-705	Sequence 705, App
C 408	32.4	4.5	8225	3	US-09-794-431-1	Sequence 1, Appl	C 481	32.2	4.5	5895	4	US-09-685-166A-705	Sequence 705, App
C 409	32.4	4.5	8591	1	US-08-462-859A-6	Sequence 6, Appl	C 482	32.2	4.5	6976	4	US-03-679-426-705	Sequence 80, Appl
C 410	32.4	4.5	8591	1	US-08-462-859A-8	Sequence 8, Appl	C 483	32.2	4.5	6976	4	US-10-204-708-80	Sequence 3, Appl
C 411	32.4	4.5	8591	1	US-08-123-659A-6	Sequence 6, Appl	C 484	32.2	4.5	8961	1	US-07-753-520B-3	Sequence 3, Appl
C 412	32.4	4.5	8591	1	US-08-123-659A-8	Sequence 8, Appl	C 485	32.2	4.5	9115	1	US-08-956-171E-37	Sequence 37, Appl
C 413	32.4	4.5	8591	1	US-08-464-247A-6	Sequence 6, Appl	C 486	32.2	4.5	9834	4	US-08-781-986A-3	Sequence 37, Appl
C 414	32.4	4.5	8591	1	US-08-464-247A-8	Sequence 8, Appl	C 487	32.2	4.5	9834	4	US-08-306-691B-19	Sequence 19, Appl
C 415	32.4	4.5	8591	1	US-08-464-248A-6	Sequence 6, Appl	C 488	32.2	4.5	35100	5	PCT-US93-06251-19	Sequence 1, Appl
C 416	32.4	4.5	8591	1	US-08-464-248A-8	Sequence 8, Appl	C 489	32.2	4.5	35100	5	PCT-US93-06251-19	Sequence 1, Appl
C 417	32.4	4.5	8614	3	US-09-247-352-5	Sequence 5, Appl	C 490	32.2	4.5	72928	3	US-09-009-913-1	Sequence 3, Appl
C 418	32.4	4.5	8614	3	US-09-247-352-5	Sequence 5, Appl	C 491	32	4.5	786431	4	US-09-751-389-3	Sequence 3, Appl
C 419	32.4	4.5	8858	3	US-09-247-352-6	Sequence 6, Appl	C 492	32	4.5	282	4	US-09-621-976-18648	Sequence 7, Appl
C 420	32.4	4.5	8858	4	US-09-466-635-6	Sequence 6, Appl	C 493	32	4.5	291	1	US-07-922-723A-7	Sequence 7, Appl
C 421	32.4	4.5	9434	4	US-08-566-921-22	Sequence 22, Appl	C 494	32	4.5	291	1	US-08-074-275-7	Sequence 7, Appl
C 422	32.4	4.5	9890	1	US-08-232-463-18	Sequence 18, Appl	C 495	32	4.5	291	1	US-08-480-366-7	Sequence 7, Appl
C 423	32.4	4.5	9916	1	US-08-232-463-17	Sequence 17, Appl	C 496	32	4.5	291	2	US-07-952-277A-7	Sequence 7, Appl
C 424	32.4	4.5	9917	1	US-08-232-463-16	Sequence 16, Appl	C 497	32	4.5	576	4	US-09-601-198-5	Sequence 5, Appl
C 425	32.4	4.5	10408	1	US-08-232-463-6	Sequence 6, Appl	C 498	32	4.5	591	3	US-09-134-001C-1812	Sequence 1812, Ap
C 426	32.4	4.5	10504	3	US-08-232-463-7	Sequence 7, Appl	C 499	32	4.5	660	1	US-07-991-867B-32	Sequence 32, Appl
C 427	32.4	4.5	10504	3	US-09-423-744A-19	Sequence 19, Appl	C 500	32	4.5	660	1	US-08-107-755A-32	Sequence 32, Appl
C 428	32.4	4.5	10580	1	US-08-196-259-1	Sequence 1, Appl	C 501	32	4.5	660	2	US-08-544-332-32	Sequence 32, Appl
C 429	32.4	4.5	10728	4	US-09-376-774-5	Sequence 5, Appl	C 502	32	4.5	660	4	US-09-370-861A-32	Sequence 32, Appl
C 430	32.4	4.5	11616	1	US-08-196-259-2	Sequence 2, Appl	C 503	32	4.5	897	4	US-09-314-701-51	Sequence 51, Appl
C 431	32.4	4.5	11958	3	US-08-927-317-7	Sequence 7, Appl	C 504	32	4.5	1065	3	US-09-512-342-13	Sequence 13, Appl
C 432	32.4	4.5	12143	3	US-09-423-744A-1	Sequence 1, Appl	C 505	32	4.5	1220	4	US-09-270-767-1667	Sequence 1667, Ap
C 433	32.4	4.5	1254	1	US-08-276-852-156	Sequence 156, App	C 506	32	4.5	1220	1	US-09-270-767-16949	Sequence 16949, A
C 434	32.4	4.5	1254	1	US-08-276-852-170	Sequence 170, App	C 507	32	4.5	1511	1	US-07-991-867B-8	Sequence 8, Appl
C 435	32.4	4.5	13254	1	US-08-899-575-156	Sequence 156, App	C 508	32	4.5	1511	2	US-08-107-755A-8	Sequence 8, Appl
C 436	32.4	4.5	13254	1	US-08-899-575-170	Sequence 170, App	C 509	32	4.5	1511	2	US-08-544-332-8	Sequence 8, Appl
C 437	32.4	4.5	13254	1	US-08-899-575-156	Sequence 156, App	C 510	32	4.5	1511	4	US-09-370-861A-8	Sequence 10914, A
C 438	32.4	4.5	13254	1	US-08-899-575-170	Sequence 170, App	C 511	32	4.5	1517	4	US-09-270-767-10914	Sequence 36, Appl
C 439	32.4	4.5	13254	5	PCT-US95-08743-156	Sequence 156, App	C 512	32	4.5	1771	4	US-09-944-457-36	Sequence 96, Appl
C 440	32.4	4.5	13254	5	PCT-US95-08743-170	Sequence 170, App	C 513	32	4.5	2022	2	US-08-505-486-96	Sequence 96, Appl
C 441	32.4	4.5	13910	3	US-09-263-933-1	Sequence 1, Appl	C 514	32	4.5	2022	3	US-08-801-028-96	Sequence 96, Appl
C 442	32.4	4.5	13910	3	US-09-263-933-8	Sequence 8, Appl	C 515	32	4.5	2022	3	US-09-340-154-96	Sequence 96, Appl
C 443	32.4	4.5	13910	3	US-09-263-933-15	Sequence 15, Appl	C 516	32	4.5	2022	4	US-09-482-611B-96	Sequence 96, Appl
C 444	32.4	4.5	13910	4	US-09-919-901-1	Sequence 1, Appl	C 517	32	4.5	2022	5	PCT-US95-09338-96	Sequence 96, Appl
C 445	32.4	4.5	13910	4	US-09-919-901-8	Sequence 8, Appl	C 518	32	4.5	2022	5	PCT-US95-09339-96	Sequence 96, Appl
C 446	32.4	4.5	13910	4	US-09-919-901-15	Sequence 15, Appl	C 519	32	4.5	2127	2	US-08-505-486-95	Sequence 95, Appl
C 447	32.4	4.5	13910	4	US-10-191-966-1	Sequence 1, Appl	C 520	32	4.5	2127	3	US-08-801-028-95	Sequence 95, Appl
C 448	32.4	4.5	13910	4	US-10-191-966-8	Sequence 8, Appl	C 521	32	4.5	2127	3	US-09-340-154-95	Sequence 95, Appl
C 449	32.4	4.5	13910	4	US-10-191-966-15	Sequence 15, Appl	C 522	32	4.5	2127	3	PCT-US95-09338-95	Sequence 95, Appl
C 450	32.4	4.5	17327	1	US-07-906-871-15	Sequence 15, Appl	C 523	32	4.5	2127	5	PCT-US95-09339-95	Sequence 95, Appl
C 451	32.4	4.5	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 524	32	4.5	2127	5	PCT-US95-09339-95	Sequence 1, Appl
C 452	32.4	4.5	193303	4	US-09-497-855A-44	Sequence 44, Appl	C 525	32	4.5	2632	4	US-09-867-915-1	Sequence 1, Appl
C 453	32.4	4.5	254366	4	US-09-822-871-3	Sequence 3, Appl	C 526	32	4.5	2632	4	US-09-867-915-26	Sequence 26, Appl
C 454	32.4	4.5	1830121	4	US-09-557-884-1	Sequence 1, Appl	C 527	32	4.5	2735	4	US-09-976-584-372	Sequence 372, App
C 455	32.4	4.5	1830121	4	US-09-643-990A-1	Sequence 1, Appl	C 528	32	4.5	2966	4	US-09-569-098A-103	Sequence 103, App
C 456	32.4	4.5	1830121	4	US-10-329-960-1	Sequence 1, Appl	C 529	32	4.5	3156	4	US-09-633-927-1	Sequence 1, Appl
C 457	32.2	4.5	141	4	US-09-513-999C-25470	Sequence 25470, A	C 530	32	4.5	3627	4	US-09-710-279-3764	Sequence 3764, Ap
C 458	32.2	4.5	401	4	US-09-513-999C-498	Sequence 498, App	C 531	32	4.5	4733	4	US-08-956-171E-433	Sequence 433, App
C 459	32.2	4.5	427	2	US-08-623-906A-5	Sequence 5, Appl	C 532	32	4.5	4733	3	US-08-781-986A-433	Sequence 11, Appl
C 460	32.2	4.5	474	4	US-09-621-976-18033	Sequence 5, Appl	C 533	32	4.5	4810	3	US-08-852-629-11	Sequence 15, Appl
C 461	32.2	4.5	550	4	US-09-010-147B-5	Sequence 5, Appl	C 534	32	4.5	4838	3	US-08-852-629-15	Sequence 74, Appl
C 462	32.2	4.5	624	4	US-09-248-796A-2078	Sequence 2078, Ap	C 535	32	4.5	5152	4	US-10-204-708-74	Sequence 3, Appl
C 463	32.2	4.5	738	4	US-09-636-215-747	Sequence 747, App	C 536	32	4.5	5793	4	US-09-869-855A-3	Sequence 2, Appl
C 464	32.2	4.5	738	4	US-09-685-166A-747	Sequence 747, App	C 537	32	4.5	5943	2	US-08-875-154-2	Sequence 1, Appl
C 465	32.2	4.5	738	4	US-09-679-426-747	Sequence 747, App	C 538	32	4.5	6169	2	US-08-869-855A-1	Sequence 1, Appl
C 466	32.2	4.5	780	4	US-09-248-796A-3195	Sequence 3195, App	C 539	32	4.5	6409	4	US-09-967-908A-1	Sequence 1, Appl

546	32	4.5	6409	4	US-10-159-L51-1	Sequence 1, Appli	619	31.6	4.4	678	4	US-09-248-796A-6649	Sequence 6649, Ap
547	32	4.5	7326	6	5304637-21	Patent No. 5304637	c 620	31.6	4.4	791	3	US-08-858-207A-219	Sequence 219, App
548	32	4.5	7336	2	US-08-418-085-3	Sequence 3, Appli	c 621	31.6	4.4	1001	4	US-09-671-317-51	Sequence 51, Appl
549	32	4.5	7336	3	US-09-099-011A-3	Sequence 3, Appli	622	31.6	4.4	1708	4	US-09-620-312D-275	Sequence 275, App
550	32	4.5	7336	3	US-08-470-369-21	Sequence 21, Appl	623	31.6	4.4	2030	2	US-08-705-937-7	Sequence 7, Appli
551	32	4.5	7336	4	US-09-098-877B-3	Sequence 3, Appli	624	31.6	4.4	2406	4	US-09-594-506-37	Sequence 37, Appl
552	32	4.5	8119	1	US-08-460-343B-1	Sequence 1, Appli	625	31.6	4.4	3497	4	US-09-110-279-4374	Sequence 4374, Ap
553	32	4.5	8119	1	US-08-398-028B-1	Sequence 1, Appli	c 626	31.6	4.4	4071	4	US-09-513-057C-5	Sequence 5, Appli
554	32	4.5	8119	2	US-08-504-265B-1	Sequence 1, Appli	c 627	31.6	4.4	4071	4	US-09-746-801A-5	Sequence 5, Appli
555	32	4.5	9144	3	US-08-556-978B-79	Sequence 79, Appl	c 628	31.6	4.4	7573	1	US-08-287-959-2	Sequence 2, Appli
556	32	4.5	19233	4	US-10-204-708-46	Sequence 46, Appl	c 629	31.6	4.4	7669	4	US-09-454-071-1	Sequence 1, Appli
557	32	4.5	29430	4	US-09-544-398B-7	Sequence 7, Appli	630	31.6	4.4	7786	4	US-09-790-988-2	Sequence 2, Appli
558	32	4.5	29430	4	US-09-543-771-7	Sequence 7, Appli	631	31.6	4.4	8239	4	US-09-029-047C-1	Sequence 1, Appli
559	32	4.5	152331	3	US-09-128-155-16	Sequence 16, Appl	632	31.6	4.4	9347	4	US-10-204-708-36	Sequence 36, Appl
560	31.8	4.5	180	4	US-09-621-976-8281	Sequence 8281, Ap	c 633	31.6	4.4	9636	1	US-08-323-170B-1	Sequence 1, Appli
561	31.8	4.5	243	1	US-07-922-723A-9	Sequence 9, Appli	c 634	31.6	4.4	9636	3	US-08-954-441-1	Sequence 1, Appli
562	31.8	4.5	243	1	US-07-799-828C-9	Sequence 9, Appli	c 635	31.6	4.4	11049	4	US-10-204-708-23	Sequence 23, Appl
563	31.8	4.5	243	1	US-08-074-275-9	Sequence 9, Appli	c 636	31.6	4.4	15418	4	US-09-783-203-1	Sequence 1, Appli
564	31.8	4.5	243	1	US-08-480-366-9	Sequence 9, Appli	c 637	31.6	4.4	15418	4	US-09-994-427A-1	Sequence 1, Appli
565	31.8	4.5	243	2	US-07-952-277A-9	Sequence 9, Appli	c 638	31.6	4.4	15418	4	US-09-244-438-1	Sequence 1, Appli
566	31.8	4.5	659	3	US-08-714-918-53	Sequence 53, Appl	c 639	31.6	4.4	16442	3	US-08-781-891-208	Sequence 208, App
567	31.8	4.5	659	3	US-09-365-315-53	Sequence 53, Appl	c 640	31.6	4.4	16844	4	US-09-618-166-208	Sequence 208, App
568	31.8	4.5	659	3	US-09-265-315-53	Sequence 53, Appl	641	31.6	4.4	18844	3	US-09-734-675-3	Sequence 3, Appli
569	31.8	4.5	659	3	US-09-266-417-53	Sequence 53, Appl	642	31.6	4.4	99500	3	US-09-798-096-10	Sequence 10, Appl
570	31.8	4.5	659	4	US-09-528-709-53	Sequence 53, Appl	c 643	31.6	4.4	118067	3	US-09-497-855A-32	Sequence 32, Appl
571	31.8	4.5	659	4	US-09-527-745-53	Sequence 53, Appl	644	31.6	4.4	152331	3	US-09-128-155-16	Sequence 16, Appl
572	31.8	4.5	665	2	US-08-883-795A-36	Sequence 36, Appl	645	31.6	4.4	246240	2	US-08-724-394A-20	Sequence 20, Appl
573	31.8	4.5	741	3	US-09-238-481-1	Sequence 1, Appli	646	31.6	4.4	246240	2	US-08-724-394A-21	Sequence 21, Appl
574	31.8	4.5	741	3	US-09-572-810A-1	Sequence 1, Appli	647	31.6	4.4	246240	2	US-08-724-394A-22	Sequence 22, Appl
575	31.8	4.5	768	4	US-09-248-796A-5700	Sequence 5700, Ap	c 648	31.6	4.4	392000	4	US-10-027-983-11	Sequence 11, Appl
576	31.8	4.5	773	3	US-08-998-416-385	Sequence 385, App	649	31.4	4.4	173	4	US-09-621-976-9851	Sequence 9851, Ap
577	31.8	4.5	1122	4	US-09-248-796A-5765	Sequence 5765, App	c 650	31.4	4.4	179	4	US-09-513-999C-17811	Sequence 17811, A
578	31.8	4.5	1457	4	US-09-270-767-26587	Sequence 26587, A	651	31.4	4.4	252	4	US-09-513-999C-35669	Sequence 35669, A
579	31.8	4.5	1603	4	US-09-270-767-11071	Sequence 11071, A	652	31.4	4.4	293	4	US-09-621-976-16965	Sequence 16965, A
580	31.8	4.5	1684	3	US-09-468-265-4	Sequence 4, Appli	653	31.4	4.4	293	4	US-09-248-796A-9575	Sequence 9575, Ap
581	31.8	4.5	1921	4	US-09-325-932A-140	Sequence 140, App	654	31.4	4.4	318	4	US-09-248-796A-3701	Sequence 3701, Ap
582	31.8	4.5	1968	4	US-09-601-198-100	Sequence 100, App	655	31.4	4.4	351	4	US-09-710-279-135	Sequence 135, App
583	31.8	4.5	2252	4	US-09-270-767-26712	Sequence 26712, A	656	31.4	4.4	639	4	US-09-482-273-49	Sequence 49, Appl
584	31.8	4.5	2662	4	US-09-270-767-11180	Sequence 11180, A	657	31.4	4.4	693	3	US-09-134-001C-772	Sequence 772, App
585	31.8	4.5	3001	4	US-09-539-333D-140	Sequence 140, App	658	31.4	4.4	810	4	US-09-792-024-52	Sequence 52, Appl
586	31.8	4.5	3404	4	US-09-710-279-4381	Sequence 4381, Ap	659	31.4	4.4	828	4	US-09-248-796A-1730	Sequence 1730, Ap
587	31.8	4.5	3454	4	US-09-710-279-4346	Sequence 4346, Ap	c 660	31.4	4.4	940	4	US-09-270-767-3469	Sequence 3469, Ap
588	31.8	4.5	3454	4	US-09-963-137-151	Sequence 151, App	c 661	31.4	4.4	940	4	US-09-270-767-18751	Sequence 18751, A
589	31.8	4.5	4648	4	US-09-963-137-178	Sequence 178, App	662	31.4	4.4	957	4	US-09-248-796A-4606	Sequence 4606, Ap
590	31.8	4.5	4648	4	US-09-207-914-24	Sequence 24, Appl	663	31.4	4.4	1129	3	US-09-183-217-1	Sequence 1, Appli
591	31.8	4.5	4655	4	US-09-207-914-20	Sequence 20, Appl	c 664	31.4	4.4	1180	4	US-09-620-312D-971	Sequence 25, Appl
592	31.8	4.5	5046	4	US-09-725-932A-13	Sequence 13, Appl	c 665	31.4	4.4	1366	3	US-08-876-885-25	Sequence 25, Appl
593	31.8	4.5	5152	4	US-10-204-708-47	Sequence 47, Appl	c 666	31.4	4.4	1374	4	US-09-601-198-158	Sequence 158, App
594	31.8	4.5	5562	4	US-10-204-708-63	Sequence 63, Appl	c 667	31.4	4.4	1641	4	US-08-988-197-8	Sequence 8, Appli
595	31.8	4.5	6251	4	US-08-956-171B-25	Sequence 25, Appl	c 668	31.4	4.4	1641	4	US-10-385-072-8	Sequence 8, Appli
596	31.8	4.5	6251	4	US-08-781-986A-25	Sequence 25, Appl	c 669	31.4	4.4	1710	4	US-09-333-999A-40	Sequence 40, Appl
597	31.8	4.5	8009	4	US-08-956-171B-61	Sequence 61, Appl	c 670	31.4	4.4	1710	4	US-09-710-279-4167	Sequence 4167, Ap
598	31.8	4.5	8009	4	US-08-781-986A-61	Sequence 61, Appl	671	31.4	4.4	1827	3	US-09-134-001C-1914	Sequence 1914, Ap
599	31.8	4.5	8478	3	US-08-676-818-1	Sequence 1, Appli	c 672	31.4	4.4	2429	4	US-09-336-115C-11	Sequence 11, Appl
600	31.8	4.5	8478	3	US-09-407-549-1	Sequence 1, Appli	673	31.4	4.4	2448	1	US-08-526-964-2	Sequence 2, Appli
601	31.8	4.5	8537	4	US-10-204-708-41	Sequence 41, Appl	c 674	31.4	4.4	2448	3	US-08-946-617-2	Sequence 2, Appli
602	31.8	4.5	8537	4	US-10-204-708-42	Sequence 42, Appl	675	31.4	4.4	2448	3	US-09-031-897-2	Sequence 2, Appli
603	31.8	4.5	10079	2	US-08-476-866-20	Sequence 20, Appl	c 676	31.4	4.4	2732	4	US-09-933-999A-40	Sequence 40, Appl
604	31.8	4.5	15144	3	US-08-458-434A-6	Sequence 6, Appli	677	31.4	4.4	3003	4	US-09-710-279-4167	Sequence 4167, Ap
605	31.8	4.5	20674	4	US-09-641-638-651	Sequence 651, App	c 678	31.4	4.4	3296	4	US-09-674-826B-3	Sequence 3, Appli
606	31.8	4.5	20674	4	US-10-170-097-651	Sequence 651, App	679	31.4	4.4	4055	4	US-09-710-279-3357	Sequence 3357, Ap
607	31.8	4.5	58407	4	US-08-916-421B-2	Sequence 2, Appli	c 680	31.4	4.4	4241	4	US-09-710-279-3577	Sequence 3577, Ap
608	31.8	4.5	58407	4	US-09-692-570-2	Sequence 2, Appli	681	31.4	4.4	5844	4	US-10-204-708-89	Sequence 89, Appl
609	31.6	4.4	246	4	US-09-621-976-13617	Sequence 13617, A	682	31.4	4.4	6070	4	US-10-204-708-9	Sequence 9, Appli
610	31.6	4.4	299	4	US-08-956-171B-1171	Sequence 1171, Ap	c 683	31.4	4.4	15071	4	US-09-358-082A-29	Sequence 29, Appl
611	31.6	4.4	299	4	US-08-781-986A-1171	Sequence 1171, Ap	c 684	31.4	4.4	15071	4	US-09-358-082A-29	Sequence 29, Appl
612	31.6	4.4	325	1	US-08-111-316-6	Sequence 6, Appli	c 685	31.4	4.4	29555	4	US-08-956-171E-206	Sequence 206, App
613	31.6	4.4	325	1	US-08-468-405-6	Sequence 6, Appli	686	31.4	4.4	29555	4	US-08-781-986A-206	Sequence 206, App
614	31.6	4.4	325	2	US-08-332-766A-11	Sequence 11, Appl	687	31.2	4.4	197	4	US-09-513-999C-21922	Sequence 21922, A
615	31.6	4.4	333	4	US-09-248-796A-11241	Sequence 11241, A	c 688	31.2	4.4	200	3	US-09-243-335-3	Sequence 3, Appli
616	31.6	4.4	394	2	US-08-623-906A-7	Sequence 7, Appli	c 689	31.2	4.4	200	4	US-09-761-116-3	Sequence 3, Appli
617	31.6	4.4	403	4	US-09-621-976-19061	Sequence 19061, A	c 690	31.2	4.4	240	4	US-09-107-532A-1443	Sequence 1443, Ap
618	31.6	4.4	546	4	US-09-248-796A-2044	Sequence 2044, Ap	691	31.2	4.4	255	4	US-09-513-999C-10299	Sequence 10299, A

c 692	31.2	4.4	370	4	US-09-513-999C-497	Sequence 497, App	c 765	31	4.3	4182	1	US-07-973-257-1	Sequence 1, Appli
c 693	31.2	4.4	396	4	US-09-640-173-16	Sequence 16, Appl	c 766	31	4.3	4185	3	US-09-417-485D-7	Sequence 7, Appli
c 694	31.2	4.4	396	4	US-09-713-550-16	Sequence 16, Appl	c 767	31	4.3	4651	3	US-08-425-843-6	Sequence 6, Appli
c 695	31.2	4.4	396	4	US-09-825-294-16	Sequence 16, Appl	c 768	31	4.3	5360	3	US-10-204-708-65	Sequence 65, Appl
c 696	31.2	4.4	429	4	US-09-970-966-16	Sequence 16, Appl	c 769	31	4.3	5433	3	US-08-929-329-1	Sequence 1, Appli
c 697	31.2	4.4	429	4	US-09-543-681A-707	Sequence 707, App	c 770	31	4.3	5455	4	US-10-204-708-34	Sequence 34, Appl
c 698	31.2	4.4	573	3	US-09-117-257-12	Sequence 12, Appl	c 771	31	4.3	7995	4	US-09-821-726A-11	Sequence 11, Appl
c 699	31.2	4.4	573	3	US-08-945-476-12	Sequence 12, Appl	c 772	31	4.3	8961	4	US-10-204-708-80	Sequence 80, Appl
c 700	31.2	4.4	573	3	US-09-489-352-12	Sequence 12, Appl	c 773	31	4.3	9048	3	US-08-973-273-4	Sequence 5, Appli
c 701	31.2	4.4	576	3	US-09-117-257-39	Sequence 39, Appl	c 774	31	4.3	10640	4	US-09-417-485D-5	Sequence 5, Appli
c 702	31.2	4.4	576	3	US-09-489-352-39	Sequence 39, Appl	c 775	30.8	4.3	266	4	US-09-513-999C-23074	Sequence 23074, A
c 703	31.2	4.4	606	4	US-09-270-767-2606	Sequence 2606, Ap	c 776	30.8	4.3	323	2	US-09-621-976-10374	Sequence 10374, A
c 704	31.2	4.4	606	4	US-09-270-767-17888	Sequence 17888, A	c 777	30.8	4.3	350	2	US-08-332-766A-20	Sequence 20, Appl
c 705	31.2	4.4	661	2	US-08-529-878B-37	Sequence 37, Appl	c 778	30.8	4.3	371	4	US-09-621-976-19223	Sequence 22, Appl
c 706	31.2	4.4	1021	4	US-09-134-000C-343	Sequence 34, App	c 779	30.8	4.3	412	3	US-09-018-584A-22	Sequence 22, Appl
c 707	31.2	4.4	1295	4	US-09-543-681A-1286	Sequence 1286, App	c 780	30.8	4.3	412	4	US-09-784-423-22	Sequence 22, Appl
c 708	31.2	4.4	1440	4	US-09-248-796A-6033	Sequence 6033, Ap	c 781	30.8	4.3	435	4	US-09-621-976-9236	Sequence 9236, Ap
c 709	31.2	4.4	1530	4	US-09-270-767-13887	Sequence 13887, A	c 782	30.8	4.3	468	4	US-09-248-796A-4315	Sequence 4315, Ap
c 710	31.2	4.4	1575	4	US-09-543-681A-615	Sequence 615, App	c 783	30.8	4.3	474	4	US-09-621-976-18033	Sequence 18033, A
c 711	31.2	4.4	1575	4	US-09-248-796A-3683	Sequence 3683, Ap	c 784	30.8	4.3	552	4	US-09-270-767-4499	Sequence 4499, Ap
c 712	31.2	4.4	1760	4	US-09-495-050A-139	Sequence 139, App	c 785	30.8	4.3	552	4	US-09-270-767-19781	Sequence 19781, A
c 713	31.2	4.4	2013	4	US-09-248-796A-3566	Sequence 3566, App	c 786	30.8	4.3	681	4	US-09-709-840-15	Sequence 15, Appl
c 714	31.2	4.4	3135	4	US-09-976-594-925	Sequence 925, App	c 787	30.8	4.3	699	4	US-09-248-796A-2685	Sequence 2685, Ap
c 715	31.2	4.4	3137	4	US-09-710-279-3615	Sequence 3615, Ap	c 788	30.8	4.3	705	4	US-09-134-000C-2941	Sequence 2941, Ap
c 716	31.2	4.4	3142	1	US-08-110-158-3	Sequence 3, Appli	c 789	30.8	4.3	762	4	US-09-586-106D-66	Sequence 66, Appl
c 717	31.2	4.4	3142	4	US-09-023-655-1090	Sequence 1090, Ap	c 790	30.8	4.3	912	4	US-09-495-406-16	Sequence 16, Appl
c 718	31.2	4.4	3144	5	PCT-US91-05059-1	Sequence 1, Appli	c 791	30.8	4.3	912	4	US-09-816-028A-28	Sequence 28, Appl
c 719	31.2	4.4	3596	4	US-09-710-279-4065	Sequence 4065, Ap	c 792	30.8	4.3	912	4	US-10-303-162-28	Sequence 28, Appl
c 720	31.2	4.4	3927	4	US-09-710-279-3926	Sequence 3926, Ap	c 793	30.8	4.3	1022	4	US-09-270-767-26538	Sequence 38, Appl
c 721	31.2	4.4	3930	2	US-09-018-787-2	Sequence 2, Appli	c 794	30.8	4.3	1229	5	PCT-US91-02714-38	Sequence 39, Appl
c 722	31.2	4.4	4586	3	US-09-335-710-2	Sequence 2, Appli	c 795	30.8	4.3	1230	1	US-07-688-352C-39	Sequence 39, Appl
c 723	31.2	4.4	4586	3	US-09-031-563-26	Sequence 26, Appl	c 796	30.8	4.3	1230	2	US-08-474-379C-39	Sequence 39, Appl
c 724	31.2	4.4	4586	4	US-09-392-277-26	Sequence 26, Appl	c 797	30.8	4.3	1230	3	US-09-146-249A-39	Sequence 39, Appl
c 725	31.2	4.4	4586	4	US-09-258-000-26	Sequence 26, Appl	c 798	30.8	4.3	1230	3	US-08-206-188B-39	Sequence 39, Appl
c 726	31.2	4.4	5562	4	US-10-204-708-64	Sequence 64, Appl	c 799	30.8	4.3	1272	4	US-09-248-796A-1909	Sequence 1909, Ap
c 727	31.2	4.4	5714	4	US-09-620-312D-393	Sequence 393, App	c 800	30.8	4.3	1437	3	US-09-446-504-63	Sequence 63, Appl
c 728	31.2	4.4	5714	4	US-08-961-527-105	Sequence 105, App	c 801	30.8	4.3	1437	3	US-09-712-266-63	Sequence 63, Appl
c 729	31.2	4.4	8537	4	US-10-204-708-42	Sequence 42, Appl	c 802	30.8	4.3	1437	3	US-09-167-206-11	Sequence 11, Appl
c 730	31.2	4.4	18443	3	US-09-078-294-6	Sequence 6, Appli	c 803	30.8	4.3	1939	1	US-07-715-751B-2	Sequence 2, Appli
c 731	31.2	4.4	56516	2	US-08-996-306-1	Sequence 1, Appli	c 804	30.8	4.3	2030	2	US-08-705-937-7	Sequence 7, Appli
c 732	31.2	4.4	56516	3	US-09-338-907-1	Sequence 1, Appli	c 805	30.8	4.3	2035	4	US-09-270-767-13760	Sequence 49, Appl
c 733	31.2	4.4	56516	3	US-09-218-207-1	Sequence 1, Appli	c 806	30.8	4.3	2328	4	US-09-601-198-49	Sequence 14386, A
c 734	31.2	4.4	56520	3	US-09-338-907-179	Sequence 179, App	c 807	30.8	4.3	2371	4	US-09-270-767-14386	Sequence 2435, Ap
c 735	31.2	4.4	56520	3	US-09-218-207-179	Sequence 179, App	c 808	30.8	4.3	2475	4	US-09-248-796A-2435	Sequence 178, App
c 736	31.2	4.4	72928	3	US-09-009-913-1	Sequence 1, Appli	c 809	30.8	4.3	3025	4	US-08-956-171E-178	Sequence 178, App
c 737	31.2	4.4	106746	4	US-09-326-402C-1	Sequence 1, Appli	c 810	30.8	4.3	3025	4	US-08-781-986A-178	Sequence 4211, Ap
c 738	31.2	4.4	106746	4	US-09-326-402C-12	Sequence 12, Appl	c 811	30.8	4.3	3211	4	US-09-710-279-4211	Sequence 4211, Ap
c 739	31	4.3	407	4	US-09-513-999C-24174	Sequence 24174, A	c 812	30.8	4.3	3254	4	US-09-710-279-4202	Sequence 442, App
c 740	31	4.3	452	4	US-09-710-279-2695	Sequence 2695, Ap	c 813	30.8	4.3	3326	4	US-08-956-171E-442	Sequence 442, App
c 741	31	4.3	517	4	US-09-621-976-17793	Sequence 17793, A	c 814	30.8	4.3	3326	4	US-08-781-986A-442	Sequence 442, App
c 742	31	4.3	540	4	US-09-248-796A-4283	Sequence 4283, Ap	c 815	30.8	4.3	3532	4	US-09-710-279-4153	Sequence 4153, Ap
c 743	31	4.3	592	4	US-09-270-767-9494	Sequence 9494, Ap	c 816	30.8	4.3	3574	3	US-09-446-504-83	Sequence 83, Appl
c 744	31	4.3	592	4	US-09-270-767-24776	Sequence 24776, A	c 817	30.8	4.3	3574	3	US-09-712-266-83	Sequence 83, Appl
c 745	31	4.3	592	4	US-08-332-766A-19	Sequence 19, Appl	c 818	30.8	4.3	3881	1	US-08-299-953-2	Sequence 2, Appli
c 746	31	4.3	666	4	US-09-107-532A-3013	Sequence 3013, Ap	c 819	30.8	4.3	3881	1	US-08-459-415-2	Sequence 2, Appli
c 747	31	4.3	666	4	US-09-134-000C-3112	Sequence 3112, Ap	c 820	30.8	4.3	3881	3	US-09-066-687-2	Sequence 2, Appli
c 748	31	4.3	696	4	US-09-270-767-14786	Sequence 14786, A	c 821	30.8	4.3	3881	5	PCT-US95-11231-2	Sequence 2, Appli
c 749	31	4.3	732	4	US-09-248-796A-1507	Sequence 1507, Ap	c 822	30.8	4.3	3974	3	US-08-467-504-3	Sequence 3, Appli
c 750	31	4.3	869	4	US-09-270-767-7756	Sequence 7756, Ap	c 823	30.8	4.3	3977	4	US-09-270-767-12208	Sequence 12208, A
c 751	31	4.3	869	4	US-09-270-767-23038	Sequence 23038, A	c 824	30.8	4.3	4010	4	US-09-710-279-4296	Sequence 4296, Ap
c 752	31	4.3	915	4	US-09-134-000C-2588	Sequence 2588, Ap	c 825	30.8	4.3	4228	4	US-09-227-421-3	Sequence 3, Appli
c 753	31	4.3	972	4	US-09-601-198-127	Sequence 127, App	c 826	30.8	4.3	4228	4	US-09-479-855-3	Sequence 3, Appli
c 754	31	4.3	1098	3	US-09-248-335-35	Sequence 35, Appl	c 827	30.8	4.3	5437	1	US-08-416-872-1	Sequence 1, Appli
c 755	31	4.3	1113	3	US-09-134-001C-1329	Sequence 1329, Ap	c 828	30.8	4.3	5437	2	US-09-035-241-1	Sequence 1, Appli
c 756	31	4.3	1148	4	US-09-665-189A-75	Sequence 75, Appl	c 829	30.8	4.3	5437	5	PCT-US94-06197-1	Sequence 1, Appli
c 757	31	4.3	1696	4	US-09-835-811-1	Sequence 1, Appli	c 830	30.8	4.3	5455	4	US-10-204-708-33	Sequence 33, Appl
c 758	31	4.3	1785	4	US-09-601-198-156	Sequence 156, App	c 831	30.8	4.3	5608	4	US-09-976-594-163	Sequence 163, App
c 759	31	4.3	2174	3	US-08-606-505B-63	Sequence 63, Appl	c 832	30.8	4.3	5735	4	US-09-734-674-1	Sequence 1, Appli
c 760	31	4.3	2174	3	US-09-616-990-63	Sequence 63, Appl	c 833	30.8	4.3	6156	4	US-10-204-708-59	Sequence 59, Appl
c 761	31	4.3	2946	4	US-09-710-279-3738	Sequence 3738, Ap	c 834	30.8	4.3	6801	4	US-10-204-708-62	Sequence 62, Appl
c 762	31	4.3	3922	4	US-09-921-099A-18	Sequence 18, Appl	c 835	30.8	4.3	10785	3	US-08-444-644-27	Sequence 27, Appl
c 763	31	4.3	3982	4	US-08-956-171E-520	Sequence 520, App	c 836	30.8	4.3	10785	3	US-08-232-246A-27	Sequence 27, Appl
c 764	31	4.3	3982	4	US-08-781-986A-520	Sequence 520, App	c 837	30.8	4.3	10844	3	US-08-444-644-41	Sequence 41, Appl

838	30.8	4.3	10844	3	US-08-232-246A-41	Sequence 41, Appl	C 911	30.6	4.3	13158	2	US-08-687-080-105	Sequence 105, App
839	30.8	4.3	11528	3	US-08-444-644-18	Sequence 18, Appl	912	30.6	4.3	16550	4	US-09-916-421B-3	Sequence 3, Appl
840	30.8	4.3	11528	3	US-08-232-246A-18	Sequence 18, Appl	913	30.6	4.3	16550	4	US-09-692-570-3	Sequence 3, Appl
841	30.8	4.3	11528	3	US-08-956-171B-136	Sequence 136, App	914	30.6	4.3	29793	3	US-09-302-812-38	Sequence 38, Appl
842	30.8	4.3	11823	4	US-08-781-986A-136	Sequence 136, App	915	30.6	4.3	29793	3	US-09-511-477-38	Sequence 38, Appl
843	30.8	4.3	12127	3	US-08-444-644-32	Sequence 32, Appl	916	30.6	4.3	29793	3	US-09-511-507-38	Sequence 19, Appl
844	30.8	4.3	12127	3	US-08-232-246A-32	Sequence 32, Appl	917	30.6	4.3	33778	4	US-09-596-002-19	Sequence 1, Appl
845	30.8	4.3	13999	3	US-08-444-644-24	Sequence 24, Appl	C 918	30.6	4.3	33778	4	US-08-545-528B-1	Sequence 10692, A
846	30.8	4.3	13999	3	US-08-232-246A-24	Sequence 24, Appl	919	30.4	4.3	234	4	US-09-621-796A-10692	Sequence 16320, A
847	30.8	4.3	15016	4	US-09-601-198-60	Sequence 60, Appl	920	30.4	4.3	242	4	US-09-428-796A-10692	Sequence 16324, A
848	30.8	4.3	15418	4	US-09-783-203-1	Sequence 1, Appl	921	30.4	4.3	242	4	US-09-621-796-16320	Sequence 18, Appl
849	30.8	4.3	15418	4	US-09-994-427A-1	Sequence 1, Appl	922	30.4	4.3	267	3	US-09-134-001C-18	Sequence 10546, A
850	30.8	4.3	15418	4	US-09-244-438-1	Sequence 1, Appl	923	30.4	4.3	297	4	US-09-248-796A-10546	Sequence 13, Appl
851	30.6	4.3	177	4	US-09-621-976-1047	Sequence 1047, Ap	924	30.4	4.3	357	3	US-09-134-001C-19	Sequence 13, Appl
852	30.6	4.3	192	3	US-09-157-177-115	Sequence 115, App	C 925	30.4	4.3	372	3	US-09-784-423-13	Sequence 10904, A
853	30.6	4.3	192	3	US-09-541-210-115	Sequence 115, App	C 926	30.4	4.3	372	4	US-09-513-999C-10504	Sequence 8976, Ap
854	30.6	4.3	212	4	US-09-513-999C-23699	Sequence 23699, A	C 927	30.4	4.3	393	4	US-09-621-376-8976	Sequence 18, Appl
855	30.6	4.3	253	4	US-09-248-796A-13808	Sequence 13808, A	C 928	30.4	4.3	399	4	US-09-018-584A-18	Sequence 16, Appl
856	30.6	4.3	276	4	US-09-248-796A-13808	Sequence 13808, A	C 929	30.4	4.3	415	3	US-09-784-423-18	Sequence 18, Appl
857	30.6	4.3	292	4	US-09-221-017B-623	Sequence 623, App	930	30.4	4.3	415	4	US-08-332-766A-16	Sequence 7777, Ap
858	30.6	4.3	309	4	US-09-134-000C-272	Sequence 272, App	C 931	30.4	4.3	500	4	US-08-270-767-7777	Sequence 23059, A
859	30.6	4.3	313	4	US-09-270-767-30450	Sequence 30450, A	C 932	30.4	4.3	500	4	US-09-270-767-7777	Sequence 4, Appl
860	30.6	4.3	354	4	US-09-270-767-29953	Sequence 29953, A	C 933	30.4	4.3	537	4	US-09-720-201A-4	Sequence 637, App
861	30.6	4.3	370	2	US-08-332-766A-8	Sequence 8, Appl	C 934	30.4	4.3	576	4	US-09-710-279-637	Sequence 6528, Ap
862	30.6	4.3	396	4	US-09-640-173-53	Sequence 53, Appl	C 935	30.4	4.3	585	4	US-09-270-767-6528	Sequence 21810, A
863	30.6	4.3	396	4	US-09-713-550-53	Sequence 53, Appl	936	30.4	4.3	585	4	US-09-270-767-21810	Sequence 6, Appl
864	30.6	4.3	396	4	US-09-825-294-53	Sequence 53, Appl	C 937	30.4	4.3	644	4	US-09-720-201A-6	Sequence 3694, Ap
865	30.6	4.3	432	4	US-09-970-966-53	Sequence 53, Appl	C 938	30.4	4.3	675	4	US-09-543-681A-3694	Sequence 805, App
866	30.6	4.3	432	4	US-09-451-651-34	Sequence 34, Appl	C 939	30.4	4.3	680	4	US-08-956-171E-805	Sequence 805, App
867	30.6	4.3	469	4	US-09-513-999C-25453	Sequence 25453, A	C 940	30.4	4.3	680	4	US-08-781-986A-805	Sequence 8427, Ap
868	30.6	4.3	490	4	US-09-621-976-2432	Sequence 2432, Ap	C 941	30.4	4.3	687	4	US-09-248-796A-8427	Sequence 10136, A
869	30.6	4.3	530	4	US-09-621-976-8993	Sequence 8993, Ap	C 942	30.4	4.3	733	3	US-09-270-767-10136	Sequence 2721, Ap
870	30.6	4.3	719	4	US-09-270-767-13269	Sequence 13269, A	C 943	30.4	4.3	834	3	US-09-134-001C-2721	Sequence 47, Appl
871	30.6	4.3	722	3	US-08-480-640A-222	Sequence 222, App	C 944	30.4	4.3	856	4	US-09-288-143-47	Sequence 105, App
872	30.6	4.3	722	3	US-08-686-968C-222	Sequence 222, App	945	30.4	4.3	1034	4	US-09-311-021-105	Sequence 11086, A
873	30.6	4.3	722	3	US-08-488-237A-222	Sequence 222, App	946	30.4	4.3	1034	4	US-09-248-796A-11086	Sequence 23, Appl
874	30.6	4.3	722	3	US-08-472-679H-222	Sequence 222, App	947	30.4	4.3	1038	4	US-09-806-708B-23	Sequence 85, Appl
875	30.6	4.3	785	4	US-09-270-767-5707	Sequence 5707, Ap	948	30.4	4.3	1055	4	US-09-378-088A-85	Sequence 85, Appl
876	30.6	4.3	785	4	US-09-270-767-14307	Sequence 14307, A	C 949	30.4	4.3	1114	3	US-09-643-596B-85	Sequence 42, Appl
877	30.6	4.3	885	4	US-09-976-594-102	Sequence 102, App	C 950	30.4	4.3	1114	3	US-08-84-188-42	Sequence 42, Appl
878	30.6	4.3	1200	4	US-08-817-913-13	Sequence 13, Appl	C 951	30.4	4.3	1152	3	US-09-547-621-42	Sequence 572, App
879	30.6	4.3	1214	3	US-08-817-913-14	Sequence 14, Appl	C 952	30.4	4.3	1192	4	US-09-976-594-572	Sequence 42, Appl
880	30.6	4.3	1232	3	US-08-971-089-1	Sequence 1, Appl	953	30.4	4.3	1241	3	US-09-378-088A-42	Sequence 42, Appl
881	30.6	4.3	1298	3	US-09-270-767-25921	Sequence 25921, A	C 954	30.4	4.3	1241	3	US-09-548-334A-42	Sequence 42, Appl
882	30.6	4.3	1336	4	US-08-817-913-15	Sequence 15, Appl	C 955	30.4	4.3	1241	4	US-09-643-596B-42	Sequence 128, App
883	30.6	4.3	1352	3	US-09-073-569-1	Sequence 1, Appl	C 956	30.4	4.3	1249	4	US-09-461-325-128	Sequence 128, App
884	30.6	4.3	1733	3	US-08-817-913-16	Sequence 16, Appl	958	30.4	4.3	1249	4	US-10-012-542-128	Sequence 128, App
885	30.6	4.3	1734	3	US-08-817-913-16	Sequence 16, Appl	C 959	30.4	4.3	1249	4	US-10-115-123-128	Sequence 93, Appl
886	30.6	4.3	1758	4	US-09-248-796A-4964	Sequence 4964, Ap	C 960	30.4	4.3	1260	4	US-09-461-325-93	Sequence 93, Appl
887	30.6	4.3	1812	4	US-09-520-781-1	Sequence 1, Appl	C 961	30.4	4.3	1260	4	US-10-012-542-93	Sequence 93, Appl
888	30.6	4.3	1890	6	5312912-3	Patent No. 5312912	C 962	30.4	4.3	1298	3	US-08-948-705-3	Sequence 16, Appl
889	30.6	4.3	1920	3	US-08-817-913-17	Sequence 17, Appl	963	30.4	4.3	1368	3	US-09-510-543-3	Sequence 13, Appl
890	30.6	4.3	2109	4	US-09-614-221A-479	Sequence 479, App	964	30.4	4.3	1368	3	US-09-134-001C-16	Sequence 13, Appl
891	30.6	4.3	2146	4	US-09-270-767-10508	Sequence 10508, A	C 965	30.4	4.3	1373	4	US-09-489-847-13	Sequence 595, App
892	30.6	4.3	2169	3	US-08-981-803-14	Sequence 14, Appl	C 966	30.4	4.3	1373	4	US-08-956-171B-595	Sequence 595, App
893	30.6	4.3	2169	3	US-08-981-803-28	Sequence 28, App	C 967	30.4	4.3	1484	4	US-08-781-986A-595	Sequence 24, Appl
894	30.6	4.3	2169	3	US-08-983-440-14	Sequence 14, Appl	968	30.4	4.3	1484	4	US-08-340-820-24	Sequence 24, Appl
895	30.6	4.3	2169	3	US-08-983-440-28	Sequence 28, App	969	30.4	4.3	1493	1	US-08-547-621-39	Sequence 39, Appl
896	30.6	4.3	2169	4	US-09-367-895-14	Sequence 14, Appl	C 970	30.4	4.3	1493	1	US-08-593-535-24	Sequence 160, App
897	30.6	4.3	2169	4	US-09-367-895-28	Sequence 28, App	C 971	30.4	4.3	1521	4	US-09-643-596B-160	Sequence 2561, Ap
898	30.6	4.3	3164	3	US-08-686-968C-1	Sequence 1, Appl	C 972	30.4	4.3	1590	4	US-09-543-681A-2561	Sequence 181, App
899	30.6	4.3	3269	4	US-09-710-279-3692	Sequence 3692, Ap	973	30.4	4.3	1624	4	US-10-140-002-181	Sequence 13, Appl
900	30.6	4.3	3828	4	US-09-710-279-3921	Sequence 3921, Ap	C 974	30.4	4.3	1662	3	US-09-668-097A-13	Sequence 39, Appl
901	30.6	4.3	5152	3	US-10-204-708-73	Sequence 73, Appl	C 975	30.4	4.3	2132	3	US-08-844-188-39	Sequence 39, Appl
902	30.6	4.3	5238	3	US-09-080-855-1	Sequence 1, Appl	C 976	30.4	4.3	2132	3	US-09-378-088A-39	Sequence 39, Appl
903	30.6	4.3	5238	4	US-09-566-076-1	Sequence 1, Appl	C 977	30.4	4.3	2132	4	US-09-548-334A-39	Sequence 39, Appl
904	30.6	4.3	5360	4	US-10-204-708-66	Sequence 66, Appl	C 978	30.4	4.3	2132	4	US-09-547-621-39	Sequence 39, Appl
905	30.6	4.3	5666	4	US-10-204-708-29	Sequence 29, Appl	C 979	30.4	4.3	2132	4	US-09-643-596B-39	Sequence 97, Appl
906	30.6	4.3	5943	1	US-08-206-176-1	Sequence 1, Appl	980	30.4	4.3	2146	3	US-08-936-165A-97	Sequence 67, Appl
907	30.6	4.3	8607	4	US-10-204-708-71	Sequence 71, Appl	981	30.4	4.3	2434	4	US-09-489-847-67	Sequence 549, App
908	30.6	4.3	11469	4	US-09-367-895-29	Sequence 29, Appl	982	30.4	4.3	2535	4	US-09-799-451-549	Sequence 1, Appl
909	30.6	4.3	11478	3	US-08-981-803-29	Sequence 29, Appl	983	30.4	4.3	2624	1	US-08-032-382B-1	
910	30.6	4.3	11478	3	US-08-983-440-29	Sequence 29, Appl							

984	30.4	4.3	2625	4	US-09-270-767-10080	Sequence 10080, A	cl1057	30.2	4.2	1565	4	US-08-956-171E-527	Sequence 527, App
C 985	30.4	4.3	2733	1	US-08-310-271-1	Sequence 1, Appli	cl1058	30.2	4.2	1565	4	US-08-781-986A-527	Sequence 527, App
C 986	30.4	4.3	2733	3	US-09-032-742-9	Sequence 9, Appli	1059	30.2	4.2	1747	4	US-09-270-767-7614	Sequence 7614, Ap
C 987	30.4	4.3	2733	4	US-09-016-434-1317	Sequence 1317, Ap	1060	30.2	4.2	1747	4	US-09-270-767-22896	Sequence 22896, A
C 988	30.4	4.3	2907	4	US-09-248-796A-3444	Sequence 3444, Ap	1061	30.2	4.2	1872	4	US-09-107-532A-1072	Sequence 1072, Ap
C 989	30.4	4.3	3001	4	US-09-539-333D-194	Sequence 194, App	1062	30.2	4.2	2069	4	US-09-678-300-3	Sequence 3, Appli
C 990	30.4	4.3	3116	4	US-09-710-279-3991	Sequence 3991, Ap	cl1063	30.2	4.2	2124	4	US-09-678-300-6	Sequence 6, Appli
991	30.4	4.3	3116	4	US-09-311-021-187	Sequence 187, App	cl1064	30.2	4.2	2124	4	US-09-678-300-9	Sequence 9, Appli
992	30.4	4.3	3116	4	US-09-710-279-4098	Sequence 4098, Ap	1065	30.2	4.2	2181	3	US-08-714-918-85	Sequence 85, Appl
993	30.4	4.3	3326	4	US-09-710-279-3438	Sequence 3438, Ap	1066	30.2	4.2	2181	3	US-09-265-315-85	Sequence 85, Appl
994	30.4	4.3	3474	4	US-09-710-279-3858	Sequence 3858, Ap	1067	30.2	4.2	2181	3	US-09-265-315-85	Sequence 85, Appl
995	30.4	4.3	3881	4	US-09-710-279-3751	Sequence 3751, Ap	1068	30.2	4.2	2181	3	US-09-266-417-85	Sequence 85, Appl
996	30.4	4.3	3994	4	US-09-710-279-3704	Sequence 3704, Ap	1069	30.2	4.2	2181	3	US-09-528-709-85	Sequence 85, Appl
C 997	30.4	4.3	4775	4	US-09-220-132-5	Sequence 5, Appli	1070	30.2	4.2	2232	4	US-09-527-745-85	Sequence 12, Appl
C 998	30.4	4.3	4877	4	US-09-566-921-8	Sequence 8, Appli	cl1071	30.2	4.2	2280	4	US-09-678-300-2	Sequence 2, Appli
C 999	30.4	4.3	5219	4	US-10-204-708-52	Sequence 52, Appl	cl1072	30.2	4.2	2863	4	US-09-678-300-5	Sequence 5, Appli
1000	30.4	4.3	6113	4	US-10-204-708-13	Sequence 13, Appl	cl1073	30.2	4.2	2904	4	US-09-678-300-8	Sequence 8, Appli
1001	30.4	4.3	6527	4	US-09-492-308A-3	Sequence 3, Appli	cl1074	30.2	4.2	2971	4	US-09-678-300-11	Sequence 11, Appl
1002	30.4	4.3	8585	1	US-08-030-096-3	Sequence 3, Appli	cl1075	30.2	4.2	3055	1	US-08-236-754-1	Sequence 1, Appli
1003	30.4	4.3	8700	2	US-08-392-625-16	Sequence 16, Appl	cl1076	30.2	4.2	3055	1	US-09-678-300-1	Sequence 1, Appli
1004	30.4	4.3	8700	2	US-08-466-961A-16	Sequence 16, Appl	cl1077	30.2	4.2	4160	3	US-09-134-218-1	Sequence 1, Appli
1005	30.4	4.3	8700	2	US-08-645-193B-18	Sequence 18, Appl	1078	30.2	4.2	4170	3	US-09-049-671-2	Sequence 1, Appli
1006	30.4	4.3	14113	3	US-08-992-801-1	Sequence 1, Appli	cl1079	30.2	4.2	4170	3	US-09-235-068-2	Sequence 2, Appli
1007	30.4	4.3	14113	3	US-08-223-134-1	Sequence 1, Appli	cl1080	30.2	4.2	4170	3	US-09-481-275-2	Sequence 2, Appli
1008	30.4	4.3	14113	3	US-08-223-535-1	Sequence 1, Appli	cl1081	30.2	4.2	4345	4	US-09-569-852B-5	Sequence 5, Appli
cl109	30.4	4.3	20966	4	US-09-776-976-7	Sequence 7, Appli	cl1082	30.2	4.2	4345	4	US-09-627-122-21	Sequence 21, Appl
cl1010	30.4	4.3	20966	4	US-09-909-547-7	Sequence 7, Appli	1083	30.2	4.2	6070	4	US-10-204-708-10	Sequence 10, Appl
cl1011	30.4	4.3	20966	4	US-09-569-852B-1	Sequence 1, Appli	cl1084	30.2	4.2	6070	4	US-10-204-708-10	Sequence 10, Appl
cl1012	30.4	4.3	41100	4	US-09-755-665-46	Sequence 46, Appl	1085	30.2	4.2	6131	4	US-09-799-451-163	Sequence 163, App
cl1013	30.4	4.3	62909	4	US-09-596-002-32	Sequence 32, Appl	1086	30.2	4.2	6265	4	US-09-129-112-3	Sequence 3, Appli
1014	30.2	4.2	145	4	US-09-621-976-8550	Sequence 8550, Ap	1087	30.2	4.2	6314	4	US-09-620-312D-98	Sequence 98, Appl
1015	30.2	4.2	147	4	US-09-621-976-8551	Sequence 8551, Ap	1088	30.2	4.2	6317	4	US-10-204-708-12	Sequence 12, Appl
1016	30.2	4.2	237	4	US-09-248-796A-10661	Sequence 10661, Ap	cl1089	30.2	4.2	6866	4	US-10-204-708-28	Sequence 28, Appl
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cl1018	30.2	4.2	276	4	US-09-248-796A-11619	Sequence 11619, A	cl1091	30.2	4.2	8607	4	US-10-204-708-3	Sequence 3, Appli
1019	30.2	4.2	350	3	US-09-157-177-110	Sequence 110, App	1092	30.2	4.2	10619	4	US-10-204-708-55	Sequence 55, Appl
1020	30.2	4.2	350	4	US-09-541-210-110	Sequence 110, App	1093	30.2	4.2	11015	4	US-10-204-708-86	Sequence 86, Appl
1021	30.2	4.2	357	4	US-09-248-796A-7735	Sequence 7735, Ap	cl1094	30.2	4.2	11050	4	US-10-204-708-86	Sequence 86, Appl
cl1022	30.2	4.2	388	2	US-08-623-906A-13	Sequence 13, Appl	1095	30.2	4.2	11131	4	US-09-488-671-10	Sequence 10, Appl
cl1023	30.2	4.2	407	4	US-09-270-767-6129	Sequence 6129, Ap	1096	30.2	4.2	12141	3	US-08-956-171E-120	Sequence 120, App
cl1024	30.2	4.2	407	4	US-09-270-767-6129	Sequence 6129, Ap	cl1097	30.2	4.2	13508	4	US-08-781-986A-120	Sequence 120, App
1025	30.2	4.2	434	4	US-09-232-785-250	Sequence 250, App	1098	30.2	4.2	13508	4	US-09-614-981-8	Sequence 8, Appli
1026	30.2	4.2	434	4	US-09-248-796A-7714	Sequence 7714, Ap	1099	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
1027	30.2	4.2	477	4	US-09-621-976-19183	Sequence 19183, A	1100	30.2	4.2	16397	4	US-08-781-986A-205	Sequence 205, App
cl1028	30.2	4.2	563	4	US-09-799-451-59	Sequence 59, Appl	1101	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1029	30.2	4.2	635	3	US-08-998-416-193	Sequence 193, App	1102	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1030	30.2	4.2	676	3	US-08-998-416-193	Sequence 193, App	1103	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1031	30.2	4.2	676	3	US-08-998-416-193	Sequence 193, App	1104	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1032	30.2	4.2	676	3	US-08-998-416-193	Sequence 193, App	1105	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1033	30.2	4.2	685	4	US-09-513-999C-13230	Sequence 13230, A	1106	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
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cl1036	30.2	4.2	727	4	US-09-270-767-9799	Sequence 9799, Ap	1109	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1037	30.2	4.2	727	4	US-09-270-767-9799	Sequence 9799, Ap	1110	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
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cl1039	30.2	4.2	771	3	US-09-277-716-19	Sequence 19, Appl	1112	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
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cl1042	30.2	4.2	1030	4	US-09-152-060-41	Sequence 41, Appl	1115	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1043	30.2	4.2	1114	3	US-09-277-716-21	Sequence 21, Appl	1116	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1044	30.2	4.2	1146	3	US-09-609-161B-21	Sequence 21, Appl	1117	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1045	30.2	4.2	1151	1	US-08-236-754-3	Sequence 3, Appli	1118	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1046	30.2	4.2	1158	4	US-09-643-596B-139	Sequence 139, App	1119	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1047	30.2	4.2	1175	3	US-09-378-088A-77	Sequence 77, Appl	1120	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1048	30.2	4.2	1175	3	US-09-643-596B-77	Sequence 77, Appl	1121	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1049	30.2	4.2	1182	4	US-09-248-796A-779	Sequence 779, App	1122	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1050	30.2	4.2	1220	4	US-09-270-767-1667	Sequence 1667, Ap	1123	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
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1052	30.2	4.2	1230	3	US-09-140-466-1	Sequence 1, Appli	1125	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1053	30.2	4.2	1308	4	US-09-107-532A-3483	Sequence 3483, Ap	1126	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1054	30.2	4.2	1371	4	US-08-956-171E-271	Sequence 271, App	1127	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1055	30.2	4.2	1371	4	US-08-781-986A-271	Sequence 271, App	1128	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
cl1056	30.2	4.2	1410	3	US-09-378-088A-81	Sequence 81, Appl	1129	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App
			1410	4	US-09-643-596B-81	Sequence 81, Appl	1130	30.2	4.2	16397	4	US-08-956-171E-205	Sequence 205, App

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c1282	29.6	4.2	257	4	US-09-270-767-17878	Sequence 17878, A	1355	29.6	4.2	51552	4	US-09-733-294A-30	Sequence 30, Appl
c1283	29.6	4.2	261	4	US-09-248-796A-12693	Sequence 12693, A	1356	29.6	4.2	53332	4	US-09-801-861-3	Sequence 3, Appli
c1284	29.6	4.2	299	2	US-08-623-906A-19	Sequence 19, Appl	c1357	29.6	4.2	53332	4	US-10-224-562-3	Sequence 3, Appli
c1285	29.6	4.2	354	4	US-09-621-376-16145	Sequence 16145, A	1358	29.6	4.2	62804	3	US-09-800-960-3	Sequence 3, Appli
c1286	29.6	4.2	372	4	US-09-328-352-920	Sequence 352, App	1359	29.6	4.2	62804	3	US-10-096-960-3	Sequence 3, Appli
c1287	29.6	4.2	446	2	US-08-332-766A-26	Sequence 26, Appl	1360	29.6	4.2	87350	3	US-08-781-891-79	Sequence 79, Appl
c1288	29.6	4.2	458	4	US-09-621-976-3216	Sequence 3216, Ap	1361	29.6	4.2	87350	3	US-09-618-166-79	Sequence 79, Appl
c1289	29.6	4.2	556	3	US-09-018-584A-25	Sequence 25, Appl	1362	29.6	4.2	87350	3	US-09-791-211-3	Sequence 3, Appli
c1290	29.6	4.2	556	3	US-09-784-423-25	Sequence 25, Appl	1363	29.6	4.2	87350	3	US-09-128-155-17	Sequence 17, Appl
c1291	29.6	4.2	563	3	US-09-276-531-38	Sequence 38, Appl	1364	29.6	4.2	176373	4	US-09-248-796A-9955	Sequence 10511, A
c1292	29.6	4.2	563	3	US-09-602-877A-95	Sequence 95, Appl	1365	29.6	4.2	176373	4	US-09-248-796A-9955	Sequence 126, App
c1293	29.6	4.2	629	3	US-09-385-982-147	Sequence 147, App	1366	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 9138, Ap
c1294	29.6	4.2	744	3	US-08-821-994-39	Sequence 39, Appl	1367	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 24420, A
c1295	29.6	4.2	801	4	US-10-039-659A-5	Sequence 5, Appli	1368	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 16058, A
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c1297	29.6	4.2	1023	4	US-09-248-796A-7824	Sequence 7824, Ap	1370	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 16019, A
c1298	29.6	4.2	1024	4	US-09-328-475C-50	Sequence 50, Appl	1371	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 16042, A
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c1302	29.6	4.2	1281	4	US-09-248-796A-5417	Sequence 5417, Ap	1375	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1303	29.6	4.2	1368	4	US-09-107-532A-3101	Sequence 3101, Ap	1376	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1304	29.6	4.2	1404	3	US-09-134-001C-615	Sequence 615, App	1377	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
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c1310	29.6	4.2	1692	3	US-09-134-001C-335	Sequence 1, Appli	1383	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1311	29.6	4.2	1771	4	US-09-270-767-11541	Sequence 11, Appl	1384	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1312	29.6	4.2	1893	4	US-09-248-796A-6172	Sequence 6172, Ap	1385	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1313	29.6	4.2	2058	3	US-08-749-391-1	Sequence 1, Appli	1386	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1314	29.6	4.2	2058	3	US-09-390-200-1	Sequence 1, Appli	1387	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1315	29.6	4.2	2061	2	US-08-960-022-11	Sequence 11, Appl	1388	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1316	29.6	4.2	2614	4	US-09-004-056-1	Sequence 1, Appli	1389	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1317	29.6	4.2	2734	3	US-08-470-369-26	Sequence 26, Appl	1390	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1318	29.6	4.2	2748	3	US-08-470-369-25	Sequence 25, Appl	1391	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1319	29.6	4.2	2872	4	US-10-204-708-92	Sequence 92, Appl	1392	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1320	29.6	4.2	3001	4	US-09-539-333D-130	Sequence 130, App	1393	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1321	29.6	4.2	3028	4	US-09-710-279-4247	Sequence 4247, Ap	1394	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1322	29.6	4.2	3110	4	US-09-710-279-4390	Sequence 4390, Ap	1395	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1323	29.6	4.2	3313	4	US-09-710-279-3923	Sequence 3923, Ap	1396	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1324	29.6	4.2	3338	4	US-09-489-847-117	Sequence 117, App	1397	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1325	29.6	4.2	3353	1	US-08-123-702-1	Sequence 1, Appli	1398	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
c1326	29.6	4.2	3353	1	US-08-456-420-12	Sequence 12, Appl	1399	29.6	4.2	176373	4	US-09-513-999C-10511	Sequence 1376, Ap
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C 638	39	5.5	5195	15	US-10-311-455-894	Sequence 894, App	C 777	38.4	5.4	1223197	15	US-10-027-632-179264	Sequence 179264, A
C 639	39	5.5	6059	15	US-10-311-455-786	Sequence 786, App	C 778	38.2	5.4	324	10	US-09-814-353-17879	Sequence 17879, A
C 640	39	5.5	7450	15	US-10-240-453-5	Sequence 5, Appli	C 779	38.2	5.4	433	18	US-10-674-124A-8934	Sequence 8934, App
C 641	39	5.5	9180	15	US-10-311-455-1937	Sequence 1937, App	C 780	38.2	5.4	456	9	US-09-864-761-15716	Sequence 15716, A
C 642	39	5.5	30304	17	US-10-367-094-128	Sequence 128, App	C 781	38.2	5.4	511	15	US-10-106-698-1256	Sequence 1256, App
C 643	38.8	5.4	199	9	US-09-728-444-981	Sequence 981, App	C 782	38.2	5.4	634	16	US-10-424-599-93966	Sequence 93966, A
C 644	38.8	5.4	263	10	US-09-814-353-18283	Sequence 18283, A	C 783	38.2	5.4	996	18	US-10-425-115-151933	Sequence 151933, A
C 645	38.8	5.4	393	9	US-09-960-352-4582	Sequence 4582, App	C 784	38.2	5.4	1121	18	US-10-425-115-115706	Sequence 115706, A
C 646	38.8	5.4	598	13	US-10-027-632-221434	Sequence 221434, A	C 785	38.2	5.4	1141	15	US-10-336-753-39	Sequence 39, Appli
C 647	38.8	5.4	598	15	US-10-027-632-221434	Sequence 221434, A	C 786	38.2	5.4	1164	18	US-10-363-345A-28253	Sequence 28253, A
C 648	38.8	5.4	745	13	US-10-027-632-33292	Sequence 33292, A	C 787	38.2	5.4	2562	15	US-10-336-753-38	Sequence 38, Appli
C 649	38.8	5.4	5641	15	US-10-027-632-33292	Sequence 33292, A	C 788	38.2	5.4	2623	17	US-10-717-597-236	Sequence 236, App
C 650	38.8	5.4	8170	15	US-10-311-455-1369	Sequence 1369, App	C 789	38.2	5.4	4756	9	US-09-982-091A-3	Sequence 3, Appli
C 651	38.8	5.4	9005	15	US-10-311-455-131	Sequence 131, App	C 790	38.2	5.4	7851	15	US-10-311-455-1733	Sequence 1733, App
C 652	38.8	5.4	9005	15	US-10-311-455-35	Sequence 35, Appli	C 791	38.2	5.4	16287	15	US-10-311-455-645	Sequence 645, App
C 653	38.6	5.4	256	11	US-09-732-627A-470	Sequence 470, App	C 792	38.2	5.4	50460	13	US-10-087-192-1633	Sequence 1633, App
C 654	38.6	5.4	316	16	US-10-424-599-20711	Sequence 20711, A	C 793	38.2	5.4	58837	9	US-09-982-091A-5	Sequence 5, Appli
C 655	38.6	5.4	526	17	US-10-021-323-14764	Sequence 14764, A	C 794	38.2	5.4	70215	13	US-10-087-192-217	Sequence 217, App
C 656	38.6	5.4	576	10	US-09-814-353-5208	Sequence 5208, App	C 795	38.2	5.4	174703	13	US-10-087-192-1336	Sequence 1336, App
C 657	38.6	5.4	576	10	US-09-814-353-11495	Sequence 11495, A	C 796	38.2	5.4	289190	17	US-10-087-192-1135	Sequence 1135, App
C 658	38.6	5.4	5376	15	US-10-311-455-2123	Sequence 2123, App	C 797	38.2	5.4	329	18	US-10-674-124A-22067	Sequence 22067, A
C 659	38.6	5.4	5416	15	US-10-311-455-1769	Sequence 1769, App	C 798	38	5.3	466	18	US-10-674-124A-17623	Sequence 17623, A
C 660	38.6	5.4	562	15	US-10-311-455-1260	Sequence 1260, App	C 799	38	5.3	647	18	US-10-425-115-40312	Sequence 40312, A
C 661	38.6	5.4	6015	15	US-10-311-455-650	Sequence 650, App	C 801	38	5.3	681	9	US-09-823-830A-26	Sequence 26, Appli
C 662	38.6	5.4	6486	17	US-10-433-793-79	Sequence 79, Appli	C 802	38	5.3	779	17	US-10-437-963-58325	Sequence 58325, A
C 663	38.6	5.4	6591	15	US-10-311-455-1223	Sequence 1223, App	C 803	38	5.3	918	18	US-10-425-115-81231	Sequence 81231, A
C 664	38.6	5.4	13376	15	US-10-311-455-556	Sequence 556, App	C 804	38	5.3	1243	18	US-10-425-115-172117	Sequence 172117, A
C 665	38.6	5.4	21537	15	US-10-311-455-1972	Sequence 1972, App	C 805	38	5.3	3251	13	US-10-027-632-255884	Sequence 255884, A
C 666	38.6	5.4	21118	9	US-09-799-462A-16	Sequence 16, Appli	C 806	38	5.3	5461	17	US-10-311-455-971	Sequence 971, App
C 667	38.6	5.4	22118	10	US-09-815-981-5	Sequence 5, Appli	C 807	38	5.3	5461	17	US-10-437-963-793-7	Sequence 7, Appli
C 668	38.6	5.4	22118	10	US-09-836-911A-16	Sequence 16, Appli	C 808	38	5.3	6754	16	US-10-221-613-266	Sequence 266, App
C 669	38.6	5.4	22118	10	US-09-815-979-5	Sequence 5, Appli	C 809	38	5.3	7615	16	US-10-257-166-54	Sequence 54, Appli
C 670	38.6	5.4	22118	13	US-10-125-767-16	Sequence 16, Appli	C 810	38	5.3	9910	15	US-10-311-455-399	Sequence 399, App
C 671	38.6	5.4	22118	14	US-10-151-081-16	Sequence 16, Appli	C 811	38	5.3	15548	15	US-10-311-455-2128	Sequence 2128, App
C 672	38.6	5.4	22118	15	US-10-287-313-16	Sequence 16, Appli	C 812	38	5.3				
C 673	38.6	5.4	22118	15	US-10-219-694-16	Sequence 16, Appli							

813	38	5.3	19233	15	US-10-204-708-45	Sequence 45, Appl	888	37.4	5.2	934	13	US-10-027-632-166719	Sequence 166719,
C 814	38	5.3	27469	15	US-10-017-161-1015	Sequence 1015, Ap	889	37.4	5.2	934	15	US-10-027-632-166719	Sequence 166719,
815	38	5.3	33456	13	US-10-087-192-103	Sequence 103, App	C 890	37.4	5.2	978	13	US-10-027-632-170163	Sequence 170163,
C 816	38	5.3	33234	17	US-10-322-696-73	Sequence 73, Appl	C 891	37.4	5.2	978	15	US-10-027-632-170163	Sequence 170163,
C 817	38	5.3	398287	17	US-10-741-601-5719	Sequence 5719, Ap	C 892	37.4	5.2	2435	13	US-10-027-632-254051	Sequence 254051,
C 818	37.8	5.3	201	17	US-10-741-601-6270	Sequence 6270, Ap	C 893	37.4	5.2	2435	15	US-10-027-632-254051	Sequence 254051,
819	37.8	5.3	284	18	US-10-674-124A-9083	Sequence 9083, Ap	894	37.4	5.2	2778	16	US-10-108-260A-164	Sequence 164, App
C 820	37.8	5.3	470	9	US-09-864-761-701	Sequence 701, App	895	37.4	5.2	5984	17	US-10-433-793-23	Sequence 23, Appl
C 821	37.8	5.3	538	18	US-10-363-345A-33383	Sequence 33383, A	C 896	37.4	5.2	6181	16	US-10-221-613-232	Sequence 232, App
C 822	37.8	5.3	538	18	US-10-363-345A-33384	Sequence 33384, A	C 897	37.4	5.2	6239	15	US-10-311-455-1749	Sequence 1749, Ap
C 823	37.8	5.3	710	17	US-10-437-963-82026	Sequence 82026, A	C 898	37.4	5.2	6239	15	US-10-240-453-171	Sequence 171, App
C 824	37.8	5.3	856	18	US-10-425-115-158031	Sequence 158031	C 899	37.4	5.2	6668	15	US-10-311-455-1191	Sequence 1191, App
C 825	37.8	5.3	1208	16	US-10-424-599-85771	Sequence 85771, A	900	37.4	5.2	6668	16	US-10-221-714A-139	Sequence 139, App
C 826	37.8	5.3	1537	16	US-10-610-473-2	Sequence 2, Appl	C 901	37.4	5.2	6917	15	US-10-311-455-2208	Sequence 2208, Ap
C 827	37.8	5.3	2000	16	US-10-260-238-2453	Sequence 2453, Ap	C 902	37.4	5.2	7231	15	US-10-240-452-23	Sequence 23, Appl
C 828	37.8	5.3	3953	16	US-10-302-172-546	Sequence 546, App	C 903	37.4	5.2	8305	15	US-10-311-455-1541	Sequence 1541, Ap
C 829	37.8	5.3	6242	15	US-10-311-455-2121	Sequence 2121, Ap	C 904	37.4	5.2	10591	17	US-10-601-807-1	Sequence 1, Appl
C 830	37.8	5.3	6731	16	US-10-257-166-44	Sequence 44, Appl	C 905	37.4	5.2	17144	16	US-10-221-714A-387	Sequence 387, App
C 831	37.8	5.3	7072	16	US-10-221-613-348	Sequence 348, App	C 906	37.4	5.2	19080	16	US-10-388-934-722	Sequence 722, App
C 832	37.8	5.3	7369	18	US-10-473-126-132	Sequence 132, App	C 907	37.4	5.2	19080	16	US-10-388-934-750	Sequence 750, App
C 833	37.8	5.3	7369	18	US-10-473-126-132	Sequence 132, App	C 908	37.4	5.2	31812	13	US-10-087-192-1279	Sequence 1279, Ap
C 834	37.8	5.3	7369	18	US-10-473-126-278	Sequence 278, App	C 909	37.4	5.2	32677	17	US-10-367-094-133	Sequence 133, App
C 835	37.8	5.3	9504	15	US-10-240-453-281	Sequence 281, App	C 910	37.4	5.2	37973	15	US-10-311-455-2170	Sequence 2170, Ap
C 836	37.8	5.3	10369	15	US-10-311-455-366	Sequence 366, App	C 911	37.4	5.2	46130	15	US-10-017-161-985	Sequence 985, App
C 837	37.8	5.3	10369	15	US-10-221-714A-26	Sequence 26, Appl	C 912	37.4	5.2	47096	17	US-10-367-094-151	Sequence 151, App
C 838	37.8	5.3	10543	16	US-10-221-613-120	Sequence 120, App	C 913	37.4	5.2	55611	15	US-10-017-161-783	Sequence 783, App
C 839	37.8	5.3	15156	17	US-10-741-601-5747	Sequence 5747, Ap	C 914	37.4	5.2	63248	13	US-10-087-192-1879	Sequence 1879, Ap
C 840	37.8	5.3	16918	15	US-10-311-455-1590	Sequence 1590, Ap	C 915	37.4	5.2	145025	13	US-10-087-192-1051	Sequence 1051, Ap
C 841	37.8	5.3	19659	15	US-10-311-455-729	Sequence 729, App	C 916	37.4	5.2	153740	17	US-10-322-696-85	Sequence 85, Appl
C 842	37.8	5.3	29556	11	US-09-997-722-229	Sequence 229, App	C 917	37.4	5.2	160771	17	US-10-450-826-86	Sequence 86, Appl
C 843	37.8	5.3	87394	18	US-10-810-788A-6	Sequence 6, Appl	C 918	37.4	5.2	164841	13	US-10-087-192-985	Sequence 985, App
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C 845	37.8	5.3	202001	14	US-10-274-590-3	Sequence 3, Appl	C 920	37.4	5.2	786431	15	US-10-412-277-3	Sequence 3, Appl
C 846	37.8	5.3	253861	17	US-10-741-601-5611	Sequence 5611, Ap	C 921	37.2	5.2	299	10	US-09-814-353-4844	Sequence 4844, Ap
C 847	37.8	5.3	26187	13	US-10-087-192-2002	Sequence 2002, Ap	C 922	37.2	5.2	299	10	US-09-814-353-11141	Sequence 1141, A
C 848	37.6	5.3	341	18	US-10-674-124A-24606	Sequence 24606, A	C 923	37.2	5.2	314	18	US-10-674-124A-13664	Sequence 13664, A
C 849	37.6	5.3	388	18	US-10-674-124A-12597	Sequence 12597, A	C 924	37.2	5.2	344	18	US-10-674-124A-13684	Sequence 13684, A
C 850	37.6	5.3	776	13	US-10-027-632-163595	Sequence 163595,	C 925	37.2	5.2	450	18	US-10-674-124A-17991	Sequence 17991, A
C 851	37.6	5.3	776	13	US-10-027-632-163595	Sequence 163595,	C 926	37.2	5.2	540	15	US-10-106-698-3077	Sequence 3077, Ap
C 852	37.6	5.3	797	13	US-10-027-632-28604	Sequence 28604, A	C 927	37.2	5.2	692	16	US-10-398-221-1133	Sequence 1133, Ap
C 853	37.6	5.3	797	13	US-10-027-632-28604	Sequence 28604, A	C 928	37.2	5.2	891	15	US-10-106-698-1496	Sequence 1496, Ap
C 854	37.6	5.3	797	13	US-10-027-632-112337	Sequence 112337,	C 929	37.2	5.2	1047	16	US-10-424-599-119405	Sequence 119405,
C 855	37.6	5.3	797	13	US-10-027-632-112337	Sequence 112337,	C 930	37.2	5.2	1601	13	US-10-027-632-258609	Sequence 258609,
C 856	37.6	5.3	797	13	US-10-027-632-112337	Sequence 112337,	C 931	37.2	5.2	1601	13	US-10-027-632-258610	Sequence 258610,
C 857	37.6	5.3	5218	15	US-10-311-455-1239	Sequence 1239, Ap	C 932	37.2	5.2	1601	13	US-10-027-632-258611	Sequence 258611,
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C 859	37.6	5.3	6240	15	US-10-311-455-22	Sequence 22, Appl	C 934	37.2	5.2	1601	13	US-10-027-632-258613	Sequence 258613,
C 860	37.6	5.3	9219	16	US-10-311-455-2400	Sequence 2400, Ap	C 935	37.2	5.2	1601	13	US-10-027-632-258614	Sequence 258614,
C 861	37.6	5.3	9219	16	US-10-311-455-2400	Sequence 2400, Ap	C 936	37.2	5.2	1601	13	US-10-027-632-258615	Sequence 258615,
C 862	37.6	5.3	11534	15	US-10-311-455-316	Sequence 316, App	C 937	37.2	5.2	1601	15	US-10-027-632-258610	Sequence 258610,
C 863	37.6	5.3	13125	15	US-10-311-455-1200	Sequence 1200, Ap	C 938	37.2	5.2	1601	15	US-10-027-632-258610	Sequence 258610,
C 864	37.6	5.3	13125	15	US-10-240-485-110	Sequence 110, App	C 939	37.2	5.2	1601	15	US-10-027-632-258611	Sequence 258611,
C 865	37.6	5.3	14798	15	US-10-311-455-1005	Sequence 1005, Ap	C 940	37.2	5.2	1601	15	US-10-027-632-258612	Sequence 258612,
C 866	37.6	5.3	17528	15	US-10-311-455-574	Sequence 574, App	C 941	37.2	5.2	1601	15	US-10-027-632-258613	Sequence 258613,
C 867	37.6	5.3	19787	15	US-10-311-455-1423	Sequence 1423, Ap	C 942	37.2	5.2	1601	15	US-10-027-632-258614	Sequence 258614,
C 868	37.6	5.3	73334	15	US-10-311-455-2098	Sequence 2098, Ap	C 943	37.2	5.2	1601	15	US-10-027-632-258615	Sequence 258615,
C 869	37.6	5.3	73334	16	US-10-240-593C-128	Sequence 128, App	C 944	37.2	5.2	1657	16	US-10-398-221-3406	Sequence 3406, Ap
C 870	37.4	5.2	210	18	US-10-674-124A-23762	Sequence 23762, A	C 945	37.2	5.2	2000	9	US-09-938-842A-3866	Sequence 3866, Ap
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C 872	37.4	5.2	399	18	US-10-674-124A-1572	Sequence 1572, Ap	C 947	37.2	5.2	2548	13	US-10-027-632-110619	Sequence 110619,
C 873	37.4	5.2	401	18	US-10-674-124A-11243	Sequence 11243, A	C 948	37.2	5.2	2548	13	US-10-027-632-110620	Sequence 110620,
C 874	37.4	5.2	403	18	US-10-674-124A-1571	Sequence 1571, Ap	C 949	37.2	5.2	2548	15	US-10-027-632-110619	Sequence 110619,
C 875	37.4	5.2	403	18	US-10-674-124A-22251	Sequence 22251, A	C 950	37.2	5.2	2548	15	US-10-027-632-110620	Sequence 110620,
C 876	37.4	5.2	468	18	US-10-674-124A-11619	Sequence 11619, A	C 951	37.2	5.2	2602	9	US-09-974-238-45	Sequence 45, Appl
C 877	37.4	5.2	489	13	US-10-027-632-170164	Sequence 170164,	C 952	37.2	5.2	2763	13	US-10-027-632-261547	Sequence 261547,
C 878	37.4	5.2	489	13	US-10-027-632-170165	Sequence 170165,	C 953	37.2	5.2	2763	13	US-10-027-632-261548	Sequence 261548,
C 879	37.4	5.2	489	15	US-10-027-632-170165	Sequence 170165,	C 954	37.2	5.2	2763	13	US-10-027-632-261549	Sequence 261549,
C 880	37.4	5.2	489	15	US-10-027-632-170165	Sequence 170165,	C 955	37.2	5.2	2763	13	US-10-027-632-261550	Sequence 261550,
C 881	37.4	5.2	510	10	US-09-814-333-18805	Sequence 18805, A	C 956	37.2	5.2	2763	13	US-10-027-632-261551	Sequence 261551,
C 882	37.4	5.2	579	10	US-09-814-333-3569	Sequence 3569, Ap	C 957	37.2	5.2	2763	13	US-10-027-632-261552	Sequence 261552,
C 883	37.4	5.2	579	10	US-09-814-333-11856	Sequence 11856, A	C 958	37.2	5.2	2763	13	US-10-027-632-261553	Sequence 261553,
C 886	37.4	5.2	715	13	US-10-027-632-231083	Sequence 231083,	C 959	37.2	5.2	2763	15	US-10-027-632-261547	Sequence 261547,
C 887	37.4	5.2	715	15	US-10-027-632-231083	Sequence 231083,	C 960	37.2	5.2	2763	15	US-10-027-632-261548	Sequence 261548,

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962	37.2	2763	15	US-10-027-632-261550	Sequence 261550, App	c1035	37	5.2	17848	16	US-10-257-166-58	Sequence 58, App
963	37.2	2763	15	US-10-027-632-261551	Sequence 261551, App	c1036	37	5.2	37278	17	US-10-322-281-21	Sequence 21, App
964	37.2	2763	15	US-10-027-632-261552	Sequence 261552, App	c1037	37	5.2	38342	16	US-10-221-714A-471	Sequence 471, App
965	37.2	2763	15	US-10-027-632-261553	Sequence 261553, App	c1038	37	5.2	47448	15	US-10-085-117-145	Sequence 145, App
966	37.2	2763	15	US-10-027-632-261554	Sequence 261554, App	c1039	37	5.2	63502	13	US-10-087-192-271	Sequence 271, App
967	37.2	2763	15	US-10-027-632-261555	Sequence 261555, App	c1040	37	5.2	63502	13	US-10-087-192-271	Sequence 271, App
968	37.2	2763	15	US-10-027-632-261556	Sequence 261556, App	c1041	37	5.2	69081	13	US-10-087-192-271	Sequence 1192, App
969	37.2	2763	15	US-10-027-632-261557	Sequence 261557, App	c1042	37	5.2	70215	13	US-10-087-192-271	Sequence 217, App
970	37.2	2763	15	US-10-027-632-261558	Sequence 261558, App	c1043	37	5.2	339234	17	US-10-087-192-271	Sequence 73, App
971	37.2	2763	15	US-10-027-632-261559	Sequence 261559, App	c1044	36.8	5.2	301	18	US-10-087-192-271	Sequence 16454, A
972	37.2	2763	15	US-10-027-632-261560	Sequence 261560, App	c1045	36.8	5.2	332	18	US-10-087-192-271	Sequence 19917, A
973	37.2	2763	15	US-10-027-632-261561	Sequence 261561, App	c1046	36.8	5.2	350	10	US-10-087-192-271	Sequence 18240, A
974	37.2	2763	15	US-10-027-632-261562	Sequence 261562, App	c1047	36.8	5.2	403	18	US-10-087-192-271	Sequence 53749, A
975	37.2	2763	15	US-10-027-632-261563	Sequence 261563, App	c1048	36.8	5.2	408	9	US-10-087-192-271	Sequence 1221, App
976	37.2	2763	15	US-10-027-632-261564	Sequence 261564, App	c1049	36.8	5.2	416	10	US-10-087-192-271	Sequence 1235, A
977	37.2	2763	15	US-10-027-632-261565	Sequence 261565, App	c1050	36.8	5.2	420	16	US-10-087-192-271	Sequence 128659, A
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979	37.2	2763	15	US-10-027-632-261567	Sequence 261567, App	c1052	36.8	5.2	453	9	US-10-087-192-271	Sequence 12148, A
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981	37.2	2763	15	US-10-027-632-261569	Sequence 261569, App	c1054	36.8	5.2	504	13	US-10-087-192-271	Sequence 14685, A
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983	37.2	2763	15	US-10-027-632-261571	Sequence 261571, App	c1056	36.8	5.2	504	15	US-10-087-192-271	Sequence 6593, App
984	37.2	2763	15	US-10-027-632-261572	Sequence 261572, App	c1057	36.8	5.2	510	17	US-10-087-192-271	Sequence 5097, App
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987	37.2	2763	15	US-10-027-632-261575	Sequence 261575, App	c1060	36.8	5.2	569	15	US-10-087-192-271	Sequence 197522, App
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993	37.2	2763	15	US-10-027-632-261581	Sequence 261581, App	c1066	36.8	5.2	1369	15	US-10-087-192-271	Sequence 266496, App
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995	37.2	2763	15	US-10-027-632-261583	Sequence 261583, App	c1068	36.8	5.2	1387	9	US-10-087-192-271	Sequence 200, App
996	37.2	2763	15	US-10-027-632-261584	Sequence 261584, App	c1069	36.8	5.2	1387	14	US-10-087-192-271	Sequence 113, App
997	37.2	2763	15	US-10-027-632-261585	Sequence 261585, App	c1070	36.8	5.2	5826	16	US-10-087-192-271	Sequence 113, App
998	37.2	2763	15	US-10-027-632-261586	Sequence 261586, App	c1071	36.8	5.2	7321	16	US-10-087-192-271	Sequence 16, App
999	37.2	2763	15	US-10-027-632-261587	Sequence 261587, App	c1072	36.8	5.2	7341	16	US-10-087-192-271	Sequence 300, App
1000	37.2	2763	15	US-10-027-632-261588	Sequence 261588, App	c1073	36.8	5.2	7341	16	US-10-087-192-271	Sequence 357, App
1001	37.2	2763	15	US-10-027-632-261589	Sequence 261589, App	c1074	36.8	5.2	7346	15	US-10-087-192-271	Sequence 318, App
1002	37.2	2763	15	US-10-027-632-261590	Sequence 261590, App	c1075	36.8	5.2	7461	15	US-10-087-192-271	Sequence 1757, App
1003	37.2	2763	15	US-10-027-632-261591	Sequence 261591, App	c1076	36.8	5.2	8056	18	US-10-087-192-271	Sequence 240, App
1004	37.2	2763	15	US-10-027-632-261592	Sequence 261592, App	c1077	36.8	5.2	10467	15	US-10-087-192-271	Sequence 386, App
1005	37.2	2763	15	US-10-027-632-261593	Sequence 261593, App	c1078	36.8	5.2	10467	15	US-10-087-192-271	Sequence 2, App
1006	37.2	2763	15	US-10-027-632-261594	Sequence 261594, App	c1079	36.8	5.2	11416	15	US-10-087-192-271	Sequence 92, App
1007	37.2	2763	15	US-10-027-632-261595	Sequence 261595, App	c1080	36.8	5.2	12176	16	US-10-087-192-271	Sequence 20, App
1008	37.2	2763	15	US-10-027-632-261596	Sequence 261596, App	c1081	36.8	5.2	38918	15	US-10-087-192-271	Sequence 8316, App
1009	37.2	2763	15	US-10-027-632-261597	Sequence 261597, App	c1082	36.8	5.2	38918	15	US-10-087-192-271	Sequence 2049, App
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1011	37.2	2763	15	US-10-027-632-261599	Sequence 261599, App	c1084	36.6	5.1	200	9	US-10-087-192-271	Sequence 319, App
1012	37.2	2763	15	US-10-027-632-261600	Sequence 261600, App	c1085	36.6	5.1	210	18	US-10-087-192-271	Sequence 8784, App
1013	37.2	2763	15	US-10-027-632-261601	Sequence 261601, App	c1086	36.6	5.1	216	9	US-10-087-192-271	Sequence 16664, A
1014	37.2	2763	15	US-10-027-632-261602	Sequence 261602, App	c1087	36.6	5.1	219	16	US-10-087-192-271	Sequence 955, App
1015	37.2	2763	15	US-10-027-632-261603	Sequence 261603, App	c1088	36.6	5.1	241	9	US-10-087-192-271	Sequence 82347, A
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1018	37.2	2763	15	US-10-027-632-261606	Sequence 261606, App	c1091	36.6	5.1	245	18	US-10-087-192-271	Sequence 7059, App
1019	37.2	2763	15	US-10-027-632-261607	Sequence 261607, App	c1092	36.6	5.1	269	18	US-10-087-192-271	Sequence 23669, A
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1021	37.2	2763	15	US-10-027-632-261609	Sequence 261609, App	c1094	36.6	5.1	386	18	US-10-087-192-271	Sequence 16881, A
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1024	37.2	2763	15	US-10-027-632-261612	Sequence 261612, App	c1097	36.6	5.1	447	17	US-10-087-192-271	Sequence 17543, A
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1027	37.2	2763	15	US-10-027-632-261615	Sequence 261615, App	c1100	36.6	5.1	615	15	US-10-087-192-271	Sequence 252767, App
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1029	37.2	2763	15	US-10-027-632-261617	Sequence 261617, App	c1102	36.6	5.1	811	14	US-10-087-192-271	Sequence 97488, A
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1031	37.2	2763	15	US-10-027-632-261619	Sequence 261619, App	c1104	36.6	5.1	925	13	US-10-087-192-271	Sequence 122519, App
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1033	37.2	2763	15	US-10-027-632-261621	Sequence 261621, App	c1106	36.6	5.1	1220	18	US-10-087-192-271	Sequence 122520, App
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c1109	36.6	5.1	1239	18	US-10-847-391-10	Sequence 10, Appl	1182	36.4	5.1	6167	15	US-10-240-453-244	Sequence 244, App
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c1112	36.6	5.1	3144	16	US-10-425-115-82095	Sequence 82095, A	c1185	36.4	5.1	8979	16	US-10-221-613-137	Sequence 137, App
1113	36.6	5.1	4018	16	US-10-336-091-29	Sequence 29, Appl	1186	36.4	5.1	9293	14	US-10-239-676-26	Sequence 26, Appl
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c1115	36.6	5.1	7000	18	US-10-847-321-3	Sequence 3, Appl	1188	36.4	5.1	9233	16	US-10-257-166-56	Sequence 56, Appl
c1116	36.6	5.1	7000	18	US-10-847-391-3	Sequence 3, Appl	c1189	36.4	5.1	10907	15	US-10-429-802-31	Sequence 31, Appl
c1117	36.6	5.1	7025	16	US-10-257-166-142	Sequence 142, App	c1190	36.4	5.1	10907	16	US-10-430-503-22	Sequence 22, Appl
c1118	36.6	5.1	7025	16	US-10-240-454-46	Sequence 46, Appl	c1191	36.4	5.1	14551	15	US-10-240-485-138	Sequence 138, App
1119	36.6	5.1	7143	15	US-10-311-455-956	Sequence 956, App	c1192	36.4	5.1	15000	9	US-09-954-531-175	Sequence 175, App
c1120	36.6	5.1	7657	14	US-10-239-676-185	Sequence 185, App	c1193	36.4	5.1	15674	15	US-10-311-455-336	Sequence 336, App
c1121	36.6	5.1	7657	15	US-10-311-455-1995	Sequence 1995, Ap	c1194	36.4	5.1	15674	15	US-10-240-485-30	Sequence 30, Appl
c1122	36.6	5.1	8143	15	US-10-311-455-1870	Sequence 1870, Ap	1195	36.4	5.1	15951	15	US-10-240-485-134	Sequence 134, App
1123	36.6	5.1	9515	14	US-10-239-676-159	Sequence 159, App	c1196	36.4	5.1	15951	15	US-10-311-455-627	Sequence 627, App
1124	36.6	5.1	9515	15	US-10-240-453-181	Sequence 181, App	c1197	36.4	5.1	17211	15	US-10-311-455-1906	Sequence 1906, Ap
1125	36.6	5.1	10640	15	US-10-304-095-5	Sequence 5, Appl	c1198	36.4	5.1	17211	15	US-10-087-193-703	Sequence 703, App
c1126	36.6	5.1	11131	15	US-10-204-708-27	Sequence 27, Appl	c1199	36.4	5.1	23871	13	US-10-087-193-703	Sequence 703, App
c1127	36.6	5.1	11131	15	US-10-311-455-725	Sequence 725, App	c1200	36.4	5.1	29163	10	US-09-764-891-7809	Sequence 7809, Ap
c1128	36.6	5.1	11131	16	US-10-240-589C-35	Sequence 35, Appl	c1201	36.4	5.1	38342	16	US-10-221-714A-471	Sequence 471, App
1129	36.6	5.1	11260	14	US-10-239-676-19	Sequence 19, Appl	c1202	36.4	5.1	42999	9	US-09-799-462A-17	Sequence 17, Appl
1130	36.6	5.1	11260	15	US-10-240-453-27	Sequence 27, Appl	c1203	36.4	5.1	42999	10	US-09-836-911A-17	Sequence 17, Appl
1131	36.6	5.1	11996	15	US-10-240-485-46	Sequence 46, Appl	c1204	36.4	5.1	42999	10	US-09-738-630-73	Sequence 73, Appl
c1132	36.6	5.1	52242	16	US-10-052-482-172	Sequence 172, App	c1205	36.4	5.1	42999	13	US-10-125-767-17	Sequence 17, Appl
c1133	36.6	5.1	61020	16	US-10-322-281-465	Sequence 465, App	c1206	36.4	5.1	42999	14	US-10-151-081-17	Sequence 17, Appl
1134	36.6	5.1	92076	17	US-10-322-281-465	Sequence 465, App	c1207	36.4	5.1	42999	15	US-10-287-313-17	Sequence 17, Appl
c1135	36.6	5.1	113515	15	US-10-311-455-2148	Sequence 2148, Ap	c1208	36.4	5.1	42999	15	US-10-219-694-17	Sequence 17, Appl
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1137	36.6	5.1	161700	17	US-10-741-601-5623	Sequence 5623, Ap	c1210	36.4	5.1	44972	13	US-10-087-192-349	Sequence 349, App
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1139	36.4	5.1	154	10	US-09-971-353-34	Sequence 34, Appl	c1212	36.4	5.1	54786	16	US-10-052-482-211	Sequence 211, App
1140	36.4	5.1	154	10	US-09-971-353-35	Sequence 35, Appl	c1213	36.4	5.1	54786	16	US-10-052-482-211	Sequence 211, App
c1141	36.4	5.1	261	18	US-10-674-124A-763	Sequence 763, App	c1214	36.4	5.1	89856	17	US-10-322-281-79	Sequence 79, Appl
c1142	36.4	5.1	288	18	US-10-674-124A-25949	Sequence 25949, A	c1215	36.4	5.1	90351	17	US-10-367-094-166	Sequence 166, App
1143	36.4	5.1	313	18	US-10-674-124A-23662	Sequence 23662, A	c1216	36.4	5.1	90351	17	US-10-002-491-10	Sequence 10, Appl
c1144	36.4	5.1	313	18	US-09-814-353-5902	Sequence 5902, Ap	c1217	36.4	5.1	95889	11	US-10-087-192-2029	Sequence 2029, Ap
c1145	36.4	5.1	318	10	US-09-814-353-12183	Sequence 12183, A	c1218	36.4	5.1	95889	11	US-09-997-722-178	Sequence 178, App
c1146	36.4	5.1	318	10	US-10-425-115-149581	Sequence 149581, A	c1219	36.4	5.1	96589	14	US-10-175-523-96	Sequence 96, Appl
c1147	36.4	5.1	324	18	US-09-960-352-13002	Sequence 13002, A	c1220	36.4	5.1	10079	14	US-10-087-192-1831	Sequence 1831, Ap
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1149	36.4	5.1	354	18	US-10-674-124A-11951	Sequence 11951, A	c1222	36.2	5.1	126413	13	US-10-674-124A-9476	Sequence 9476, Ap
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c1151	36.4	5.1	399	18	US-10-674-124A-5992	Sequence 5992, Ap	c1224	36.2	5.1	275	18	US-10-674-124A-7930	Sequence 7930, Ap
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1153	36.4	5.1	430	18	US-10-674-124A-1124	Sequence 1124, Ap	c1226	36.2	5.1	286	9	US-10-027-632-165041	Sequence 165041, A
c1154	36.4	5.1	447	18	US-10-425-115-115729	Sequence 115729, A	c1227	36.2	5.1	300	13	US-10-027-632-165042	Sequence 165042, A
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c1157	36.4	5.1	479	16	US-10-152-319A-315	Sequence 315, App	c1230	36.2	5.1	300	15	US-10-027-632-165042	Sequence 165042, A
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c1162	36.4	5.1	504	13	US-10-027-632-45154	Sequence 45154, A	c1235	36.2	5.1	424	18	US-10-674-124A-15283	Sequence 15283, A
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c1167	36.4	5.1	837	13	US-10-027-632-165955	Sequence 165955, A	c1240	36.2	5.1	517	17	US-10-021-323-11054	Sequence 11054, A
c1168	36.4	5.1	837	13	US-10-027-632-165955	Sequence 165955, A	c1241	36.2	5.1	517	17	US-10-021-323-11054	Sequence 11054, A
c1169	36.4	5.1	837	15	US-10-027-632-165955	Sequence 165955, A	c1242	36.2	5.1	538	10	US-09-814-353-5090	Sequence 5090, Ap
c1170	36.4	5.1	837	15	US-10-027-632-165955	Sequence 165955, A	c1243	36.2	5.1	538	10	US-09-814-353-5090	Sequence 11382, A
c1171	36.4	5.1	926	14	US-09-866-050A-570	Sequence 570, App	c1244	36.2	5.1	543	17	US-10-021-323-12208	Sequence 12208, A
c1172	36.4	5.1	926	14	US-10-152-661-570	Sequence 570, App	c1245	36.2	5.1	543	17	US-10-021-323-12208	Sequence 12208, A
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1174	36.4	5.1	1946	9	US-10-376-564-83	Sequence 83, Appl	c1247	36.2	5.1	543	17	US-10-021-323-12208	Sequence 12208, A
c1175	36.4	5.1	3152	15	US-10-172-118-138	Sequence 138, App	c1248	36.2	5.1	564	13	US-10-027-632-161759	Sequence 61759, A
1176	36.4	5.1	3152	15	US-10-172-118-1860	Sequence 1860, Ap	c1249	36.2	5.1	564	13	US-10-027-632-161759	Sequence 61759, A
c1177	36.4	5.1	3152	16	US-10-342-887-138	Sequence 138, App	c1250	36.2	5.1	564	13	US-10-027-632-161759	Sequence 61759, A
c1178	36.4	5.1	3152	16	US-10-342-887-1860	Sequence 1860, Ap	1251	36.2	5.1	725	15	US-10-195-730-92	Sequence 92, Appl
1179	36.4	5.1	3152	15	US-10-311-455-930	Sequence 930, App	1252	36.2	5.1	786	17	US-10-437-963-98277	Sequence 98277, A

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1254	36.2	5.1	919	15	US-10-017-161-1701	Sequence 1701, Ap	c1327	36	5.0	472	18	US-10-674-124A-3674	Sequence 3674, Ap
1255	36.2	5.1	919	15	US-10-292-798-1357	Sequence 1357, Ap	1328	36	5.0	473	18	US-10-674-124A-7300	Sequence 7300, Ap
1256	36.2	5.1	928	13	US-10-027-632-173095	Sequence 173095,	1329	36	5.0	479	18	US-10-674-124A-4491	Sequence 4491, Ap
1257	36.2	5.1	928	13	US-10-027-632-173096	Sequence 173096,	c1330	36	5.0	543	13	US-10-027-632-6785	Sequence 6785, Ap
1258	36.2	5.1	928	13	US-10-027-632-173097	Sequence 173097,	c1331	36	5.0	543	13	US-10-027-632-324549	Sequence 324549,
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1264	36.2	5.1	1580	16	US-10-282-122A-10992	Sequence 10992, A	1337	36	5.0	549	13	US-10-027-632-37033	Sequence 37033, A
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1267	36.2	5.1	2396	17	US-10-181-530-19	Sequence 19, Appl	c1340	36	5.0	561	13	US-10-027-632-277057	Sequence 277057,
1268	36.2	5.1	2569	18	US-10-425-115-41167	Sequence 41167, A	c1341	36	5.0	561	15	US-10-027-632-277057	Sequence 277057,
1269	36.2	5.1	5339	15	US-10-240-485-180	Sequence 180, App	1342	36	5.0	592	13	US-10-027-632-70333	Sequence 70333, A
1270	36.2	5.1	5647	15	US-10-311-455-1539	Sequence 1539, Ap	1343	36	5.0	592	15	US-10-027-632-70333	Sequence 70333, A
1271	36.2	5.1	5647	16	US-10-221-613-281	Sequence 281, App	1344	36	5.0	594	13	US-10-027-632-246735	Sequence 246735,
1272	36.2	5.1	5845	15	US-10-311-455-1635	Sequence 1635, Ap	1345	36	5.0	594	15	US-10-027-632-246735	Sequence 246735,
1273	36.2	5.1	6113	15	US-10-204-708-14	Sequence 14, Appl	1346	36	5.0	602	13	US-10-027-632-278226	Sequence 278226,
1274	36.2	5.1	6113	15	US-10-311-455-404	Sequence 404, App	1347	36	5.0	602	15	US-10-027-632-278226	Sequence 278226,
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1276	36.2	5.1	6121	15	US-10-311-455-1947	Sequence 1947, Ap	1349	36	5.0	612	13	US-10-027-632-307822	Sequence 307822,
1277	36.2	5.1	6121	15	US-10-221-613-69	Sequence 69, Appl	1350	36	5.0	612	15	US-10-027-632-93923	Sequence 93923, A
1278	36.2	5.1	6222	15	US-10-311-455-656	Sequence 656, App	1351	36	5.0	612	15	US-10-027-632-307822	Sequence 307822,
1279	36.2	5.1	6244	15	US-10-311-455-457	Sequence 457, App	1352	36	5.0	612	15	US-10-027-632-185483	Sequence 185483,
1280	36.2	5.1	7441	16	US-10-257-166-139	Sequence 139, App	c1353	36	5.0	634	13	US-10-027-632-185484	Sequence 185484,
1281	36.2	5.1	7479	16	US-10-240-454-39	Sequence 39, Appl	c1354	36	5.0	634	13	US-10-027-632-185484	Sequence 185484,
1282	36.2	5.1	7589	15	US-10-311-455-921	Sequence 921, App	c1355	36	5.0	634	15	US-10-027-632-185485	Sequence 185485,
1283	36.2	5.1	7900	16	US-10-221-714A-486	Sequence 486, App	c1356	36	5.0	634	15	US-10-027-632-185484	Sequence 185484,
1284	36.2	5.1	9005	15	US-10-311-455-36	Sequence 36, Appl	c1357	36	5.0	634	15	US-10-027-632-185485	Sequence 185485,
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1286	36.2	5.1	10543	16	US-10-221-613-119	Sequence 119, App	1359	36	5.0	636	13	US-10-027-632-308922	Sequence 308922,
1287	36.2	5.1	11944	15	US-10-311-455-2160	Sequence 2160, Ap	1360	36	5.0	636	15	US-10-027-632-308921	Sequence 308921,
1288	36.2	5.1	12356	16	US-10-221-714A-231	Sequence 231, App	1361	36	5.0	636	15	US-10-027-632-308922	Sequence 308922,
1289	36.2	5.1	12986	16	US-10-221-714A-276	Sequence 276, App	c1362	36	5.0	636	15	US-10-027-632-156409	Sequence 156409,
1290	36.2	5.1	14615	16	US-10-221-714A-429	Sequence 429, App	c1363	36	5.0	762	13	US-10-027-632-156410	Sequence 156410,
1291	36.2	5.1	15923	16	US-10-221-613-90	Sequence 90, Appl	c1364	36	5.0	762	15	US-10-027-632-156409	Sequence 156409,
1292	36.2	5.1	17674	15	US-10-311-455-1317	Sequence 1317, Ap	c1365	36	5.0	762	15	US-10-027-632-156410	Sequence 156410,
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1294	36.2	5.1	23695	17	US-10-433-793-11	Sequence 11, Appl	c1367	36	5.0	1130	13	US-10-027-632-254186	Sequence 254186,
1295	36.2	5.1	45736	17	US-10-322-281-767	Sequence 767, App	c1368	36	5.0	1130	15	US-10-027-632-254186	Sequence 254186,
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1301	36	5.0	211	18	US-10-674-124A-23391	Sequence 23391, A	1374	36	5.0	2231	16	US-10-424-599-90659	Sequence 90659, A
1302	36	5.0	296	16	US-10-242-535A-54757	Sequence 54757, A	1375	36	5.0	2645	9	US-09-764-870-76	Sequence 76, Appl
1303	36	5.0	296	16	US-10-085-783A-54757	Sequence 54757, A	1376	36	5.0	2645	14	US-10-125-540-76	Sequence 76, Appl
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1305	36	5.0	339	18	US-10-674-124A-16089	Sequence 16089, A	c1378	36	5.0	3664	18	US-10-473-126-268	Sequence 268, App
1306	36	5.0	350	18	US-10-674-124A-16089	Sequence 16089, A	1379	36	5.0	4985	14	US-10-094-240-10	Sequence 10, Appl
1307	36	5.0	360	18	US-10-674-124A-22374	Sequence 22374, A	c1380	36	5.0	4985	15	US-10-056-405-10	Sequence 10, Appl
1308	36	5.0	367	18	US-10-674-124A-1121	Sequence 11210, A	c1381	36	5.0	5204	15	US-10-311-455-874	Sequence 874, App
1309	36	5.0	375	9	US-09-960-352-15014	Sequence 15014, A	c1382	36	5.0	5204	15	US-10-311-455-1745	Sequence 1745, Ap
1310	36	5.0	420	18	US-10-674-124A-991	Sequence 991, App	1383	36	5.0	5666	15	US-10-311-455-1493	Sequence 1493, Ap
1311	36	5.0	424	9	US-09-960-352-11218	Sequence 11218, A	c1384	36	5.0	6061	15	US-10-311-455-1538	Sequence 1538, Ap
1312	36	5.0	439	13	US-10-027-632-68339	Sequence 68339, A	1385	36	5.0	6061	16	US-10-221-613-272	Sequence 272, App
1313	36	5.0	439	13	US-10-027-632-68340	Sequence 68340, A	c1386	36	5.0	6123	15	US-10-311-455-793	Sequence 793, App
1314	36	5.0	439	13	US-10-027-632-295071	Sequence 295071, A	1387	36	5.0	6317	15	US-10-204-708-11	Sequence 11, Appl
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1316	36	5.0	439	15	US-10-027-632-68339	Sequence 68339, A	1389	36	5.0	6343	18	US-10-473-126-333	Sequence 333, App
1317	36	5.0	439	15	US-10-027-632-295071	Sequence 295071, A	1390	36	5.0	8085	15	US-10-172-086-39	Sequence 39, Appl
1318	36	5.0	439	15	US-10-027-632-295072	Sequence 295072, A	1391	36	5.0	8085	16	US-10-221-714A-201	Sequence 201, App
1319	36	5.0	442	9	US-09-960-352-12911	Sequence 12911, A	1392	36	5.0	8085	17	US-10-311-507-71	Sequence 71, Appl
1320	36	5.0	443	17	US-10-021-323-2953	Sequence 2953, Ap	1393	36	5.0	8085	18	US-10-480-846-39	Sequence 39, Appl
1321	36	5.0	446	18	US-10-674-124A-5557	Sequence 5557, Ap	1394	36	5.0	8246	15	US-10-311-455-175	Sequence 175, App
1322	36	5.0	447	18	US-10-425-115-148961	Sequence 148961, A	c1395	36	5.0	9270	15	US-10-311-455-5	Sequence 5, Appli
1323	36	5.0	448	18	US-10-674-124A-8499	Sequence 8499, Ap	c1396	36	5.0	10957	15	US-10-311-455-1083	Sequence 1083, Ap
1324	36	5.0	451	18	US-10-674-124A-23571	Sequence 23571, A	1397	36	5.0	11050	15	US-10-204-708-86	Sequence 86, Appl
1325	36	5.0	451	18	US-10-674-124A-23571	Sequence 23571, A	1398	36	5.0	11155	15	US-10-311-455-577	Sequence 577, App

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1404	36	5.0	17848	16	US-10-257-166-58	Sequence 58, Appl	1477	35.8	5.0	1191	15	US-10-027-632-204582	Sequence 204582,
c1405	36	5.0	51365	11	US-09-997-722-256	Sequence 256, App	1478	35.8	5.0	1424	9	US-09-729-674-71	Sequence 71, Appl
1406	36	5.0	71251	13	US-10-087-192-356	Sequence 356, App	1479	35.8	5.0	1508	18	US-10-425-115-101424	Sequence 101424,
c1407	36	5.0	100534	17	US-10-367-094-160	Sequence 160, App	1480	35.8	5.0	1723	16	US-10-424-599-98252	Sequence 98252, A
1408	36	5.0	151152	17	US-10-775-169-243	Sequence 243, App	c1481	35.8	5.0	1862	16	US-10-424-599-133068	Sequence 133068,
c1409	36	5.0	151858	17	US-10-322-281-653	Sequence 653, App	c1482	35.8	5.0	2111	16	US-10-108-260A-379	Sequence 379, App
c1410	36	5.0	465237	9	US-09-933-2678-1	Sequence 1, Appl	1483	35.8	5.0	2971	18	US-10-425-115-103107	Sequence 103107,
c1411	36	5.0	513509	10	US-09-754-853A-4	Sequence 4, Appl	c1484	35.8	5.0	3172	13	US-10-027-632-261535	Sequence 261535,
c1412	35.8	5.0	139	18	US-10-674-124A-14551	Sequence 14551, A	c1485	35.8	5.0	3172	15	US-10-027-632-261535	Sequence 261535,
c1413	35.8	5.0	144	9	US-09-867-701-8729	Sequence 8729, App	c1486	35.8	5.0	3410	9	US-09-745-288-100	Sequence 100, App
1414	35.8	5.0	196	9	US-09-867-701-9264	Sequence 9264, App	c1487	35.8	5.0	3410	9	US-09-759-143-110	Sequence 110, App
c1415	35.8	5.0	220	17	US-10-741-601-22209	Sequence 22209, A	c1488	35.8	5.0	3410	9	US-09-780-669-110	Sequence 110, App
1416	35.8	5.0	230	18	US-10-674-124A-26644	Sequence 26644, A	c1489	35.8	5.0	3410	9	US-09-030-606-110	Sequence 110, App
1417	35.8	5.0	313	18	US-10-674-124A-2498	Sequence 2498, App	c1490	35.8	5.0	3410	9	US-09-822-827-110	Sequence 110, App
1418	35.8	5.0	319	17	US-10-021-323-7947	Sequence 7947, App	c1491	35.8	5.0	3410	9	US-09-115-453-110	Sequence 110, App
1419	35.8	5.0	326	18	US-10-674-124A-21108	Sequence 21108, A	c1492	35.8	5.0	3410	9	US-09-232-880-110	Sequence 110, App
c1420	35.8	5.0	333	11	US-09-876-143-359	Sequence 359, App	c1493	35.8	5.0	3410	9	US-09-895-793-110	Sequence 110, App
1421	35.8	5.0	341	16	US-10-424-599-134459	Sequence 134459, A	c1494	35.8	5.0	3410	9	US-09-895-814-110	Sequence 110, App
1422	35.8	5.0	347	18	US-10-674-124A-10561	Sequence 10561, A	c1495	35.8	5.0	3410	13	US-10-012-896-110	Sequence 110, App
1423	35.8	5.0	352	18	US-10-674-124A-19241	Sequence 19241, A	c1496	35.8	5.0	3410	14	US-10-010-940-110	Sequence 110, App
c1424	35.8	5.0	356	18	US-10-674-124A-26079	Sequence 26079, A	c1497	35.8	5.0	3410	15	US-10-144-678A-110	Sequence 110, App
c1425	35.8	5.0	375	10	US-09-814-353-5244	Sequence 5244, App	c1498	35.8	5.0	3410	15	US-10-294-025-110	Sequence 110, App
c1426	35.8	5.0	375	10	US-09-814-353-11531	Sequence 11531, A	c1499	35.8	5.0	3410	16	US-10-453-915-100	Sequence 100, App
c1427	35.8	5.0	379	18	US-10-674-124A-3003	Sequence 3003, App	c1500	35.8	5.0	3410	17	US-10-688-838-110	Sequence 110, App
c1428	35.8	5.0	380	18	US-10-674-124A-17011	Sequence 17011, A							
1429	35.8	5.0	386	18	US-10-674-124A-15766	Sequence 15766, A							
c1430	35.8	5.0	394	18	US-10-674-124A-5612	Sequence 5612, App							
1431	35.8	5.0	395	18	US-10-674-124A-14269	Sequence 14269, A							
1432	35.8	5.0	411	18	US-10-674-124A-4095	Sequence 4095, App							
c1433	35.8	5.0	413	10	US-09-918-995-17359	Sequence 17359, A							
c1434	35.8	5.0	413	18	US-10-674-124A-24659	Sequence 24659, A							
c1435	35.8	5.0	441	18	US-10-425-115-48377	Sequence 48377, A							
c1436	35.8	5.0	442	18	US-10-674-124A-26017	Sequence 26017, A							
1437	35.8	5.0	461	10	US-10-674-124A-19209	Sequence 19209, A							
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1440	35.8	5.0	471	18	US-10-674-124A-8358	Sequence 8358, App							
1441	35.8	5.0	498	15	US-10-029-386-20772	Sequence 20772, A							
1442	35.8	5.0	499	17	US-10-021-323-10189	Sequence 10189, A							
1443	35.8	5.0	503	15	US-10-029-386-7065	Sequence 7065, App							
c1444	35.8	5.0	520	17	US-10-021-323-7699	Sequence 7699, App							
c1445	35.8	5.0	560	17	US-10-437-963-85832	Sequence 85832, A							
1446	35.8	5.0	565	17	US-10-021-323-11125	Sequence 11125, A							
1447	35.8	5.0	585	13	US-10-027-632-204583	Sequence 204583, A							
1448	35.8	5.0	585	13	US-10-027-632-204584	Sequence 204584, A							
1449	35.8	5.0	585	15	US-10-027-632-204583	Sequence 204583, A							
1450	35.8	5.0	585	15	US-10-027-632-204584	Sequence 204584, A							
c1451	35.8	5.0	601	13	US-10-027-632-20599	Sequence 20599, A							
c1452	35.8	5.0	601	15	US-10-027-632-20599	Sequence 20599, A							
c1453	35.8	5.0	608	10	US-09-814-353-5190	Sequence 5190, App							
c1454	35.8	5.0	608	10	US-09-814-353-11478	Sequence 11478, A							
1455	35.8	5.0	609	13	US-10-027-632-113109	Sequence 113109, A							
1456	35.8	5.0	609	13	US-10-027-632-113110	Sequence 113110, A							
1457	35.8	5.0	609	15	US-10-027-632-113109	Sequence 113109, A							
1458	35.8	5.0	609	15	US-10-027-632-113110	Sequence 113110, A							
c1459	35.8	5.0	618	13	US-10-027-632-186424	Sequence 186424, A							
c1460	35.8	5.0	618	13	US-10-027-632-186425	Sequence 186425, A							
c1461	35.8	5.0	618	13	US-10-027-632-186426	Sequence 186426, A							
c1462	35.8	5.0	618	15	US-10-027-632-186425	Sequence 186425, A							
c1463	35.8	5.0	618	15	US-10-027-632-186426	Sequence 186426, A							
c1464	35.8	5.0	702	13	US-10-027-632-126555	Sequence 126555, A							
c1465	35.8	5.0	702	13	US-10-027-632-126555	Sequence 126555, A							
c1466	35.8	5.0	914	13	US-10-027-632-121898	Sequence 121898, A							
1467	35.8	5.0	914	13	US-10-027-632-121899	Sequence 121899, A							
1468	35.8	5.0	914	15	US-10-027-632-121898	Sequence 121898, A							
1469	35.8	5.0	914	15	US-10-027-632-121899	Sequence 121899, A							
1470	35.8	5.0	914	15	US-10-027-632-121899	Sequence 121899, A							
1471	35.8	5.0	928	16	US-10-424-599-4980	Sequence 4980, App							

Search completed: December 2, 2004, 01:10:28

Job time : 661.405 secs

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OM nucleic - nucleic search, using sw model

Run on: December 1, 2004, 23:06:11 ; Search time 3567.89 Seconds
(without alignments)
7282.038 Million cell updates/sec

Title: US-09-989-293A-376
Perfect score: 713
Sequence: 1 aatatacatcattatcata.....tgggtccaaaggaagaaaaaaa 713

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database: EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description
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C 1 527.8 74.0 663 1 AU185777 AU185777
C 2 268.2 37.6 800 6 CB958894 AGENCOURT
C 3 147.6 20.7 663 8 AZ121459 RPCI-23-3
C 4 138.4 19.4 659 4 B1018962 IL3-MT026
5 120 16.8 673 1 AV721179 AV721179
6 104.8 14.7 582 6 CB420818 593806 MA
7 76.6 10.7 363 5 BY547544 BY547544
8 76.6 10.7 419 5 BY536666 BY536666
9 73.8 10.4 855 4 BI107684 BI107684
C 10 58.6 8.2 1101 9 CNS0039G CNS0039G
11 56 7.9 759 9 CNS06QXV CNS06QXV
12 55.6 7.8 996 9 CNS06FSV CNS06FSV
13 54.2 7.6 895 9 CNS044QP CNS044QP
C 14 54 7.6 1043 9 CNS044Q CNS044Q
15 53.2 7.5 583 9 CNS044Q CNS044Q
C 16 52.8 7.4 1029 9 CNS01ZGM CNS01ZGM
C 17 51.4 7.2 661 9 AG160661 AG160661
C 18 51.2 7.2 928 9 CNS00DKY CNS00DKY
19 50 7.0 1184 9 CNS04P4P CNS04P4P
C 20 49.6 7.0 1204 9 CNS016E2 CNS016E2
21 49.4 6.9 460 4 BI14616 BI14616
C 22 49.4 6.9 1225 9 CNS0161D CNS0161D
23 49 6.9 987 9 CNS014PQ CNS014PQ
24 48.6 6.8 734 9 CNS010MP CNS010MP

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C 26	48	6.7	1391	4	BM754863
C 27	47.6	6.7	524	4	BM883775
C 28	47.6	6.7	527	4	BM883968
C 29	47.6	6.7	1101	9	CNS00EVL
C 30	47.2	6.6	584	8	AQ565915
C 31	47.2	6.6	1061	8	BZ504404
C 32	47.2	6.6	1225	9	CNS0161D
C 33	47.2	6.6	1340	9	AG360815
C 34	47.2	6.6	1456	9	CL119201
C 35	47	6.6	1393	9	AG280161
C 36	47	6.6	2330	3	BC020201
C 37	46.8	6.6	543	7	CNS567288
C 38	46.8	6.6	725	8	BH202291
C 39	46.8	6.6	764	8	AZ193158
C 40	46.8	6.6	1101	9	CNS0161D
C 41	46.8	6.6	1201	9	CNS015YI
C 42	46.6	6.5	729	9	AG602398
C 43	46.6	6.5	1043	9	CNS0145P
C 44	46.6	6.5	1206	5	BQ709824
C 45	46.4	6.5	1101	9	CNS01219
C 46	46.4	6.5	1139	8	AQ897537
C 47	46.4	6.5	1152	4	BG309087
C 48	46.4	6.5	1168	8	CC203002
C 49	46.4	6.5	1177	9	AG365683
C 50	46.2	6.5	319	4	BM154986
C 51	46.2	6.5	699	8	BZ036412
C 52	46.2	6.5	868	7	CK160531
C 53	46.2	6.5	949	9	CNS04AIH
C 54	46	6.5	521	8	AQ881547
C 55	46	6.5	922	8	BH016093
C 56	46	6.5	922	9	CNS015W0
C 57	46	6.5	1201	9	CNS0163T
C 58	45.8	6.4	437	9	CNS010VU
C 59	45.8	6.4	532	6	CD682496
C 60	45.8	6.4	642	8	AZ347309
C 61	45.8	6.4	1001	9	CNS0064G
C 62	45.8	6.4	1271	9	AG360730
C 63	45.6	6.4	538	9	CE718428
C 64	45.6	6.4	680	6	BY717385
C 65	45.6	6.4	886	8	BH177277
C 66	45.6	6.4	886	9	CNS07JUX
C 67	45.6	6.4	965	9	CL486691
C 68	45.6	6.4	1101	9	CNS0039L
C 69	45.6	6.4	1151	9	CNS02100
C 70	45.4	6.4	398	8	AZ071875
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C 72	45.4	6.4	798	8	BH727390
C 73	45.4	6.4	798	8	BZ048130
C 74	45.4	6.4	928	9	CNS00DKY
C 75	45.4	6.4	1101	9	CNS0039R
C 76	45.4	6.4	1277	9	AG365949
C 77	45.4	6.4	1334	8	AG321337
C 78	45.2	6.3	814	8	AQ957286
C 79	45.2	6.3	996	9	CNS00FUH
C 80	45.2	6.3	1092	9	CNS020K7
C 81	45.2	6.3	1200	3	CR681220
C 82	45.2	6.3	1333	9	AG390651
C 83	45	6.3	799	9	CNS01ISA
C 84	45	6.3	852	8	AQ894184
C 85	45	6.3	1086	9	CNS00YXK
C 86	45	6.3	1101	9	CNS0106X
C 87	45	6.3	1166	2	BE966404
C 88	44.8	6.3	717	8	BZ047056
C 89	44.8	6.3	718	9	CE752057
C 90	44.8	6.3	748	8	AQ745260
C 91	44.8	6.3	1101	9	CNS017V2
C 92	44.6	6.3	466	1	AU087529
C 93	44.6	6.3	625	9	CNS016A2
C 94	44.6	6.3	649	8	AQ576178
C 95	44.6	6.3	1202	8	CC262481
C 96	44.6	6.3	1255	9	AG346372
C 97	44.6	6.3	1268	8	BZ577630

AL108171	Drosophil
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BM883775	rc22f10.Y
BM883968	rc24b04.Y
AL069706	Drosophil
AQ565915	HS_5318_A
BZ504404	BONHA47TF
AL106171	Drosophil
AG360815	Mus muscu
CL119201	ISB1-76J1
AG280161	Mus muscu
BC020201	Homo sapi
CNS567288	tag10F04.
BH202291	Sm1-56110
AZ193158	SP_1022_B
AL106896	Drosophil
AL106068	Drosophil
AG602398	Mus muscu
AL103735	Drosophil
BQ709824	AGENCOURT
AL101595	Drosophil
AQ897537	HS_3153_A
BG309087	HVSMC000
CC203002	CH261-182
AG365683	Mus muscu
BM154986	fv92b02.Y
BZ036412	oea4e08.
CK160531	FGAS04212
AL281906	Tetraodon
AQ881547	HS_5263_A
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CD682496	rj25f09.Y
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AL062781	Drosophil
AG360730	Mus muscu
CE718428	tigr-gss-
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BH177277	008_L_22-
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CL486691	SAIL_440
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AL176289	Tetraodon
AZ071875	RPCI-23-4
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BZ048130	lkg91h08.
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AL063932	Drosophil
AG365949	Mus muscu
AG321337	Mus muscu
AQ957286	LERAO91TR
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CR681220	Tetraodon
AG390651	Mus muscu
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AQ894184	HS_3072_A
AL069692	Drosophil
AL098595	Drosophil
BE966404	601660455
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CE752057	tigr-gss-
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AL108536	Drosophil
AU087529	AU087529
AL229763	Tetraodon
AQ576178	nbxb0088P
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AG346372	Mus muscu
BZ577630	msb2_550.

98	44.4	6.2	398	5	BP645979	BP645979	171	43.4	6.1	729	9	AG441276	AG441276	Mus muscu
99	44.4	6.2	648	7	CK956218	CK956218	172	43.4	6.1	732	9	AG280613	AG280613	Mus muscu
100	44.4	6.2	705	7	CK934221	CK934221	173	43.4	6.1	762	9	AG280613	AG280613	Mus muscu
101	44.4	6.2	789	7	CNS87139	CNS87139	174	43.4	6.1	827	9	AG280613	AG280613	Mus muscu
102	44.4	6.2	864	7	CNS87139	CNS87139	175	43.4	6.1	867	9	AG280613	AG280613	Mus muscu
103	44.4	6.2	870	4	CG290874	CG290874	176	43.4	6.1	933	6	AG280613	AG280613	Mus muscu
104	44.4	6.2	939	9	CNS033887	CNS033887	177	43.4	6.1	938	8	AG280613	AG280613	Mus muscu
105	44.4	6.2	959	9	CNS006555	CNS006555	178	43.4	6.1	982	8	AG280613	AG280613	Mus muscu
106	44.4	6.2	1101	9	CNS01737Q	CNS01737Q	179	43.4	6.1	997	9	AG280613	AG280613	Mus muscu
107	44.4	6.2	1201	9	CNS010338	CNS010338	180	43.4	6.1	1086	9	AG280613	AG280613	Mus muscu
108	44.4	6.2	1265	9	CG754359	CG754359	181	43.4	6.1	1101	9	AG280613	AG280613	Mus muscu
109	44.4	6.2	1846	9	AG321458	AG321458	182	43.4	6.1	1101	9	AG280613	AG280613	Mus muscu
110	44.4	6.2	2312	3	HSMB00502	HSMB00502	183	43.4	6.1	1201	9	AG280613	AG280613	Mus muscu
111	44.2	6.2	473	7	CN194290	CN194290	184	43.4	6.1	1356	9	AG280613	AG280613	Mus muscu
112	44.2	6.2	500	8	BH892508	BH892508	185	43.2	6.1	332	9	AG280613	AG280613	Mus muscu
113	44.2	6.2	563	8	AQ326762	AQ326762	186	43.2	6.1	391	7	AG280613	AG280613	Mus muscu
114	44.2	6.2	737	9	AG434531	AG434531	187	43.2	6.1	459	7	AG280613	AG280613	Mus muscu
115	44.2	6.2	741	9	AG453968	AG453968	188	43.2	6.1	493	7	AG280613	AG280613	Mus muscu
116	44.2	6.2	760	9	AG597074	AG597074	189	43.2	6.1	520	5	AG280613	AG280613	Mus muscu
117	44.2	6.2	762	9	BX192385	BX192385	190	43.2	6.1	534	8	AG280613	AG280613	Mus muscu
118	44.2	6.2	831	9	CNS0111FZ	CNS0111FZ	191	43.2	6.1	543	4	AG280613	AG280613	Mus muscu
119	44.2	6.2	846	7	CO245816	CO245816	192	43.2	6.1	571	4	AG280613	AG280613	Mus muscu
120	44.2	6.2	901	7	CK422466	CK422466	193	43.2	6.1	639	9	AG280613	AG280613	Mus muscu
121	44.2	6.2	974	9	AG388918	AG388918	194	43.2	6.1	654	8	AG280613	AG280613	Mus muscu
122	44.2	6.2	1101	9	CNS0000GX	CNS0000GX	195	43.2	6.1	674	9	AG280613	AG280613	Mus muscu
123	44.2	6.2	1101	9	CNS0000FG	CNS0000FG	196	43.2	6.1	683	9	AG280613	AG280613	Mus muscu
124	44.2	6.2	1211	9	AG349657	AG349657	197	43.2	6.1	726	8	AG280613	AG280613	Mus muscu
125	44.2	6.2	1432	9	AG381846	AG381846	198	43.2	6.1	791	8	AG280613	AG280613	Mus muscu
126	44	6.2	626	5	BQ246250	BQ246250	199	43.2	6.1	804	9	AG280613	AG280613	Mus muscu
127	44	6.2	839	5	HU151187	HU151187	200	43.2	6.1	842	9	AG280613	AG280613	Mus muscu
128	44	6.2	856	8	BZ475136	BZ475136	201	43.2	6.1	851	7	AG280613	AG280613	Mus muscu
129	44	6.2	914	2	BF273072	BF273072	202	43.2	6.1	857	9	AG280613	AG280613	Mus muscu
130	44	6.2	957	9	CL094619	CL094619	203	43.2	6.1	891	8	AG280613	AG280613	Mus muscu
131	44	6.2	968	2	BF274563	BF274563	204	43.2	6.1	897	8	AG280613	AG280613	Mus muscu
132	44	6.2	970	9	CNS0102BE	CNS0102BE	205	43.2	6.1	925	8	AG280613	AG280613	Mus muscu
133	44	6.2	1101	9	CNS0102JN	CNS0102JN	206	43.2	6.1	1101	9	AG280613	AG280613	Mus muscu
134	44	6.2	1172	9	AG324265	AG324265	207	43.2	6.1	1191	9	AG280613	AG280613	Mus muscu
135	44	6.2	1332	9	AG310802	AG310802	208	43.2	6.1	1201	9	AG280613	AG280613	Mus muscu
136	43.8	6.1	492	8	AZ892258	AZ892258	209	43.2	6.1	2142	3	AG280613	AG280613	Mus muscu
137	43.8	6.1	496	8	BH182183	BH182183	210	43	6.0	262	7	AG280613	AG280613	Mus muscu
138	43.8	6.1	496	9	CNS070NMZ	CNS070NMZ	211	43	6.0	365	8	AG280613	AG280613	Mus muscu
139	43.8	6.1	571	9	CE719270	CE719270	212	43	6.0	370	1	AG280613	AG280613	Mus muscu
140	43.8	6.1	617	9	CE633648	CE633648	213	43	6.0	392	7	AG280613	AG280613	Mus muscu
141	43.8	6.1	651	9	CE733772	CE733772	214	43	6.0	412	9	AG280613	AG280613	Mus muscu
142	43.8	6.1	684	9	CE773519	CE773519	215	43	6.0	567	6	AG280613	AG280613	Mus muscu
143	43.8	6.1	684	9	CNS0255WB	CNS0255WB	216	43	6.0	576	9	AG280613	AG280613	Mus muscu
144	43.8	6.1	777	9	CNS04039H	CNS04039H	217	43	6.0	644	9	AG280613	AG280613	Mus muscu
145	43.8	6.1	779	9	CNS0101PP	CNS0101PP	218	43	6.0	658	8	AG280613	AG280613	Mus muscu
146	43.8	6.1	783	9	BX137081	BX137081	219	43	6.0	672	9	AG280613	AG280613	Mus muscu
147	43.8	6.1	805	9	CNS009F8	CNS009F8	220	43	6.0	760	8	AG280613	AG280613	Mus muscu
148	43.8	6.1	882	2	BF262461	BF262461	221	43	6.0	777	8	AG280613	AG280613	Mus muscu
149	43.8	6.1	937	4	B1667198	B1667198	222	43	6.0	785	8	AG280613	AG280613	Mus muscu
150	43.8	6.1	1201	9	CNS0106RQ	CNS0106RQ	223	43	6.0	899	9	AG280613	AG280613	Mus muscu
151	43.6	6.1	515	6	CN922508	CN922508	224	43	6.0	904	9	AG280613	AG280613	Mus muscu
152	43.6	6.1	617	7	CE737049	CE737049	225	43	6.0	941	7	AG280613	AG280613	Mus muscu
153	43.6	6.1	634	9	LBAP080B03	LBAP080B03	226	43	6.0	945	9	AG280613	AG280613	Mus muscu
154	43.6	6.1	640	8	AQ957285	AQ957285	227	43	6.0	990	9	AG280613	AG280613	Mus muscu
155	43.6	6.1	660	8	AQ957285	AQ957285	228	43	6.0	1101	9	AG280613	AG280613	Mus muscu
156	43.6	6.1	660	8	LBAP049H02	LBAP049H02	229	43	6.0	1246	9	AG280613	AG280613	Mus muscu
157	43.6	6.1	728	9	LBAP049H02	LBAP049H02	230	43	6.0	1306	9	AG280613	AG280613	Mus muscu
158	43.6	6.1	741	9	LBAP049H02	LBAP049H02	231	43	6.0	1524	9	AG280613	AG280613	Mus muscu
159	43.6	6.1	773	8	BH186746	BH186746	232	43	6.0	312	7	AG280613	AG280613	Mus muscu
160	43.6	6.1	773	9	CNS007R5M	CNS007R5M	233	42.8	6.0	466	4	AG280613	AG280613	Mus muscu
161	43.6	6.1	1032	9	CNS0610P	CNS0610P	234	42.8	6.0	487	6	AG280613	AG280613	Mus muscu
162	43.6	6.1	1085	9	CNS0102AK	CNS0102AK	235	42.8	6.0	618	9	AG280613	AG280613	Mus muscu
163	43.6	6.1	1169	9	CNS06KHQ	CNS06KHQ	236	42.8	6.0	625	8	AG280613	AG280613	Mus muscu
164	43.6	6.1	1191	9	CNS0104745	CNS0104745	237	42.8	6.0	650	7	AG280613	AG280613	Mus muscu
165	43.6	6.1	1201	9	CNS01063T	CNS01063T	238	42.8	6.0	697	8	AG280613	AG280613	Mus muscu
166	43.6	6.1	1235	9	AG361148	AG361148	239	42.8	6.0	716	6	AG280613	AG280613	Mus muscu
167	43.6	6.1	1265	6	CF238805	CF238805	240	42.8	6.0	734	9	AG280613	AG280613	Mus muscu
168	43.4	6.1	1628	9	CK382297	CK382297	241	42.8	6.0	751	8	AG280613	AG280613	Mus muscu
169	43.4	6.1	659	9	CE170323	CE170323	242	42.8	6.0	775	6	AG280613	AG280613	Mus muscu
170	43.4	6.1	661	8	AZ704427	AZ704427	243	42.8	6.0					

C 244	42.8	42.8	6.0	780	7	CK595444	AGENCYCOURT	CK595444	AGENCYCOURT	C 317	42.2	5.9	674	7	CK696709	ZF101-P00
C 245	42.8	42.8	6.0	860	4	BG855042	1024041F0	BG855042	1024041F0	C 318	42.2	5.9	697	9	BX137123	Danio rer
C 246	42.8	42.8	6.0	957	6	CB197929	AGENCYCOURT	CB197929	AGENCYCOURT	C 319	42.2	5.9	730	9	AL242211	Tetraodon
C 247	42.8	42.8	6.0	991	9	CL139092	ISB1-1110	CL139092	ISB1-1110	C 320	42.2	5.9	802	9	BX138239	Danio rer
C 248	42.8	42.8	6.0	1001	9	CNS011400	AGENCYCOURT	AL103554	Drosophil	C 321	42.2	5.9	835	5	BUR43034	AGENCYCOURT
C 249	42.8	42.8	6.0	1004	9	CNS016483	Drosophil	AL106485	Drosophil	C 322	42.2	5.9	848	9	CR319963	Medicago
C 250	42.8	42.8	6.0	1071	9	CNS05AJ7	Tetraodon	AL328588	Tetraodon	C 323	42.2	5.9	1101	9	CR319963	Medicago
C 251	42.8	42.8	6.0	1071	9	CNS05AJ7	Tetraodon	AL328588	Tetraodon	C 324	42.2	5.9	1101	9	CNS00339Q	Drosophil
C 252	42.8	42.8	6.0	1101	9	CNS0033BP	Drosophil	AL064091	Drosophil	C 325	42.2	5.9	1178	9	AG324373	Mus muscu
C 253	42.8	42.8	6.0	1101	9	CNS0010CR	Drosophil	AL078809	Drosophil	C 326	42.2	5.9	1201	9	AG324373	Mus muscu
C 254	42.8	42.8	6.0	1205	9	CL509381	SAIL_811	CL509381	SAIL_811	C 327	42.2	5.9	1327	9	AG350127	Mus muscu
C 255	42.6	42.6	6.0	153	9	CE744496	tigr-gss-	BJ766950	BJ766950	C 328	42.2	5.9	1661	8	CC208142	CH261-183
C 256	42.6	42.6	6.0	348	4	BJ696950	BJ696950	BJ696950	BJ696950	C 329	42.2	5.9	1758	9	CL509408	SAIL_811
C 257	42.6	42.6	6.0	473	8	AQ964344	LBRGV48TR	AQ964344	LBRGV48TR	C 330	42	5.9	474	8	AZ551911	RPCI-23-2
C 258	42.6	42.6	6.0	474	7	CE213068	tigr-gss-	CE213068	tigr-gss-	C 331	42	5.9	503	9	CE803771	tigr-gss-
C 259	42.6	42.6	6.0	545	9	CE213068	tigr-gss-	CE213068	tigr-gss-	C 332	42	5.9	516	5	BP122793	BP122793
C 260	42.6	42.6	6.0	558	9	CL513914	SAIL_880	CL513914	SAIL_880	C 333	42	5.9	530	4	AZ522110	202PBC04
C 261	42.6	42.6	6.0	611	8	AZ980273	2M0257E18	AZ980273	2M0257E18	C 334	42	5.9	600	4	BG587790	EST489565
C 262	42.6	42.6	6.0	666	9	CE457756	tigr-gss-	CE457756	tigr-gss-	C 335	42	5.9	660	8	BH183498	O23_L_07-
C 263	42.6	42.6	6.0	724	9	CE117666	tigr-gss-	CE117666	tigr-gss-	C 336	42	5.9	660	9	CNS070NU	T3 end of
C 264	42.6	42.6	6.0	754	5	BUI30687	603118887	BUI30687	603118887	C 337	42	5.9	690	8	CE640616	tigr-gss-
C 265	42.6	42.6	6.0	878	9	AG595634	Mus muscu	AG595634	Mus muscu	C 338	42	5.9	722	9	CE620984	tigr-gss-
C 266	42.6	42.6	6.0	878	9	CNS0187R	Drosophil	AL108993	Drosophil	C 339	42	5.9	725	9	AG583119	Mus muscu
C 267	42.6	42.6	6.0	884	4	BM358117	GA_Ea000	BM358117	GA_Ea000	C 340	42	5.9	738	9	AQ897874	HS_3153_A
C 268	42.6	42.6	6.0	943	9	CL145947	ISB1-1461	CL145947	ISB1-1461	C 341	42	5.9	759	8	AL411257	T7 end of
C 269	42.6	42.6	6.0	988	9	CNS0074D	Drosophil	AL066801	Drosophil	C 342	42	5.9	810	9	CC944048	BOIGT90TR
C 270	42.6	42.6	6.0	984	9	CNS07EBR	T7 end of	AL441457	T7 end of	C 343	42	5.9	810	9	AG591303	Mus muscu
C 271	42.6	42.6	6.0	1061	9	CL145135	ISB1-145G	CL145135	ISB1-145G	C 344	42	5.9	833	9	AG591303	Mus muscu
C 272	42.6	42.6	6.0	1101	9	CNS0166GE	Drosophil	AL106712	Drosophil	C 345	42	5.9	836	9	CG815514	ENTD081TF
C 273	42.6	42.6	6.0	1200	9	CNS0166CO	Drosophil	AL106578	Drosophil	C 346	42	5.9	852	8	AZ551577	ENTD192TF
C 274	42.6	42.6	6.0	1228	9	CL104752	ISB1-4311	CL104752	ISB1-4311	C 347	42	5.9	860	8	AZ533345	ENTD192TF
C 275	42.6	42.6	6.0	1269	9	AG387055	Mus muscu	AG387055	Mus muscu	C 348	42	5.9	875	8	AZ677696	ENTD192TF
C 276	42.6	42.6	6.0	1380	9	AG311242	Mus muscu	AG311242	Mus muscu	C 349	42	5.9	880	8	AZ542811	ENTD201TR
C 277	42.4	42.4	5.9	322	7	CK378425	lan96b04	CK378425	lan96b04	C 350	42	5.9	890	8	AZ670474	ENTD081TF
C 278	42.4	42.4	5.9	380	6	CD673674	fs02h12.x	CD673674	fs02h12.x	C 351	42	5.9	890	8	AZ670474	ENTD081TF
C 279	42.4	42.4	5.9	436	9	AG244102	Lotus cor	AG244102	Lotus cor	C 352	42	5.9	899	8	AZ533645	ENTD081TF
C 280	42.4	42.4	5.9	481	7	CF801372	rf65c12.y	CF801372	rf65c12.y	C 353	42	5.9	905	8	BH159805	ENTD081TF
C 281	42.4	42.4	5.9	483	9	CNS02CV8	Tetraodon	AL191645	Tetraodon	C 354	42	5.9	913	6	CB571874	AGENCYCOURT
C 282	42.4	42.4	5.9	496	8	AZ876082	2M0190N21	AZ876082	2M0190N21	C 355	42	5.9	913	6	CB571874	AGENCYCOURT
C 283	42.4	42.4	5.9	509	9	CR018272	Forward s	CR018272	Forward s	C 356	42	5.9	960	8	AQ899712	HS_2087_B
C 284	42.4	42.4	5.9	514	9	CR253345	Reverse s	CR253345	Reverse s	C 357	42	5.9	976	9	CNS004E5M	Tetraodon
C 285	42.4	42.4	5.9	517	9	CR236635	Reverse s	CR236635	Reverse s	C 358	42	5.9	991	9	CNS004E5M	Tetraodon
C 286	42.4	42.4	5.9	526	8	BH001873	BMBAC0111	BH001873	BMBAC0111	C 359	42	5.9	1006	6	CD388644	AGENCYCOURT
C 287	42.4	42.4	5.9	548	9	CNS03F00	Tetraodon	AL241065	Tetraodon	C 360	42	5.9	1065	9	CL091273	ISB1-20C1
C 288	42.4	42.4	5.9	556	1	AJ443654	AJ443654	AJ443654	AJ443654	C 361	42	5.9	1101	9	CNS0029U	Drosophil
C 289	42.4	42.4	5.9	560	8	AZ358243	1M0100P03	AZ358243	1M0100P03	C 362	42	5.9	1278	9	CNS0121P	Mus muscu
C 290	42.4	42.4	5.9	582	8	AZ324437	1M0046E23	AZ324437	1M0046E23	C 363	42	5.9	1278	9	AG278227	Mus muscu
C 291	42.4	42.4	5.9	610	8	BZ483628	BONEB17TR	BZ483628	BONEB17TR	C 364	42	5.9	1416	5	CL026432	CH216-23B
C 292	42.4	42.4	5.9	666	5	BU298528	603742701	BU298528	603742701	C 365	41.8	5.9	231	5	BX646093	DFP2P781E
C 293	42.4	42.4	5.9	696	8	BZ263683	CH230-409	BZ263683	CH230-409	C 366	41.8	5.9	354	9	CE759586	tigr-gss-
C 294	42.4	42.4	5.9	697	5	BU265286	Mus muscu	BU265286	Mus muscu	C 367	41.8	5.9	445	1	AI601337	fc09h09.x
C 295	42.4	42.4	5.9	710	9	AG363557	Mus muscu	AG363557	Mus muscu	C 368	41.8	5.9	517	8	BH098804	RPCI-24-3
C 296	42.4	42.4	5.9	725	9	CE216155	tigr-gss-	CE216155	tigr-gss-	C 369	41.8	5.9	574	9	CE793680	tigr-gss-
C 297	42.4	42.4	5.9	835	6	CA464213	AGENCYCOURT	CA464213	AGENCYCOURT	C 370	41.8	5.9	574	9	CG963210	MBE888TF
C 298	42.4	42.4	5.9	843	9	CNS00CS1	Drosophil	AL059666	Drosophil	C 371	41.8	5.9	638	8	AQ329262	nxbx0044N
C 299	42.4	42.4	5.9	858	8	BZ635529	OGCCV89TC	BZ635529	OGCCV89TC	C 372	41.8	5.9	652	9	CE468748	tigr-gss-
C 300	42.4	42.4	5.9	981	9	AL189701	Tetraodon	AL189701	Tetraodon	C 373	41.8	5.9	637	9	CNS04707	Tetraodon
C 301	42.4	42.4	5.9	1061	6	CB589276	AGENCYCOURT	CB589276	AGENCYCOURT	C 374	41.8	5.9	707	8	BZ045910	lj135B02
C 302	42.4	42.4	5.9	1061	6	CB589276	AGENCYCOURT	CB589276	AGENCYCOURT	C 375	41.8	5.9	711	8	BZ019696	oe76h09
C 303	42.4	42.4	5.9	1201	9	CNS0152Z	Mus muscu	AL106121	Drosophil	C 376	41.8	5.9	726	8	AQ083754	CP0612A
C 304	42.4	42.4	5.9	1296	9	AG310637	Mus muscu	AG310637	Mus muscu	C 377	41.8	5.9	736	9	CNS06C1X	AL392575 T3 end of
C 305	42.4	42.4	5.9	1370	9	AG320909	Mus muscu	AG320909	Mus muscu	C 378	41.8	5.9	742	9	CE636306	tigr-gss-
C 306	42.4	42.4	5.9	1386	9	AG067592	Pan trogl	AG067592	Pan trogl	C 379	41.8	5.9	750	8	AQ855356	CP01889B
C 307	42.4	42.4	5.9	299	8	AQ469876	CITBI-E1-	AQ469876	CITBI-E1-	C 380	41.8	5.9	757	9	BX967295	Reverse s
C 308	42.2	42.2	5.9	452	1	AI173958	ui43ail.x	AI173958	ui43ail.x	C 381	41.8	5.9	785	9	CNS00ZAC	AL097422 Drosophil
C 309	42.2	42.2	5.9	496	8	AZ197072	SP_1033_B	AZ197072	SP_1033_B	C 382	41.8	5.9	880	8	AZ668224	ENTMGT3TF
C 310	42.2	42.2	5.9	506	9	CPA562538	Cryptospo	CPA562538	Cryptospo	C 383	41.8	5.9	896	9	CG950526	MBENI41TF
C 311	42.2	42.2	5.9	506	9	CR350422	Medicago	CR350422	Medicago	C 384	41.8	5.9	920	9	CNS01UOL	AL168150 Tetraodon
C 312	42.2	42.2	5.9	515	9	CR350418	Medicago	CR350418	Medicago	C 385	41.8	5.9	948	9	CNS0159T	AL105179 Drosophil
C 313	42.2	42.2	5.9	534	9	CR350253	Medicago	CR350253	Medicago	C 386	41.8	5.9	964	9	CNS07EBR	AL441457 T7 end of
C 314	42.2	42.2	5.9	584	9	CE129322	tigr-gss-	CE129322	tigr-gss-	C 387	41.8	5.9	967	6	CE235041	CE235041
C 315	42.2	42.2	5.9	640	7	CF370476	rg5g06.y	CF370476	rg5g06.y	C 388	41.8	5.9	970	9	CNS0182A	AL108796 Drosophil
C 316	42.2	42.2	5.9	662	8	AZ607599	1M0430E07	AZ607599	1M0430E07	C 389	41.8	5.9	980	9	CNS0180A	AL108724 Drosophil

C 390	41.8	5.9	1025	9	CL113815	CL113815	ISB1-59A2	463	41.2	5.8	319	2	BB221721	BB221721
C 391	41.8	5.9	1091	9	AG365350	Mus muscu	AG365350	C 464	41.2	5.8	357	4	BM606297	BM606297
C 392	41.8	5.9	1092	9	CNS020K7	Tetraodon	AL175696	465	41.2	5.8	438	7	CF369638	CF369638
C 393	41.8	5.9	1101	9	CNS00039G	Drosophill	AL063921	466	41.2	5.8	491	7	CO866143	CO866143
C 394	41.8	5.9	1101	9	CNS0000QL	Drosophill	AL069526	467	41.2	5.8	496	8	BH045272	BH045272
C 395	41.8	5.9	1201	9	AG390842	Mus muscu	AG390842	C 468	41.2	5.8	514	5	BQ558252	BQ558252
C 396	41.8	5.9	1210	9	AG390601	Mus muscu	AG390601	469	41.2	5.8	533	8	AO283337	AO283337
C 397	41.8	5.9	1213	9	AG365686	Mus muscu	AG365686	470	41.2	5.8	541	7	CK984035	CK984035
C 398	41.8	5.9	1265	9	AG305265	Mus muscu	AG305265	C 471	41.2	5.8	566	4	BM205179	BM205179
C 399	41.8	5.9	1303	9	AG320687	Mus muscu	AG320687	472	41.2	5.8	567	8	BH498360	BH498360
C 400	41.8	5.9	1363	9	AG3221466	Mus muscu	AG3221466	473	41.2	5.8	580	9	CR159502	CR159502
C 401	41.6	5.8	393	4	BM572740	fx56H09.Y	BM572740	474	41.2	5.8	581	9	CE660060	CE660060
C 402	41.6	5.8	411	8	AZ2620396	RPCI-23-4	AZ2620396	475	41.2	5.8	592	8	BH546310	BH546310
C 403	41.6	5.8	571	9	CNS0183N	Drosophill	AL109421	C 476	41.2	5.8	603	7	DR13155	DR13155
C 404	41.6	5.8	592	5	BP182067	BP182067	BP182067	477	41.2	5.8	657	7	CM478364	CM478364
C 405	41.6	5.8	627	9	AG248977	Lotus cor	AG248977	C 478	41.2	5.8	658	8	BH059614	BH059614
C 406	41.6	5.8	634	9	CE105413	tigr-gss-	CE105413	C 479	41.2	5.8	684	9	CR062946	CR062946
C 407	41.6	5.8	639	7	CNS0702709	E0465F07-	CNS0702709	480	41.2	5.8	737	4	BG288558	BG288558
C 408	41.6	5.8	701	8	BZ121674	CH230-317	BZ121674	481	41.2	5.8	751	9	CR123066	CR123066
C 409	41.6	5.8	759	9	AG358278	Mus muscu	AG358278	C 482	41.2	5.8	777	9	AG550277	AG550277
C 410	41.6	5.8	764	6	CF289381	Mus muscu	CF289381	C 483	41.2	5.8	788	9	CNS000AK8	CNS000AK8
C 411	41.6	5.8	796	7	CK353924	AGENCOURT	CK353924	C 484	41.2	5.8	810	9	AG543801	AG543801
C 412	41.6	5.8	817	9	CC591946	CH240-392	CC591946	C 485	41.2	5.8	844	9	AG316587	AG316587
C 413	41.6	5.8	887	9	CNS0606V4	T3 end of	AL408566	486	41.2	5.8	864	9	CNS010J3	CNS010J3
C 414	41.6	5.8	889	8	AZ530823	ENTBO66TF	AZ530823	487	41.2	5.8	904	9	CNS00P2V	CNS00P2V
C 415	41.6	5.8	892	9	CL101621	ISB1-38N5	CL101621	C 488	41.2	5.8	916	7	CNS078839	CNS078839
C 416	41.6	5.8	937	7	CNS78551	29383-125	CNS78551	C 489	41.2	5.8	950	1	AL551397	AL551397
C 417	41.6	5.8	984	9	CNS00055A	Drosophill	AL057854	490	41.2	5.8	966	6	CD388381	CD388381
C 418	41.6	5.8	1101	9	CNS0000QL	Drosophill	AL069526	C 491	41.2	5.8	969	9	CL469446	CL469446
C 419	41.6	5.8	1101	9	CNS0000RVE	Drosophill	AL071298	C 492	41.2	5.8	1032	9	CL053914	CL053914
C 420	41.6	5.8	1237	6	CD389086	AGENCOURT	CD389086	493	41.2	5.8	1101	9	CNS0022U	CNS0022U
C 421	41.6	5.8	1241	9	AG278438	Mus muscu	AG278438	494	41.2	5.8	1101	9	CNS016WK	CNS016WK
C 422	41.6	5.8	1260	9	CL491610	Mus muscu	CL491610	C 495	41.2	5.8	1101	9	CNS0181N	CNS0181N
C 423	41.6	5.8	1398	9	AG305186	Mus muscu	AG305186	C 496	41.2	5.8	1132	5	BUS20654	BUS20654
C 424	41.6	5.8	1454	9	CG747614	P041-2-A0	CG747614	C 497	41.2	5.8	1137	8	BL3042	BL3042
C 425	41.6	5.8	1509	9	AG280428	Mus muscu	AG280428	C 498	41.2	5.8	1316	7	CF945677	CF945677
C 426	41.6	5.8	2019	9	CL019437	CH216-5E9	CL019437	C 499	41.2	5.8	1346	9	AG382256	AG382256
C 427	41.6	5.8	3775	3	CR627381	Homo sapi	CR627381	C 500	41.2	5.8	1348	9	CG749499	CG749499
C 428	41.6	5.8	316	9	CR049653	Reverse s	CR049653	C 501	41.2	5.8	1505	9	AG310923	AG310923
C 429	41.4	5.8	320	7	CO294973	Reverse s	CO294973	C 502	41.2	5.8	1736	3	CR627200	CR627200
C 430	41.4	5.8	443	2	BE133068	uf34n01.x	BE133068	C 503	41	5.8	302	7	N40928	N40928
C 431	41.4	5.8	460	9	DR24L12S	Danio rer	AL747183	C 504	41	5.8	351	6	C24643	C24643
C 432	41.4	5.8	510	9	CR192601	Reverse s	CR192601	C 505	41	5.8	359	9	BX960267	BX960267
C 433	41.4	5.8	522	4	BM604387	170006870	BM604387	C 506	41	5.8	361	9	CE263281	CE263281
C 434	41.4	5.8	546	8	BZ273071	lae79b07	CF545424	C 507	41	5.8	389	7	CF383048	CF383048
C 435	41.4	5.8	538	7	CP545424	lae79b07	CP545424	C 508	41	5.8	405	5	BUS05967	BUS05967
C 436	41.4	5.8	666	8	BZ273071	CH230-365	BZ273071	C 509	41	5.8	437	9	CE599899	CE599899
C 437	41.4	5.8	692	8	BZ273071	CH230-365	BZ273071	C 510	41	5.8	442	5	BQ196752	BQ196752
C 438	41.4	5.8	703	5	BU465640	603775703	BU465640	C 511	41	5.8	447	8	AZ103930	AZ103930
C 439	41.4	5.8	707	9	AG556861	Mus muscu	AG556861	C 512	41	5.8	470	4	BG656359	BG656359
C 440	41.4	5.8	716	9	AG308116	Mus muscu	AG308116	C 513	41	5.8	524	8	BH891734	BH891734
C 441	41.4	5.8	733	9	CE079698	tigr-gss-	CE079698	C 514	41	5.8	527	2	BE684443	BE684443
C 442	41.4	5.8	735	9	AG424724	Mus muscu	AG424724	C 515	41	5.8	530	8	BH891822	BH891822
C 443	41.4	5.8	851	7	BU945277	AGENCOURT	BU945277	C 516	41	5.8	537	6	CA854863	CA854863
C 444	41.4	5.8	877	5	CNS015W7	Drosophill	AL105985	C 517	41	5.8	563	4	CE108988	CE108988
C 445	41.4	5.8	957	9	CNS006CU	Drosophill	AL065103	C 518	41	5.8	565	4	BM733389	BM733389
C 446	41.4	5.8	960	9	CNS000BEU	Drosophill	AL065103	C 519	41	5.8	576	9	CE765620	CE765620
C 447	41.4	5.8	1101	9	CNS000RVE	Drosophill	AL069526	C 520	41	5.8	600	6	CA854899	CA854899
C 448	41.4	5.8	1101	9	CNS000RVE	Drosophill	AL069526	C 521	41	5.8	641	8	BH892451	BH892451
C 449	41.4	5.8	1101	9	CNS000RVE	Drosophill	AL069526	C 522	41	5.8	645	7	CK537044	CK537044
C 450	41.4	5.8	1101	9	CNS000RVE	Drosophill	AL069526	C 523	41	5.8	666	8	BZ000810	BZ000810
C 451	41.4	5.8	1101	9	CNS016SB	Drosophill	AL107141	C 524	41	5.8	670	8	BH061898	BH061898
C 452	41.4	5.8	1101	9	CNS0180W	Drosophill	AL108746	C 525	41	5.8	681	8	BH963391	BH963391
C 453	41.4	5.8	1149	9	AG499729	Mus muscu	AG499729	C 526	41	5.8	686	9	CE198758	CE198758
C 454	41.4	5.8	1186	9	CL649642	CH213-243	CL649642	C 527	41	5.8	691	9	CE556859	CE556859
C 455	41.4	5.8	1200	9	CNS016CO	Drosophill	AL106578	C 528	41	5.8	698	9	CE200136	CE200136
C 456	41.4	5.8	1204	9	AG305327	Mus muscu	AG305327	C 529	41	5.8	704	8	BZ036375	BZ036375
C 457	41.4	5.8	1276	9	AG304722	Mus muscu	AG304722	C 530	41	5.8	709	9	AG115454	AG115454
C 458	41.4	5.8	1280	9	AG337879	Mus muscu	AG337879	C 531	41	5.8	732	9	AG528559	AG528559
C 459	41.4	5.8	1315	9	AG376867	Mus muscu	AG376867	C 532	41	5.8	753	5	BP116862	BP116862
C 460	41.4	5.8	1614	9	AG365768	Mus muscu	AG365768	C 533	41	5.8	763	9	CE763086	CE763086
C 461	41.2	5.8	215	4	BM598965	170006870	BM598965	C 534	41	5.8	774	5	BP163925	BP163925
C 462	41.2	5.8	292	5	BQ739690	PfESToab4	BQ739690	C 535	41	5.8	775	8	BZ487794	BZ487794

C 536	41	5.8	779	9	CNS02WAR	AL216828	Tetraodon	609	40.6	5.7	411	4	BG212083	BG212083	RST31547
537	41	5.8	795	9	CG256730	QG0EU47TV	610	40.6	5.7	422	5	BO472970	BO472970	IC81ld05.Y	
538	41	5.8	813	5	B0957828	AGENCOURT	611	40.6	5.7	437	7	CO649087	CO649087	ILLUMIGEN	
539	41	5.8	872	9	CG340152	OGKDR34TV	612	40.6	5.7	450	5	BP117361	BP117361	BP117361	
540	41	5.8	894	5	AZ675220	ENTLF78TF	C 613	40.6	5.7	463	1	AI117589	AI117589	u43f12.x	
541	41	5.8	929	5	B0588911	AGENCOURT	C 614	40.6	5.7	466	1	AI086846	AI086846	O286a10.x	
C 542	41	5.8	975	8	BH179465	014_P_10-	615	40.6	5.7	487	8	AZ748111	AZ748111	RPCI-24-9	
543	41	5.8	993	6	CD389545	AGENCOURT	616	40.6	5.7	501	8	BH084802	BH084802	RPCI-23-2	
544	41	5.8	1022	5	B0529542	AGENCOURT	C 617	40.6	5.7	511	8	AQ923268	AQ923268	RPCI-23-2	
C 545	41	5.8	1031	9	CL113349	ISB1-58G1	C 618	40.6	5.7	511	8	AZ080495	AZ080495	2M0072M01	
C 546	41	5.8	1080	8	CC202937	CH261-122	619	40.6	5.7	521	9	CE520915	CE520915	tigr-gss-	
547	41	5.8	1101	8	CC297727	CH261-125	620	40.6	5.7	535	2	AW937024	AW937024	PMO-DT003	
C 548	41	5.8	1101	9	CNS00F6E	AL070196	621	40.6	5.7	574	8	AZ491741	AZ491741	1M0325C02	
C 549	41	5.8	1101	9	CNS0150H	AL104843	C 622	40.6	5.7	577	2	AW861551	AW861551	RC2-CT032	
C 550	41	5.8	1101	9	CL505531	SAIL_751	C 623	40.6	5.7	577	2	CO334579	CO334579	EX314489	
C 551	41	5.8	1150	9	AG288827	Mus muscu	C 624	40.6	5.7	577	9	DR32H178	DR32H178	Danio rer	
C 552	41	5.8	1224	9	CL077121	CH216-143	625	40.6	5.7	581	9	BX209996	BX209996	Danio rer	
C 553	41	5.8	1272	8	CC264939	CH261-19L	626	40.6	5.7	597	2	AW857769	AW857769	RC2-CT032	
C 554	41	5.8	1375	9	AG347159	Mus muscu	627	40.6	5.7	597	8	BZ500853	BZ500853	BONG150TF	
C 555	41	5.8	2140	9	CL037904	CH216-44D	C 628	40.6	5.7	628	9	CR326595	CR326595	Medicago	
C 556	40.8	5.7	288	4	BM650458	BM650458	629	40.6	5.7	658	9	CNS03NK1	CNS03NK1	Tetraodon	
557	40.8	5.7	294	9	CNS04G0C	AL289029	C 630	40.6	5.7	673	9	CC574601	CC574601	CH240_451	
558	40.8	5.7	333	7	CNS61067	taf78a02	C 631	40.6	5.7	692	8	BH964324	BH964324	o105C08	
559	40.8	5.7	365	9	CNS00GWR	AL072643	632	40.6	5.7	695	8	BH677868	BH677868	BOMF55TF	
560	40.8	5.7	465	8	AQ927340	RPCI-23-2	633	40.6	5.7	703	5	BQ321087	BQ321087	RC2-CT032	
561	40.8	5.7	489	7	CK623392	mi09b10.Y	634	40.6	5.7	714	8	BH982367	BH982367	ode93h06	
C 562	40.8	5.7	521	9	CE466716	CH261-125	635	40.6	5.7	714	9	CE110565	CE110565	tigr-gss-	
C 563	40.8	5.7	529	9	AZ413678	IM0197J15	C 636	40.6	5.7	723	8	BZ030456	BZ030456	ode81h07	
564	40.8	5.7	540	8	AQ793665	HS_5421_B	C 637	40.6	5.7	737	9	CE112409	CE112409	tigr-gss-	
C 565	40.8	5.7	553	8	BH098161	RPCI-24-3	638	40.6	5.7	739	8	AQ035563	AQ035563	CIT-HSP-2	
C 566	40.8	5.7	568	8	AZ026419	RPCI-23-3	C 639	40.6	5.7	750	9	AG380954	AG380954	Mus muscu	
C 567	40.8	5.7	570	5	BM956073	BM956073	C 640	40.6	5.7	777	9	CC498010	CC498010	CH240_334	
568	40.8	5.7	589	9	CNS0301Z	AL253412	C 641	40.6	5.7	784	9	AG578072	AG578072	Mus muscu	
569	40.8	5.7	592	9	CE008918	tigr-gss-	642	40.6	5.7	818	9	CR175371	CR175371	Reverse s	
C 570	40.8	5.7	620	8	BH545181	BOHFS27TF	643	40.6	5.7	831	8	BH605742	BH605742	BOMF55TF	
C 571	40.8	5.7	643	9	CE144352	tigr-gss-	C 644	40.6	5.7	831	8	AZ692775	AZ692775	ENTL195TR	
C 572	40.8	5.7	685	9	CE024560	tigr-gss-	C 645	40.6	5.7	838	8	AZ545154	AZ545154	ENTFW38TF	
C 573	40.8	5.7	695	9	CR089569	Reverse s	C 646	40.6	5.7	855	8	AZ674859	AZ674859	ENTLV50TR	
C 574	40.8	5.7	720	8	BH072778	RPCI-24-3	647	40.6	5.7	882	8	AZ692146	AZ692146	ENTLV37TR	
C 575	40.8	5.7	725	5	BH026537	603817149	C 648	40.6	5.7	886	8	AZ671419	AZ671419	ENTJ44TR	
C 576	40.8	5.7	725	5	BH180166	016_I_02-	C 649	40.6	5.7	906	9	AG555384	AG555384	Mus muscu	
577	40.8	5.7	733	9	AG545919	Mus muscu	650	40.6	5.7	964	5	B0953880	B0953880	AGENCOURT	
C 578	40.8	5.7	757	9	AG580281	AG580281	651	40.6	5.7	994	9	CNS015XG	CNS015XG	CL106030	
C 579	40.8	5.7	772	6	CR320132	AGENCOURT	652	40.6	5.7	1027	9	CL464098	CL464098	SAIL_1213	
C 580	40.8	5.7	804	9	CNS03G0X	AL243474	C 653	40.6	5.7	1045	9	CNS03YB4	CNS03YB4	Tetraodon	
C 581	40.8	5.7	822	5	BM159356	BM159356	C 654	40.6	5.7	1059	9	CNS00Z2B	CNS00Z2B	Drosophil	
C 582	40.8	5.7	848	9	BX204849	Danio rer	655	40.6	5.7	1068	9	CNS00JAX	CNS00JAX	Drosophil	
583	40.8	5.7	903	9	CNS0011C	AL074609	C 656	40.6	5.7	1099	9	CNS00DWB	CNS00DWB	Drosophil	
584	40.8	5.7	912	6	CB182673	CB182673	657	40.6	5.7	1101	9	CNS00JVK	CNS00JVK	Drosophil	
585	40.8	5.7	928	9	CL496696	SAIL_62_B	C 658	40.6	5.7	1101	9	CNS01609	CNS01609	Drosophil	
C 586	40.8	5.7	951	9	CG689836	ZMBBGO13	C 659	40.6	5.7	1267	9	AG376975	AG376975	Mus muscu	
587	40.8	5.7	967	6	CB202462	AGENCOURT	C 660	40.6	5.7	1318	9	CL643965	CL643965	CH213-60J	
C 588	40.8	5.7	987	9	CNS014PQ	AL104456	C 661	40.4	5.7	226	6	CF214092	CF214092	CGF100081	
C 589	40.8	5.7	994	9	CNS04NOJ	AL298972	C 662	40.4	5.7	341	9	CNS00606	CNS00606	Drosophil	
590	40.8	5.7	1049	5	BX457978	BX457978	663	40.4	5.7	380	4	BI945693	BI945693	sc57e12.Y	
591	40.8	5.7	1101	9	CNS003BB	AL064089	C 664	40.4	5.7	433	7	CF421593	CF421593	jaal2c08	
592	40.8	5.7	1101	9	CNS008VN	AL058694	C 665	40.4	5.7	437	6	CA346692	CA346692	677624_NC	
593	40.8	5.7	1210	9	CG749728	CG749728	C 666	40.4	5.7	447	1	AI418337	AI418337	tg48a12.x	
C 594	40.8	5.7	1210	9	CG749728	CG749728	C 667	40.4	5.7	492	9	CR194165	CR194165	Reverse s	
C 595	40.8	5.7	1342	9	AG288357	AG288357	668	40.4	5.7	494	7	CF544979	CF544979	lad85g10	
C 596	40.8	5.7	1349	9	AG288967	Mus muscu	669	40.4	5.7	500	1	AU086771	AU086771	AU086771	
C 597	40.8	5.7	1352	9	AG381852	AG381852	C 670	40.4	5.7	526	8	BH294102	BH294102	CH230-122	
C 598	40.8	5.7	1426	9	CG757286	CG757286	C 671	40.4	5.7	526	8	AZ029356	AZ029356	RPCI-23-3	
C 599	40.8	5.7	1434	8	BZ576813	BZ576813	672	40.4	5.7	560	5	BP179243	BP179243	BP179243	
C 600	40.8	5.7	1515	9	AG280359	AG280359	C 673	40.4	5.7	563	8	BZ109112	BZ109112	CH230-158	
C 601	40.8	5.7	1653	3	CR679590	CR679590	C 674	40.4	5.7	585	9	CR333510	CR333510	Medicago	
C 602	40.8	5.7	1745	9	AG338221	AG338221	675	40.4	5.7	593	1	AU002045	AU002045	AU002045	
603	40.6	5.7	266	5	BF704434	BF704434	676	40.4	5.7	594	1	AV400666	AV400666	AV400666	
604	40.6	5.7	291	7	CNS01465	CNS01465	677	40.4	5.7	598	4	BI507466	BI507466	BB170007B	
C 605	40.6	5.7	374	1	AI689559	AI689559	C 678	40.4	5.7	604	5	BQ394396	BQ394396	NISC_1908	
606	40.6	5.7	387	4	BG185511	BG185511	679	40.4	5.7	609	9	CR048694	CR048694	Reverse s	
607	40.6	5.7	397	8	BZ761137	BZ761137	680	40.4	5.7	613	8	AZ403526	AZ403526	IM0171C23	
608	40.6	5.7	410	7	CK428714	CK428714	C 681	40.4	5.7	618	4	BI678933	BI678933	SWS934_SW	

682	40.4	5.7	628	5	BP116935	BP116935	C 755	40.2	5.6	562	9	DR33N2S	AL977814	Danio rer
683	40.4	5.7	633	1	AU004482	AU004482	756	40.2	5.6	594	9	C5629928	CE629928	tigr-gss-
684	40.4	5.7	644	9	CE020369	tigr-gss-	757	40.2	5.6	605	5	BQ522342	BQ522342	NISC_nll16
685	40.4	5.7	646	9	CE507309	tigr-gss-	758	40.2	5.6	612	8	AZ405868	AZ405868	IM0174F20
686	40.4	5.7	647	1	AV399591	AV399591	759	40.2	5.6	616	8	AZ385417	AZ385417	IM0143F24
687	40.4	5.7	651	8	AZ088394	AV399591	C 760	40.2	5.6	624	8	BH589908	BH589908	BOHO90TF
688	40.4	5.7	656	6	CD640173	CD640173	C 761	40.2	5.6	624	8	CE810275	CE810275	tigr-gss-
689	40.4	5.7	669	2	BE563301	BE563301	C 762	40.2	5.6	667	8	BH720694	BH720694	BOMJP85TF
690	40.4	5.7	673	8	BZ400849	BZ400849	C 763	40.2	5.6	721	7	CF517899	CF517899	CAP0005_I
691	40.4	5.7	683	9	CE847318	CE847318	C 764	40.2	5.6	727	9	AG482573	AG482573	Mus muscu
692	40.4	5.7	688	1	AU0001063	AU0001063	C 765	40.2	5.6	752	8	BZ061754	BZ061754	lky33904
693	40.4	5.7	693	5	BP177891	BP177891	C 766	40.2	5.6	757	9	AG496423	AG496423	Mus muscu
694	40.4	5.7	692	5	BP179069	BP179069	C 767	40.2	5.6	766	9	AG423155	AG423155	Mus muscu
695	40.4	5.7	700	1	AU0066427	AU0066427	C 768	40.2	5.6	791	9	AG474238	AG474238	Mus muscu
696	40.4	5.7	701	5	BP121539	BP121539	C 769	40.2	5.6	810	8	BZ1210	BZ1210	T2N2-Sp6_T
697	40.4	5.7	704	5	BP177739	BP177739	C 770	40.2	5.6	882	5	BQ151299	BQ151299	NF073E05L
698	40.4	5.7	711	8	AZ442067	AZ442067	C 771	40.2	5.6	888	5	CNS00519	CNS00519	Drosophil
699	40.4	5.7	717	1	AU000694	AU000694	C 772	40.2	5.6	914	9	CL028356	CL028356	CH216-27G
700	40.4	5.7	723	5	BP178342	BP178342	C 773	40.2	5.6	934	9	CNS00COA	CNS00COA	Drosophil
701	40.4	5.7	724	5	BP178072	BP178072	C 774	40.2	5.6	973	9	CNS071LE	CNS071LE	clone_BAO
702	40.4	5.7	724	5	BP178533	BP178533	C 775	40.2	5.6	987	9	CNS00KXT	CNS00KXT	Drosophil
703	40.4	5.7	734	1	AV757071	AV757071	C 776	40.2	5.6	995	9	CNS01R37	CNS01R37	Anopheles
704	40.4	5.7	735	9	CNS068P7	AL399281 T3 end of	C 777	40.2	5.6	998	8	BZ695174	BZ695174	SP_Ba005
705	40.4	5.7	737	1	AV399367	AV399367	C 778	40.2	5.6	1004	9	CNS006TX	CNS006TX	Drosophil
706	40.4	5.7	739	1	CR335933	CR335933	C 779	40.2	5.6	1010	8	BZ144919	BZ144919	CH230-413
707	40.4	5.7	748	1	AV400437	AV400437	C 780	40.2	5.6	1101	9	CNS008WG	CNS008WG	Drosophil
708	40.4	5.7	749	1	AV400884	AV400884	C 781	40.2	5.6	1101	9	CNS002BM	CNS002BM	Drosophil
709	40.4	5.7	754	9	AG454046	AG454046	C 782	40.2	5.6	1308	2	BE873325	BE873325	601450277
710	40.4	5.7	759	5	BP121009	BP121009	C 783	40.2	5.6	1315	3	CR657214	CR657214	Tetraodon
711	40.4	5.7	769	9	AG134867	AG134867	C 784	40.2	5.6	1325	9	AG341551	AG341551	Mus muscu
712	40.4	5.7	770	8	AQ740708	AQ740708	C 785	40.2	5.6	1389	9	CG744469	CG744469	P037-1-C0
713	40.4	5.7	775	9	CE234561	CE234561	C 786	40.2	5.6	1473	9	AG278179	AG278179	Mus muscu
714	40.4	5.7	793	8	BZ882481	BZ882481	C 787	40.2	5.6	1542	9	AG386981	AG386981	Mus muscu
715	40.4	5.7	793	9	AG477411	AG477411	C 788	40.2	5.6	1833	9	AG280520	AG280520	Mus muscu
716	40.4	5.7	795	8	BH077425	BH077425	C 789	40.2	5.6	1858	9	AG387213	AG387213	Mus muscu
717	40.4	5.7	813	9	CNS0119M	AL099988 Drosophil	C 790	40	5.6	286	5	BQ597243	BQ597243	PfESTOab3
718	40.4	5.7	817	5	BUS56618	BUS56618	C 791	40	5.6	287	2	BE278937	BE278937	BB278937
719	40.4	5.7	824	8	AZ692676	AZ692676	C 792	40	5.6	348	8	AZ942517	AZ942517	2M020M12
720	40.4	5.7	826	4	BM358125	BM358125	C 793	40	5.6	370	7	CN750572	CN750572	APD7-XVII
721	40.4	5.7	828	9	CNS011TX	AL100719 Drosophil	C 794	40	5.6	371	8	AQ551578	AQ551578	RPCI-11-4
722	40.4	5.7	854	5	BH077786	BH077786	C 795	40	5.6	382	4	BM181109	BM181109	IV94C04_Y
723	40.4	5.7	857	5	BUS34369	BUS34369	C 796	40	5.6	389	8	AZ767065	AZ767065	IM0566G02
724	40.4	5.7	865	5	BUS943819	BUS943819	C 797	40	5.6	432	4	B1815860	B1815860	PfESTOa3
725	40.4	5.7	867	9	CR235120	CR235120	C 798	40	5.6	474	7	CF369899	CF369899	IG57F08_Y
726	40.4	5.7	870	9	CR214613	CR214613	C 799	40	5.6	491	7	CF370341	CF370341	IG63F05_Y
727	40.4	5.7	878	8	BH131582	BH131582	C 800	40	5.6	501	7	CN194264	CN194264	IG91F10_Y
728	40.4	5.7	893	5	BUS51134	BUS51134	C 801	40	5.6	534	6	CB572418	CB572418	AGENCOURT
729	40.4	5.7	893	7	CK158199	CK158199	C 802	40	5.6	556	9	CE797755	CE797755	tigr-gss-
730	40.4	5.7	934	8	AZ184244	AZ184244	C 803	40	5.6	564	9	CE668952	CE668952	tigr-gss-
731	40.4	5.7	966	9	CNS0052C	CNS0052C	C 804	40	5.6	565	8	AZ814901	AZ814901	2M0082A21
732	40.4	5.7	997	6	CD247514	CD247514	C 805	40	5.6	567	9	CR113380	CR113380	Forward_s
733	40.4	5.7	1018	4	BM416001	BM416001	C 806	40	5.6	568	6	CF104660	CF104660	maJ14b09
734	40.4	5.7	1050	8	CR2210320	CR2210320	C 807	40	5.6	603	9	CB409347	CB409347	tigr-gss-
735	40.4	5.7	1101	9	CNS00LH1	CNS00LH1	C 808	40	5.6	608	9	CE127306	CE127306	tigr-gss-
736	40.4	5.7	1172	3	CR734084	CR734084	C 809	40	5.6	623	9	CNS04MNO	CNS04MNO	Tetraodon
737	40.4	5.7	1251	9	AG332167	AG332167	C 810	40	5.6	626	8	AZ862189	AZ862189	2M0169H13
738	40.4	5.7	1313	9	AG288588	AG288588	C 811	40	5.6	634	5	BP764939	BP764939	BP764939
739	40.4	5.7	1342	9	AG305185	AG305185	C 812	40	5.6	637	9	CE196464	CE196464	tigr-gss-
740	40.4	5.7	1488	9	AG305166	AG305166	C 813	40	5.6	668	8	AZ428307	AZ428307	IM0210E17
741	40.4	5.7	1592	9	CG750135	CG750135	C 814	40	5.6	673	9	CNS06UWL	CNS06UWL	T7 end of
742	40.2	5.6	249	7	CN004667	CN004667	C 815	40	5.6	676	2	BE291862	BE291862	601084574
743	40.2	5.6	329	4	B1142703	B1142703	C 816	40	5.6	682	9	CE288793	CE288793	tigr-gss-
744	40.2	5.6	368	4	BM130428	BM130428	C 817	40	5.6	685	9	CE153461	CE153461	tigr-gss-
745	40.2	5.6	393	4	BG288289	BG288289	C 818	40	5.6	693	9	CNS006MN	CNS006MN	Drosophil
746	40.2	5.6	398	5	BP770612	BP770612	C 819	40	5.6	706	8	BZ436317	BZ436317	BONFW39TR
747	40.2	5.6	436	4	BM386258	BM386258	C 820	40	5.6	714	8	AZ869828	AZ869828	2M0182A09
748	40.2	5.6	439	7	CO195511	CO195511	C 821	40	5.6	735	9	BX181770	BX181770	Danio rer
749	40.2	5.6	455	9	CL495883	CL495883	C 822	40	5.6	737	8	AZ145325	AZ145325	SP_0017_A
750	40.2	5.6	458	1	CK336571	CK336571	C 823	40	5.6	739	6	CD239179	CD239179	ENPBLE02
751	40.2	5.6	466	1	AU087195	AU087195	C 824	40	5.6	778	8	BH022395	BH022395	GH_MBB000
752	40.2	5.6	480	1	CA302324	CA302324	C 825	40	5.6	779	9	BX164018	BX164018	Danio rer
753	40.2	5.6	502	6	AU087738	AU087738	C 826	40	5.6	797	8	BZ065067	BZ065067	lkz73a10
754	40.2	5.6	519	9	CE032406	CE032406	C 827	40	5.6					

828	40	5.6	822	9	CNS009CW	AL053618 Drosophil	901	39.8	5.6	861	8	AZ672851	AZ672851 ENTKU09TR
829	40	5.6	824	7	CK238978	CK238978 AGENCOURT	C 902	39.8	5.6	866	8	AQ258984	AQ258984 nbxb0021P
830	40	5.6	824	7	AG446668	AG446668 Mus muscu	C 903	39.8	5.6	866	8	AG133042	AG133042 Pan trogl
831	40	5.6	829	8	AZ684608	AZ684608 ENTLQ20TR	C 904	39.8	5.6	883	6	CD757089	CD757089 AGENCOURT
832	40	5.6	844	9	CR123595	CR123595 Reverse s	905	39.8	5.6	908	7	CK158270	CK158270 FGAS03950
833	40	5.6	867	9	CNS00CX5	AL060052 Drosophil	906	39.8	5.6	910	7	AG136203	AG136203 Pan trogl
834	40	5.6	868	5	BX359221	BX359221 Drosophil	907	39.8	5.6	954	4	BG075101	BG075101 K1343C10-
835	40	5.6	890	9	CNS00AFU	AL055222 Drosophil	908	39.8	5.6	975	6	CD386803	CD386803 AGENCOURT
836	40	5.6	900	8	AZ529844	AZ529844 ENTCF11TF	C 909	39.8	5.6	1003	9	CL472292	CL472292 SAIL_175
837	40	5.6	914	7	CK157980	CK157980 FGAS03918	C 910	39.8	5.6	1007	9	CNS005FT	AL059951 Drosophil
838	40	5.6	925	9	CG932920	CG932920 MBEPJ28TR	911	39.8	5.6	1022	9	CL147472	CL147472 ISB1-234F
839	40	5.6	955	7	CK415026	CK415026 AUF IPeIT	912	39.8	5.6	1031	9	AL098657	AL098657 Drosophil
840	40	5.6	968	9	CL129826	CL129826 ISB1-97E1	913	39.8	5.6	1038	9	CNS0108N	AL03832 T3 end of
841	40	5.6	970	6	CD050836	CD050836 AGENCOURT	914	39.8	5.6	1043	6	CD385012	CD385012 AGENCOURT
842	40	5.6	974	9	CNS00ITT	AL075432 Drosophil	C 915	39.8	5.6	1052	8	CC260385	CC260385 CH261-72G
843	40	5.6	988	9	CL087333	CL087333 ISB1-9A17	C 916	39.8	5.6	1085	9	CL056555	CL056555 CH216-83E
844	40	5.6	994	3	CR719889	CR719889 Tetraodon	C 917	39.8	5.6	1101	9	AL097228	AL097228 Drosophil
845	40	5.6	994	8	CC244611	CC244611 CH261-120	C 918	39.8	5.6	1101	9	CNS0106X	AL098595 Drosophil
846	40	5.6	1003	9	CL481897	CL481897 SAIL 350	919	39.8	5.6	1101	9	CNS0145U	AL103740 Drosophil
847	40	5.6	1010	6	CD171719	CD171719 AGENCOURT	920	39.8	5.6	1104	6	CD048990	CD048990 AGENCOURT
848	40	5.6	1073	8	BZ211205	BZ211205 CH230-475	C 921	39.8	5.6	1164	8	CC218891	CC218891 CH261-14M
849	40	5.6	1085	4	BM807297	BM807297 AGENCOURT	922	39.8	5.6	1201	9	CNS0167M	AL106396 Drosophil
850	40	5.6	1101	9	CNS008WC	AL052719 Drosophil	C 923	39.8	5.6	1259	9	CL104895	CL104895 ISB1-43M2
851	40	5.6	1101	9	CNS00BO1	AL057419 Drosophil	C 924	39.8	5.6	1390	9	AG347224	AG347224 Mus muscu
852	40	5.6	1101	9	CNS0183Y	AL108856 Drosophil	C 925	39.8	5.6	1396	9	CL019762	CL019762 CH216-50I
853	40	5.6	1124	9	CNS073BM	AL427304 clone_BAO	C 926	39.8	5.6	1456	9	AG280032	AG280032 Mus muscu
854	40	5.6	1166	9	CL477258	CL477258 SAIL_26_D	C 927	39.8	5.6	1460	5	BU505085	BU505085 AGENCOURT
855	40	5.6	1197	9	AG288120	AG288120 Mus muscu	C 928	39.8	5.6	1797	9	AG390564	AG390564 Mus muscu
856	40	5.6	1378	9	AG350209	AG350209 Mus muscu	C 929	39.8	5.6	1990	9	AG278470	AG278470 Mus muscu
857	40	5.6	1416	9	CL499036	CL499036 SAIL 662	C 930	39.8	5.6	2045	9	AG278108	AG278108 Mus muscu
858	40	5.6	1430	9	CG758458	CG758458 P053-4-H0	C 931	39.6	5.6	170	9	CE272446	CE272446 tigr-gss-
859	40	5.6	1437	9	CL647657	CL647657 CH213-144	C 932	39.6	5.6	178	9	CE076420	CE076420 tigr-gss-
860	40	5.6	1550	9	CL019750	CL019750 CH216-505	C 933	39.6	5.6	239	2	BE086400	BE086400 QV1-BT067
861	40	5.6	2087	9	AG333887	AG333887 Mus muscu	C 934	39.6	5.6	242	2	BE086435	BE086435 QV1-BT067
862	40	5.6	2182	9	CL515383	CL515383 SAIL 89_F	935	39.6	5.6	260	2	BE086606	BE086606 Drosophil
863	40	5.6	2266	3	CR686752	CR686752 Tetraodon	C 936	39.6	5.6	294	2	BF947901	BF947901 QM2-NN021
864	40	5.6	3257	3	AK030788	AK030788 Mus muscu	937	39.6	5.6	308	4	BM342759	BM342759 fw47f10-Y
865	40	5.6	3597	3	AK030890	AK030890 Mus muscu	938	39.6	5.6	308	4	BM342759	BM342759 fw47f10-Y
866	39.8	5.6	215	5	BQ396717	BQ396717 NISC RG22	939	39.6	5.6	309	5	BU761114	BU761114 sas63506-
867	39.8	5.6	220	6	CA802987	CA802987 sau45d09	940	39.6	5.6	359	1	AV817258	AV817258 AV817258
868	39.8	5.6	231	6	CA814303	CA814303 CA48LN09I	941	39.6	5.6	368	7	CK242028	CK242028 rx04f08.Y
869	39.8	5.6	303	7	CO752990	CO752990 MdfR3022e	942	39.6	5.6	379	4	BG520852	BG520852 ps52h02.Y
870	39.8	5.6	325	7	CN959538	CN959538 MdfR3003n	C 943	39.6	5.6	389	5	BQ010950	BQ010950 UI-1-BC1P
871	39.8	5.6	367	1	AL638061	AL638061 AL638061	C 944	39.6	5.6	410	8	AZ390431	AZ390431 LM0151J16
872	39.8	5.6	373	5	EX692255	EX692255 BX692255	C 945	39.6	5.6	420	1	AL094118	AL094118 qa34a12.s
873	39.8	5.6	394	9	CE554324	CE554324 tigr-gss-	C 946	39.6	5.6	424	1	AU045697	AU045697 AU045697
874	39.8	5.6	405	8	AQ147628	AQ147628 HS 3067_B	947	39.6	5.6	432	5	BY379699	BY379699 BY379699
875	39.8	5.6	444	5	BQ596235	BQ596235 PFESToab3	C 948	39.6	5.6	472	2	AW295536	AW295536 UI-H-BI2-
876	39.8	5.6	460	6	CB973771	CB973771 CAB30003	C 949	39.6	5.6	490	5	BQ010814	BQ010814 UI-1-BC1-
877	39.8	5.6	477	9	CE010305	CE010305 tigr-gss-	950	39.6	5.6	498	4	BI450682	BI450682 kt73d02.Y
878	39.8	5.6	506	9	CE533268	CE533268 tigr-gss-	C 951	39.6	5.6	500	8	AQ978308	AQ978308 RPCI-23-3
879	39.8	5.6	530	5	EX566754	EX566754 BX566754	C 952	39.6	5.6	502	9	CL596671	CL596671 OB_Ba005
880	39.8	5.6	630	9	CE823727	CE823727 tigr-gss-	C 953	39.6	5.6	504	7	CF529184	CF529184 UI-1-BC1P
881	39.8	5.6	633	9	CE006893	CE006893 tigr-gss-	C 954	39.6	5.6	511	2	AW449058	AW449058 UI-H-BI3-
882	39.8	5.6	650	8	BZ001651	BZ001651 oeh09b02	955	39.6	5.6	513	7	CF364781	CF364781 834783 MA
883	39.8	5.6	652	9	CR208773	CR208773 Reverse s	956	39.6	5.6	517	8	AZ887704	AZ887704 RPCI-24-1
884	39.8	5.6	652	9	CE565871	CE565871 tigr-gss-	C 957	39.6	5.6	518	4	BM661932	BM661932 UI-E-CK1-
885	39.8	5.6	668	7	CK655242	CK655242 AGENCOURT	C 958	39.6	5.6	521	8	B91975	B91975 CIT-HSP-216
886	39.8	5.6	678	9	AL187941	AL187941 Tetraodon	959	39.6	5.6	536	8	AZ861147	AZ861147 2M0167P21
887	39.8	5.6	688	8	BZ033911	BZ033911 oeh89g12	C 960	39.6	5.6	539	4	BJ350911	BJ350911 BJ350911
888	39.8	5.6	694	4	BI088925	BI088925 602854290	961	39.6	5.6	554	9	CE427799	CE427799 tigr-gss-
889	39.8	5.6	696	8	BZ009393	BZ009393 oeg71d05	C 962	39.6	5.6	563	5	BU622757	BU622757 UI-H-FL1-
890	39.8	5.6	704	9	AQ319108	AQ319108 RPCI11-99	963	39.6	5.6	565	8	AZ458284	AZ458284 1M0262C13
891	39.8	5.6	710	9	CE290816	CE290816 tigr-gss-	C 964	39.6	5.6	566	4	BM579974	BM579974 170006872
892	39.8	5.6	726	7	CR536325	CR536325 CR536325	C 965	39.6	5.6	580	4	BM646722	BM646722 170006873
893	39.8	5.6	735	9	AG104830	AG104830 Pan trogl	966	39.6	5.6	581	9	CR189938	CR189938 Forward s
894	39.8	5.6	737	8	BH580095	BH580095 BOHCC74TF	967	39.6	5.6	584	8	AZ640832	AZ640832 1M0503K03
895	39.8	5.6	749	9	AG590361	AG590361 Mus muscu	C 968	39.6	5.6	593	9	CR336920	CR336920 Medicago
896	39.8	5.6	750	9	AG592110	AG592110 Mus muscu	C 969	39.6	5.6	594	8	AZ051488	AZ051488 RPCI-23-4
897	39.8	5.6	775	9	AG491924	AG491924 Mus muscu	970	39.6	5.6	595	9	CE215511	CE215511 tigr-gss-
898	39.8	5.6	782	9	CNS06RMZ	AL412161 T7 end of	971	39.6	5.6	597	7	CN443846	CN443846 Mdfw2001a
899	39.8	5.6	806	9	CC474589	CC474589 CH240 299	972	39.6	5.6	604	2	BF130874	BF130874 601819663
900	39.8	5.6	822	8	BH506300	BH506300 BOGRV16TR	C 973	39.6	5.6	610	5	BU429740	BU429740 UI-HF-BN0

C 974	39.6	5.6	610	8	AZ589893	1M0399111	1047	39.6	5.6	1101	9	CNS00LT2	AL078714 Drosophil
C 975	39.6	5.6	619	4	BM589915	170006873	1048	39.6	5.6	1101	9	CNS015M2	AL105653 Drosophil
C 976	39.6	5.6	620	9	CE242164	tigr-gss-	1049	39.6	5.6	1101	9	CNS017ZQ	AL108704 Drosophil
C 977	39.6	5.6	631	9	CE237245	tigr-gss-	1050	39.6	5.6	1158	4	BM557070	BM557070 AGENCOURT
C 978	39.6	5.6	642	7	CN006695	CSECS137F	1051	39.6	5.6	1205	9	CL143963	CL143963 TSBI-1230
C 979	39.6	5.6	647	7	BH118274	RPCI-24-2	1052	39.6	5.6	1227	9	AG430010	AG430010 Mus muscu
C 980	39.6	5.6	653	8	BZ520255	BOMQ077F	1053	39.6	5.6	1248	8	B11336	B11336 F19M10-Sp6
C 981	39.6	5.6	657	4	BM603344	170006870	1054	39.6	5.6	1252	9	AG324070	AG324070 Mus muscu
C 982	39.6	5.6	664	7	CN331012	AGENCOURT	1055	39.6	5.6	1353	9	AG279839	AG279839 Mus muscu
C 983	39.6	5.6	664	8	BH043002	RPCI-24-2	1056	39.6	5.6	1359	9	AG280065	AG280065 Mus muscu
C 984	39.6	5.6	673	4	BM677382	UI-B-EOI-	1057	39.6	5.6	1389	9	AG310977	AG310977 Mus muscu
C 985	39.6	5.6	673	9	CE340431	tigr-gss-	1058	39.6	5.6	1432	9	AG305088	AG305088 Mus muscu
C 986	39.6	5.6	680	9	CE535319	tigr-gss-	1059	39.6	5.6	1450	9	AG290296	AG290296 Mus muscu
C 987	39.6	5.6	682	8	BH301335	CH230-166	1060	39.6	5.6	1463	9	AG310669	AG310669 Mus muscu
C 988	39.6	5.6	684	8	BZ010697	oea43b02.	1061	39.6	5.6	1503	9	AG280454	AG280454 Mus muscu
C 989	39.6	5.6	686	8	BH930560	odi165b02.	1062	39.6	5.6	1506	9	AG278469	AG278469 Mus muscu
C 990	39.6	5.6	689	5	BM969651	UI-CF-DU1	1063	39.6	5.6	2322	9	AG321011	AG321011 Mus muscu
C 991	39.6	5.6	696	8	BZ009033	oei126b08.	1064	39.6	5.6	2972	3	BC025324	BC025324 Homo sapi
C 992	39.6	5.6	698	9	CNS033327	Tetraodon	1065	39.6	5.5	271	8	AZ943719	AZ943719 2M0204D03
C 993	39.6	5.6	699	8	AQ323327	RPCI11-10	1066	39.4	5.5	284	4	BM752078	BM752078 K-EST0028
C 994	39.6	5.6	701	7	CN757203	ID0AAA1BF	1067	39.4	5.5	313	6	CD650541	CD650541 CBG110124
C 995	39.6	5.6	706	9	CE784276	tigr-gss-	1068	39.4	5.5	325	2	BZ237833	BZ237833 BVG217833
C 996	39.6	5.6	707	4	BM677412	UI-B-EOI-	1069	39.4	5.5	340	8	AZ036018	AZ036018 RPCI-23-3
C 997	39.6	5.6	709	9	CE645828	tigr-gss-	1070	39.4	5.5	352	7	CK375192	CK375192 lai4ce04.
C 998	39.6	5.6	709	9	CE846248	tigr-gss-	1071	39.4	5.5	364	7	CN750985	CN750985 ApDT-XXXI
C 999	39.6	5.6	714	8	BZ145311	CH230-266	1072	39.4	5.5	367	5	BP629668	BP629668 BP629668
C1000	39.6	5.6	715	8	BH556033	BOG2035FF	1073	39.4	5.5	389	9	T09756	T09756 0350m7 gmbp
C1001	39.6	5.6	723	8	BH961719	oddsod12.	1074	39.4	5.5	402	6	CB768924	CB768924 AMGNNUC.S
C1002	39.6	5.6	725	8	BZ164494	CH230-258	1075	39.4	5.5	403	1	AV813199	AV813199 AV813199
C1003	39.6	5.6	727	5	BU620998	UI-H-F11-	1076	39.4	5.5	412	1	AU001005	AU001005 AU001005
C1004	39.6	5.6	733	9	AG604083	Mus muscu	1077	39.4	5.5	419	7	CK379231	CK379231 lai34f12.
C1005	39.6	5.6	740	5	BH033582	AG492664	1078	39.4	5.5	420	1	AV810228	AV810228 AV810228
C1006	39.6	5.6	741	9	AG492664	Mus muscu	1079	39.4	5.5	427	6	CA335318	CA335318 NISC-1t09
C1007	39.6	5.6	742	2	BE254376	601109131	1080	39.4	5.5	438	7	CF658775	CF658775 tacs8all.
C1008	39.6	5.6	743	9	AG609084	Mus muscu	1081	39.4	5.5	449	9	CE722106	CE722106 tigr-gss-
C1009	39.6	5.6	756	6	CA107340	SCFRH100	1082	39.4	5.5	453	6	CB048215	CB048215 NISC GJ03
C1010	39.6	5.6	757	9	CR310760	Medicago	1083	39.4	5.5	456	7	BH077694	BH077694 R87a09.Y
C1011	39.6	5.6	798	9	BX192137	Danio rer	1084	39.4	5.5	470	8	BM307145	BM307145 Medicago
C1012	39.6	5.6	802	5	BUS30891	AGENCOURT	1085	39.4	5.5	481	9	CE664149	CE664149 tigr-gss-
C1013	39.6	5.6	802	9	AG150148	Pan trogl	1086	39.4	5.5	485	9	CB856349	CB856349 r15ic10.Y
C1014	39.6	5.6	803	5	BH843390	AGENCOURT	1087	39.4	5.5	486	6	CB856349	CB856349 r15ic10.Y
C1015	39.6	5.6	819	9	AG292604	Mus muscu	1088	39.4	5.5	496	1	A1862532	A1862532 wj15b08.X
C1016	39.6	5.6	824	2	BF780254	602103353	1089	39.4	5.5	496	8	AZ890003	AZ890003 RPCI-24-2
C1017	39.6	5.6	828	8	BZ452626	BOCAT28TR	1090	39.4	5.5	499	2	BF000038	BF000038 Ph16b12.X
C1018	39.6	5.6	834	9	AG417745	Mus muscu	1091	39.4	5.5	502	8	AZ409199	AZ409199 1M0180K10
C1019	39.6	5.6	836	8	AZ547027	ENTPE96TR	1092	39.4	5.5	505	7	CK374763	CK374763 lai82b07.
C1020	39.6	5.6	838	7	CK795139	AGENCOURT	1093	39.4	5.5	510	1	AA916758	AA916758 on10b03.s
C1021	39.6	5.6	838	9	AG489918	Mus muscu	1094	39.4	5.5	516	9	CE212957	CE212957 tigr-gss-
C1022	39.6	5.6	855	9	CNS04P5D	Tetraodon	1095	39.4	5.5	548	1	AV556820	AV556820 AV556820
C1023	39.6	5.6	865	9	CC523593	CH240.372	1096	39.4	5.5	555	8	BH891811	BH891811 3526.1.19
C1024	39.6	5.6	870	9	CNS06UZZ	T7 end of	1097	39.4	5.5	570	4	BM619215	BM619215 170006874
C1025	39.6	5.6	872	8	BZ500395	BONOA69TF	1098	39.4	5.5	573	9	EX990795	EX990795 Forward s
C1026	39.6	5.6	874	8	BH131968	ENTPE28TR	1099	39.4	5.5	582	9	BX147754	BX147754 Danilo rer
C1027	39.6	5.6	891	9	CNS0095U	Drosophil	1100	39.4	5.5	597	4	BI378474	BI378474 BFLG1.000
C1028	39.6	5.6	907	8	AZ529993	ENTCE117R	1101	39.4	5.5	600	8	BH530205	BH530205 BOGSG28TR
C1029	39.6	5.6	923	9	CNS01509	Drosophil	1102	39.4	5.5	601	9	CE472841	CE472841 tigr-gss-
C1030	39.6	5.6	926	8	AG405311	Mus muscu	1103	39.4	5.5	604	7	CO312735	CO312735 BK229834.
C1031	39.6	5.6	928	8	AZ546297	ENTFQ65TF	1104	39.4	5.5	608	8	BH765132	BH765132 BMBAC353G
C1032	39.6	5.6	936	9	CNS038V5	Tetraodon	1105	39.4	5.5	619	9	CE802728	CE802728 tigr-gss-
C1033	39.6	5.6	948	5	BQ877388	AGENCOURT	1106	39.4	5.5	630	9	CE721057	CE721057 tigr-gss-
C1034	39.6	5.6	956	8	CO077238	CSU-K33R.	1107	39.4	5.5	637	4	BI381942	BI381942 BFLG2.000
C1035	39.6	5.6	957	6	CNS90657	AGENCOURT	1108	39.4	5.5	637	8	AZ097834	AZ097834 RPCI-23-4
C1036	39.6	5.6	960	9	AG031602	Pan trogl	1109	39.4	5.5	640	5	BP126360	BP126360 BP126360
C1037	39.6	5.6	962	6	CD387035	AGENCOURT	1110	39.4	5.5	649	7	CNS90604	CNS90604 TTE000139
C1038	39.6	5.6	970	7	CC723061	OGLBM02TV	1111	39.4	5.5	650	9	CE284277	CE284277 tigr-gss-
C1039	39.6	5.6	971	9	CNS01815	AGENCOURT	1112	39.4	5.5	652	8	AQ553213	AQ553213 RPCI-11-4
C1040	39.6	5.6	975	6	CD387746	AGENCOURT	1113	39.4	5.5	665	7	CK533631	CK533631 rswgbo.00
C1041	39.6	5.6	983	9	CL461143	SAIL.113	1114	39.4	5.5	665	9	CE565840	CE565840 tigr-gss-
C1042	39.6	5.6	988	2	BF275105	GA_Eb002	1115	39.4	5.5	668	9	CR097976	CR097976 Reverse s
C1043	39.6	5.6	1078	8	BH150342	ENTPW09TF	1116	39.4	5.5	674	9	CE131494	CE131494 tigr-gss-
C1044	39.6	5.6	1097	6	CD048504	AGENCOURT	1117	39.4	5.5	684	6	CD832362	CD832362 BN40.063A
C1045	39.6	5.6	1101	9	AL061936	Drosophil	1118	39.4	5.5	686	8	BZ240002	BZ240002 CH230-324
C1046	39.6	5.6	1101	9	CNS006TE	AL065901	1119	39.4	5.5	691	9	AG339634	AG339634 Mus muscu

c1120	39.4	5.5	692	7	CF935715	TrEST-B05	CF935715	1732	9	CL019669	CL019669	CH216-5U1
c1121	39.4	5.5	692	9	AG339721	Mus muscu	AG339721	1733	9	AG278266	AG278266	Mus muscu
c1122	39.4	5.5	696	9	CE454509	tigr-gss-	CE454509	2155	9	CL019444	CL019444	SAU87F10.
c1123	39.4	5.5	700	8	BH940292	obf76h04.	BH940292	301	6	CA820343	CA820343	saue87f10.
c1124	39.4	5.5	700	8	CE183051	tigr-gss-	CE183051	307	6	BY750907	BY750907	QGESB18.Y
c1125	39.4	5.5	704	8	BH596231	BOGLO79TF	BH596231	311	5	BQ984794	BQ984794	QGESB18.Y
c1126	39.4	5.5	706	6	CB348184	CAB2SG000	CB348184	317	7	CN569510	CN569510	tad39d05.
c1127	39.4	5.5	716	9	BX234097	Danio rer	BX234097	326	1	AG611408	AG611408	vos1e06.r
c1128	39.4	5.5	716	9	CE457503	tigr-gss-	CE457503	341	2	B8992538	B8992538	UI-M-B21
c1129	39.4	5.5	723	9	CE055794	tigr-gss-	CE055794	361	5	BM942837	BM942837	UI-N-B21
c1130	39.4	5.5	726	9	CE668211	tigr-gss-	CE668211	419	1	AU000851	AU000851	AU000851
c1131	39.4	5.5	730	1	AG473215	Mus muscu	AG473215	424	8	BZ263903	BZ263903	CH230-420
c1132	39.4	5.5	736	1	AU001091	AU001091	AU001091	461	5	BQ453555	BQ453555	sa05a06.
c1133	39.4	5.5	737	9	CNS008BU	Drosophil	CNS008BU	476	6	CA738318	CA738318	wpi2s.pK0
c1134	39.4	5.5	738	8	BH944916	obu8ic12.	BH944916	484	9	CE148240	CE148240	tigr-gss-
c1135	39.4	5.5	738	9	CE252180	tigr-gss-	CE252180	507	1	AI432229	AI432229	th43c03.x
c1136	39.4	5.5	741	9	CNS007YN	Mus muscu	CNS007YN	516	1	AV882594	AV882594	AV882594
c1137	39.4	5.5	753	9	AG398161	Drosophil	AG398161	541	7	CF980110	CF980110	rg85a09.Y
c1138	39.4	5.5	761	9	CE193517	tigr-gss-	CE193517	553	8	AZ213270	AZ213270	Sheared D
c1139	39.4	5.5	770	1	AV758087	AV758087	AV758087	573	8	AZ897242	AZ897242	RPC1-24-2
c1140	39.4	5.5	772	5	BH361079	603788508	BH361079	579	7	CK593976	CK593976	tad36e08.
c1141	39.4	5.5	792	6	CB315935	AGENCOURT	CB315935	579	9	CE230952	CE230952	tigr-gss-
c1142	39.4	5.5	799	8	BH421229	BOGXY71TR	BH421229	588	8	AZ409768	AZ409768	1M0181N06
c1143	39.4	5.5	799	9	AG498655	Mus muscu	AG498655	589	7	CK593565	CK593565	tad33e09.
c1144	39.4	5.5	808	7	CO128111	GR_Eb14B	CO128111	591	7	CN569040	CN569040	tad35d04.
c1145	39.4	5.5	817	9	CNS072EB	AL426105	AL426105	594	2	AM640635	AM640635	bl97c07.w
c1146	39.4	5.5	820	9	CL542043	OB_Ba006	CL542043	599	6	CA877228	CA877228	K0954B03-
c1147	39.4	5.5	827	9	CNS008BU	Drosophil	CNS008BU	602	1	AV996730	AV996730	AV996730
c1148	39.4	5.5	835	7	CF411135	CH3H071.G	CF411135	610	4	BJ337190	BJ337190	BJ337190
c1149	39.4	5.5	836	9	BX195755	Danio rer	BX195755	618	9	CE628935	CE628935	tigr-gss-
c1150	39.4	5.5	839	8	BH484892	BOGJW79TR	BH484892	619	9	CE459612	CE459612	tigr-gss-
c1151	39.4	5.5	856	9	CC517114	CH240_363	CC517114	629	5	CE303242	CE303242	tigr-gss-
c1152	39.4	5.5	881	8	BH149084	ENTPX51TR	BH149084	651	8	BH559890	BH559890	BOHMH78TF
c1153	39.4	5.5	886	7	CK159064	FGA04044	CK159064	663	9	CE251668	CE251668	tigr-gss-
c1154	39.4	5.5	886	7	AG2671247	ENTLO96TF	AG2671247	667	2	BB466825	BB466825	BB466825
c1155	39.4	5.5	888	8	BH136016	ENTNMU11TR	BH136016	676	9	CNS003XU	CNS003XU	Drosophil
c1156	39.4	5.5	895	8	AZ692422	ENTNMU11TR	AZ692422	679	9	CE576403	CE576403	tigr-gss-
c1157	39.4	5.5	899	8	BH136627	ENTNR76TF	BH136627	680	5	BA366641	BA366641	BA366641
c1158	39.4	5.5	902	8	BH148690	ENTPH49TR	BH148690	680	9	CE315861	CE315861	tigr-gss-
c1159	39.4	5.5	907	8	AZ550893	ENTPU62TF	AZ550893	683	9	CE131552	CE131552	tigr-gss-
c1160	39.4	5.5	908	9	CG920649	ENTPU62TF	CG920649	688	9	CE678744	CE678744	tigr-gss-
c1161	39.4	5.5	929	8	BH132712	ENTYOY73TR	BH132712	690	9	CR311789	CR311789	Medicago
c1162	39.4	5.5	932	5	BQ888143	AGENCOURT	BQ888143	698	9	CE079486	CE079486	tigr-gss-
c1163	39.4	5.5	944	9	AG044059	Pan trogl	AG044059	703	5	BM404792	BM404792	BM404792
c1164	39.4	5.5	945	8	BH158204	ENTST43TF	BH158204	718	9	AG160666	AG160666	Pan trogl
c1165	39.4	5.5	946	8	BH158543	ENTPL83TF	BH158543	719	8	B21675	B21675	F17P15-Sp6
c1166	39.4	5.5	969	6	CD388513	AGENCOURT	CD388513	734	8	BZ051694	BZ051694	jinr58G09.
c1167	39.4	5.5	976	6	CB209639	AGENCOURT	CB209639	738	9	AG584201	AG584201	Mus muscu
c1168	39.4	5.5	998	9	CNS033GA	Tetraodon	CNS033GA	740	9	CNS01106	CNS01106	Drosophil
c1169	39.4	5.5	1000	6	CNS00YXQ	AGENCOURT	CNS00YXQ	765	8	BZ068689	BZ068689	ljt54e03.
c1170	39.4	5.5	1017	9	CL101048	ISB1-3604	CL101048	769	5	BM015161	BM015161	BM015161
c1171	39.4	5.5	1032	9	CL144058	ISB1-124E	CL144058	775	5	BM023821	BM023821	BM023821
c1172	39.4	5.5	1052	5	BUS60001	AGENCOURT	BUS60001	780	8	BZ084906	BZ084906	ljt55e03.
c1173	39.4	5.5	1094	9	CNS012FZ	Drosophil	CNS012FZ	810	4	BG029588	BG029588	602296766
c1174	39.4	5.5	1101	8	CC226592	CH261-99P	CC226592	827	9	CG929549	CG929549	MBEGL15TR
c1175	39.4	5.5	1101	9	CNS00B01	Drosophil	CNS00B01	834	8	BZ849035	BZ849035	CH240_-277
c1176	39.4	5.5	1101	9	CNS012UQ	Drosophil	CNS012UQ	839	9	EX191452	EX191452	Danio rer
c1177	39.4	5.5	1152	8	BZ696911	SP_Ba009	BZ696911	857	5	BM023481	BM023481	BM023481
c1178	39.4	5.5	1180	8	CL288642	CH261-25L	CL288642	886	6	CB205144	CB205144	AGENCOURT
c1179	39.4	5.5	1188	9	CL650084	CH213-275	CL650084	895	5	BUS63980	BUS63980	AGENCOURT
c1180	39.4	5.5	1203	3	CR722667	Tetraodon	CR722667	901	9	AL429211	AL429211	clone BAO
c1181	39.4	5.5	1214	5	BUL67807	AGENCOURT	BUL67807	905	9	CG936966	CG936966	MBEHC03TF
c1182	39.4	5.5	1224	9	AG365518	Mus muscu	AG365518	905	9	CNS00KHX	CNS00KHX	CK077798
c1183	39.4	5.5	1258	9	CL508886	SAIL_804	CL508886	907	7	CK403875	CK403875	AUF IFHdk
c1184	39.4	5.5	1260	8	BZ695485	SP_Ba006	BZ695485	915	4	BG520365	BG520365	PDJFN92TD
c1185	39.4	5.5	1268	9	CL063191	CH216-99L	CL063191	915	9	CG087264	CG087264	CG087264
c1186	39.4	5.5	1289	9	CL647725	CH213-147	CL647725	933	9	CL498254	CL498254	SAIL_654
c1187	39.4	5.5	1308	9	CL642491	CH213-31J	CL642491	937	1	AL539679	AL539679	AL539679
c1188	39.4	5.5	1308	9	CL647502	CH213-139	CL647502	992	6	CNS06E49	CNS06E49	T7 end of
c1189	39.4	5.5	1458	4	BG766741	602740034	BG766741	1024	8	BZ601217	BZ601217	WHADC85TR
c1190	39.4	5.5	1549	9	CL019527	CH216-5H9	CL019527	1041	6	CD389041	CD389041	AGENCOURT
c1191	39.4	5.5	1615	9	AG311072	Mus muscu	AG311072	1041	6	CD389041	CD389041	AGENCOURT

1266	39.2	5.5	1067	6	CD386564	CD386564	AGENCYCOURT	1339	39	5.5	526	6	CD419153	CD419153	ri82b12.y
1267	39.2	5.5	1068	9	AG112950	AG112950	CH216-20I	c1340	39	5.5	529	1	CA543871	CA543871	C0640F12-
1268	39.2	5.5	1097	9	CL024868	CL024868		c1341	39	5.5	530	1	AA521371	AA521371	aa77f12.s
1269	39.2	5.5	1101	9	CNS0042W	CNS0042W	Drosophil	c1342	39	5.5	538	2	BF114633	BF114633	7j65e10.x
1270	39.2	5.5	1101	9	CNS000H9E	CNS000H9E	Drosophil	c1343	39	5.5	550	6	CA4112962	CA4112962	UI-H-EZO
1271	39.2	5.5	1101	9	CNS014NP	CNS014NP	Drosophil	c1344	39	5.5	554	8	BQ394230	BQ394230	NISC-ng08
1272	39.2	5.5	1101	9	CNS016VO	CNS016VO	Drosophil	c1345	39	5.5	555	8	AQ500528	AQ500528	V37B7 m7n
1273	39.2	5.5	1101	9	CNS0177R	CNS0177R	Drosophil	c1346	39	5.5	555	8	CNS040CR	CNS040CR	AL299844
1274	39.2	5.5	1101	9	CNS017Y0	CNS017Y0	Drosophil	c1347	39	5.5	561	6	CA854462	CA854462	PfESToac2
1275	39.2	5.5	1115	6	AG477617	AG477617	Mus muscu	c1348	39	5.5	564	9	CR031329	CR031329	Reverse s
1276	39.2	5.5	1118	6	CF218947	CF218947	AGENCYCOURT	c1349	39	5.5	565	9	CR360366	CR360366	tigr-gss-
1277	39.2	5.5	1163	9	CL081338	CL081338	CH216-161	c1350	39	5.5	567	9	DR22KL8S	DR22KL8S	Danio rer
1278	39.2	5.5	1167	9	CL050792	CL050792	CH216-720	c1351	39	5.5	573	9	CE697776	CE697776	tigr-gss-
1279	39.2	5.5	1183	9	CL108008	CL108008	ISB1-49C1	c1352	39	5.5	575	6	CA362396	CA362396	636521 NC
1280	39.2	5.5	1184	9	AG278197	AG278197	Mus muscu	c1353	39	5.5	577	9	CE687545	CE687545	tigr-gss-
1281	39.2	5.5	1201	9	CNS0070U	CNS0070U	Drosophil	c1354	39	5.5	578	9	CE622546	CE622546	tigr-gss-
1282	39.2	5.5	1201	9	CNS0167B	CNS0167B	Drosophil	c1355	39	5.5	580	9	CE190275	CE190275	tigr-gss-
1283	39.2	5.5	1226	9	AG288300	AG288300	Mus muscu	c1356	39	5.5	581	7	CO334736	CO334736	EX315203
1284	39.2	5.5	1244	9	AG360765	AG360765	Mus muscu	c1357	39	5.5	587	7	CK680717	CK680717	ZF101-P00
1285	39.2	5.5	1268	9	AG347098	AG347098	Mus muscu	c1358	39	5.5	594	2	AW861371	AW861371	CM1-CT030
1286	39.2	5.5	1280	9	AG382224	AG382224	Mus muscu	c1359	39	5.5	595	9	AX235645	AX235645	Danio rer
1287	39.2	5.5	1285	9	AG311168	AG311168	Mus muscu	c1360	39	5.5	602	1	AI078595	AI078595	oz49q02.x
1288	39.2	5.5	1297	9	AG305140	AG305140	Mus muscu	c1361	39	5.5	606	9	CNS044D1	CNS044D1	Tetraodon
1289	39.2	5.5	1311	9	AG280063	AG280063	Mus muscu	c1362	39	5.5	611	1	AA538201	AA538201	Vj56907.r
1290	39.2	5.5	1431	9	AG280463	AG280463	Mus muscu	c1363	39	5.5	619	8	AZ421576	AZ421576	IM0199H20
1291	39.2	5.5	1439	3	AK084227	AK084227	Mus muscu	c1364	39	5.5	624	8	AZ118263	AZ118263	RPCI-23-4
1292	39.2	5.5	1452	3	CC184244	CC184244	CH261-3M5	c1365	39	5.5	628	4	BM640724	BM640724	170006872
1293	39.2	5.5	1533	9	CL081968	CL081968	CH216-165	c1366	39	5.5	628	8	AZ647830	AZ647830	IM0514K02
1294	39.2	5.5	1721	9	CL019385	CL019385	CH216-5C1	c1367	39	5.5	635	9	CE697777	CE697777	tigr-gss-
1295	39.2	5.5	1805	9	CL080711	CL080711	CH216-159	c1368	39	5.5	637	8	AQ985177	AQ985177	RPCI-23-3
1296	39.2	5.5	2266	9	AG429710	AG429710	Mus muscu	c1369	39	5.5	642	8	AZ025078	AZ025078	RPCI-23-4
1297	39	5.5	188	1	AU094213	AU094213		c1370	39	5.5	645	6	CA142282	CA142282	SCMCR208
1298	39	5.5	279	1	AI280233	AI280233	GM66907.x	c1371	39	5.5	659	8	BH042654	BH042654	RPCI-24-2
1299	39	5.5	290	6	CB045528	CB045528	NISC-gc10	c1372	39	5.5	660	9	AG055603	AG055603	Pan trogl
1300	39	5.5	290	6	CB045528	CB045528	NISC-gc10	c1373	39	5.5	665	6	CD742384	CD742384	UI-H-FT1-
1301	39	5.5	311	6	CB264177	CB264177	84-E01499	c1374	39	5.5	667	4	BG965643	BG965643	UI-H-FT1-
1302	39	5.5	326	2	BE857393	BE857393	7g35H09.x	c1375	39	5.5	667	6	BY747850	BY747850	UI-H-FT1-
1303	39	5.5	334	1	AI246359	AI246359	q113b10.x	c1376	39	5.5	668	6	CG818901	CG818901	SOYAP30TV
1304	39	5.5	352	5	BU761134	BU761134	aa63e10.	c1377	39	5.5	668	8	AZ649306	AZ649306	IM0518F23
1305	39	5.5	367	9	CE474441	CE474441	tigr-gss-	c1378	39	5.5	671	8	CE517378	CE517378	tigr-gss-
1306	39	5.5	376	9	CE730958	CE730958	tigr-gss-	c1379	39	5.5	673	5	BQ448209	BQ448209	UI-H-EU1-
1307	39	5.5	390	4	BI815811	BI815811	PfESToaa3	c1380	39	5.5	675	5	BQ448209	BQ448209	UI-H-EU1-
1308	39	5.5	398	8	AQ816540	AQ816540	HS-4555.A	c1381	39	5.5	677	8	BH967482	BH967482	oj32a08.
1309	39	5.5	398	8	CR159157	CR159157	Forward's	c1382	39	5.5	677	8	BH967482	BH967482	oj32a08.
1310	39	5.5	409	4	BG191283	BG191283	RST10371	c1383	39	5.5	677	8	BH967482	BH967482	oj32a08.
1311	39	5.5	413	5	BQ559588	BQ559588	H4059807-	c1384	39	5.5	684	5	BU626705	BU626705	UI-H-FT0-
1312	39	5.5	413	5	BQ011437	BQ011437	UI-1-BC1p	c1385	39	5.5	684	6	CB058266	CB058266	NISC-jx02
1313	39	5.5	422	9	CE714097	CE714097	tigr-gss-	c1386	39	5.5	684	8	BZ007540	BZ007540	ehh21a07.
1314	39	5.5	430	5	BM991242	BM991242	UI-H-D10-	c1387	39	5.5	686	9	CE611161	CE611161	tigr-gss-
1315	39	5.5	440	5	BQ577017	BQ577017	PfESToab1	c1388	39	5.5	687	9	CE552849	CE552849	tigr-gss-
1316	39	5.5	450	5	BY565904	BY565904		c1389	39	5.5	693	8	BZ458943	BZ458943	BONDW877R
1317	39	5.5	454	7	CF370326	CF370326	tg63d10.y	c1390	39	5.5	694	9	AG276136	AG276136	Mus muscu
1318	39	5.5	455	1	AI439315	AI439315	t159F05.x	c1391	39	5.5	695	8	BZ227162	BZ227162	CH230-305
1319	39	5.5	455	8	AQ210262	AQ210262	HS-3214.B	c1392	39	5.5	705	9	AG078824	AG078824	Pan trogl
1320	39	5.5	461	8	AZ279678	AZ279678	RPCI-23-1	c1393	39	5.5	708	9	CE213985	CE213985	tigr-gss-
1321	39	5.5	462	1	AI287686	AI287686	GL53d01.x	c1394	39	5.5	711	9	AG286222	AG286222	Mus muscu
1322	39	5.5	463	8	AZ041950	AZ041950	RPCI-23-3	c1395	39	5.5	714	9	AG279355	AG279355	Danio rer
1323	39	5.5	464	9	CE339203	CE339203	tigr-gss-	c1396	39	5.5	715	9	AG031744	AG031744	Mus muscu
1324	39	5.5	466	8	BH678695	BH678695	BONDW707R	c1397	39	5.5	715	6	BY764960	BY764960	Pan trogl
1325	39	5.5	473	2	BE045819	BE045819	hg83d06.x	c1398	39	5.5	716	9	CNS044W5	CNS044W5	Tetraodon
1326	39	5.5	475	1	AI818172	AI818172	wk42a08.x	c1399	39	5.5	716	9	AG339819	AG339819	Mus muscu
1327	39	5.5	475	7	CF370630	CF370630	tg51g03.y	c1400	39	5.5	718	9	AG424558	AG424558	Mus muscu
1328	39	5.5	476	9	CNS04TOC	CNS04TOC	Tetraodon	c1401	39	5.5	719	9	AG247193	AG247193	1kg76a12.
1329	39	5.5	477	9	CE710706	CE710706	tigr-gss-	c1402	39	5.5	727	8	BZ047193	BZ047193	1lf50b05.
1330	39	5.5	481	8	AZ336252	AZ336252	IM066L24	c1403	39	5.5	730	8	BZ089086	BZ089086	1lf50b05.
1331	39	5.5	492	9	CR052706	CR052706	Reverse s	c1404	39	5.5	731	7	CK020682	CK020682	AGENCYCOURT
1332	39	5.5	496	8	AZ821894	AZ821894	2M0094A22	c1405	39	5.5	731	8	AZ709037	AZ709037	RPCI-24-8
1333	39	5.5	503	9	CE693931	CE693931	tigr-gss-	c1406	39	5.5	735	9	AX143418	AX143418	Danio rer
1334	39	5.5	507	1	AI125981	AI125981	q446c12.x	c1407	39	5.5	735	9	AX165277	AX165277	Danio rer
1335	39	5.5	508	1	AI147865	AI147865	q446c12.x	c1408	39	5.5	736	9	AG442804	AG442804	Mus muscu
1336	39	5.5	514	4	BI678667	BI678667	SW430.SW	c1409	39	5.5	737	5	BQ932514	BQ932514	AGENCYCOURT
1337	39	5.5	520	2	AW957444	AW957444	EST369409	c1410	39	5.5	742	9	AG438941	AG438941	Mus muscu
1338	39	5.5	524	4	BG221295	BG221295	RST41100	c1411	39	5.5	752	7	CF519392	CF519392	AGENCYCOURT


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1412 39 5.5 752 9 AG601348 Mus muscu
c1413 39 5.5 753 8 BH655103 BOMFF91TF
1414 39 5.5 753 9 AG383423 Mus muscu
1415 39 5.5 756 9 AG410849 Mus muscu
c1416 39 5.5 760 9 AG574377 Mus muscu
c1417 39 5.5 770 9 CR319783 Medicago
c1418 39 5.5 772 9 AG397006 Mus muscu
c1419 39 5.5 773 9 AG514109 Mus muscu
c1420 39 5.5 781 6 CB852134 UI-CF-PNO
c1421 39 5.5 791 8 BH055583 RPC1-24-2
c1422 39 5.5 802 8 BH331278 CH230-46L
c1423 39 5.5 811 9 AG398081 Mus muscu
c1424 39 5.5 816 9 CNS02KJY Tetraodon
c1425 39 5.5 819 9 CR241576 Reverse s
c1426 39 5.5 822 5 BU930638 AGENCOURT
c1427 39 5.5 823 9 CC931632 ZUAGJ42TH
c1428 39 5.5 840 2 BF274129 GA_EB002
c1429 39 5.5 841 6 CA970412 CcLL03a08
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c1431 39 5.5 843 9 CC483944 CH240-312
c1432 39 5.5 855 9 AJ599212 Arabidops
c1433 39 5.5 863 4 BM395523 50072-2-9
c1434 39 5.5 875 9 CNS03PJV Tetraodon
c1435 39 5.5 876 9 CL836279 OR_CBA006
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c1437 39 5.5 893 9 CG030682 PUFP83TB
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c1439 39 5.5 930 9 CNS02RYB Tetraodon
c1440 39 5.5 934 9 CNS00DH9 AL070621 Drosophil
c1441 39 5.5 935 8 B10881 F24H6-Sp6.1
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c1443 39 5.5 955 9 AG388848 Mus muscu
c1444 39 5.5 961 9 CNS008HI AL051882 Drosophil
c1445 39 5.5 977 9 CNS014WC AL04701 Drosophil
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c1447 39 5.5 1002 9 AG387799 Mus muscu
c1448 39 5.5 1011 8 CC239214 CH261-127
c1449 39 5.5 1015 4 B1490178 603031949
c1450 39 5.5 1021 9 CL078509 CH216-150
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c1460 39 5.5 1138 9 AG310974 Mus muscu
c1461 39 5.5 1152 8 AQ779752 HS_5572_B
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c1464 39 5.5 1178 9 CL491661 SAIL_559
c1465 39 5.5 1201 5 BU162562 AGENCOURT
c1466 39 5.5 1201 9 CNS007E3 AL067050 Drosophil
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c1468 39 5.5 1201 9 CNS0163W AL106262 Drosophil
c1469 39 5.5 1211 9 AG346553 Mus muscu
c1470 39 5.5 1221 9 CNS0169U AL106476 Drosophil
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c1474 39 5.5 1271 9 AG371391 Mus muscu
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c1476 39 5.5 1313 9 AG347035 Mus muscu
c1477 39 5.5 1336 9 AG516595 Mus muscu
c1478 39 5.5 1336 9 CL501990 SAIL_706
c1479 39 5.5 1394 9 CL507523 SAIL_781
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c1481 39 5.5 1448 9 CG754506 P049-4-H0
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c1483 39 5.5 1581 9 AG280125 Mus muscu
c1484 39 5.5 1850 9 AG279978 Mus muscu
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c1485 39 5.5 2020 9 AG311121 Mus muscu
1486 38.8 5.4 234 1 AV326655 AV326655
1487 38.8 5.4 242 2 BE086569 QV1-BT067
1488 38.8 5.4 258 1 AV221965 AV221965
1489 38.8 5.4 276 2 BF794994 602256104
1490 38.8 5.4 278 9 CE646245 tigr-ges-
c1491 38.8 5.4 305 6 CD672586 fg13h02.x
c1492 38.8 5.4 326 6 CD682571 rj26h03.y
c1493 38.8 5.4 350 4 BM522061 ESS00598
c1494 38.8 5.4 363 6 CB855593 r141a11.y
c1495 38.8 5.4 365 6 CD722984 OJ16f01.y
c1496 38.8 5.4 382 7 N97718 170303 czap
c1497 38.8 5.4 383 7 CK386182 lah33b07
c1498 38.8 5.4 405 9 CNS03OJM CK386182 lah33b07
c1499 38.8 5.4 411 6 CB072974 taa26d11.
c1500 38.8 5.4 427 5 BP178454 BP178454
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ALIGNMENTS

RESULT 1
AUI85777/c

LOCUS AUI85777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens
DEFINITION AUI85777 Homo sapiens Mast cell mRNA linear EST 05-JUL-2001
CDNA clone B02302-019, mRNA sequence.

ACCESSION AUI85777 GI:14623690
VERSION AUI85777.1

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 663)

AUTHORS Sugita, Y., Oshida, T. and Oya, Y.
TITLE Human cDNA sequencing
JOURNAL Unpublished (2001)

COMMENT Contact: Yuji Sugita
Genox Research, Inc.
907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan
Tel: 81-44-797-2281
Fax: 81-44-797-2622
Email: syuji@genox.co.jp, URL: http://www.genox.co.jp.

FEATURES
source

Location/Qualifiers
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B02302-019"
/cell_type="Mast cell"
/clone_lib="Homo sapiens Mast cell library (Sugita Y)"

ORIGIN

Query Match 74.0%; Score 527.8; DB 1; Length 663;
Best Local Similarity 95.3%; Pred. No. 3.2e-109;
Matches 573; Conservative 0; Mismatches 23; Indels 5; Gaps 3;
Qy 2 ATATATCATCTATTATCAATTAATCAATGATTTCTTTTATTCCAATAACATTTGGGT 61
Db 597 AAATATCATCTATTATCAATTAATCAATGATTTCTTTTATTCCAATAAATTTGGGT 538
Qy 62 TTGGGATTTTAAATTTTCAACACACAGATGACATTTTCTGTCTACATTTATTATG 121
Db 537 TTGGGATTTTAAATTTTCAACACACAGATGACATTTTCTGTCTACATTTATTATG 478
Qy 122 TTGGTATGTGAAGCTATTGG-AGATCCCAATTCAGGAAGCAACACATTTGAGATGGCTA 180
Db 477 TTGGTATGTGAAGCTATTGGTATGATCCCAATTCAGNAAG---CACATTGNAGATGGCTA 421
Qy 181 CTTTCTTATCAAGAAATATAAGAGAACACAGTCAACCCACACATTCATCTTTAGAGACAG 240
Db 420 CTTTCTTATCAAGAAATATAAGAGAACACAGTCAACCCACACATTCATCTTTAGAGACAG 361

241 TGTGACTCTACCAAGGCTGTCAAAACACACAGGCAAGGCGATAGTTAAAGACGGAATCT 300
Db |||||||
360 TG-GACTCTACCAAGGCTGTCAAAACACACAGGCAAGGCGATAGTTAAAGACGGAATCT 302
Qy |||||||
301 TGACTCAAGAGGGTTAAATCTTGTGCTGTAAGCCCTGGGCGAGGGGTGTAAGAAAAACAC 360
Db |||||||
301 TGACTCAAGAGGGTTAAATCTTGTGCTGTAAGCCCTGGGCGAGGGGTGTAAGAAAAACAC 242
Qy |||||||
361 TTAGATCAAGATGTAATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT 420
Db |||||||
241 TTAGATCAAGATGTAATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT 182
Qy |||||||
421 GTATCCCTGTCATATATACATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT 480
Db |||||||
181 GTATCCCTGTCATATATACATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT 122
Qy |||||||
481 AGTTCTAAATGGACTTTATTAATTTTAAATCAAGTAACTGATTTATCATCTGGCTATGT 540
Db |||||||
121 AGTTCTAAATGGACTTTATTAATTTTAAATCAAGTAACTGATTTATCATCTGGCTATGT 62
Qy |||||||
541 GCTTAGATCTACAGAGATCATATAATTTGATACAAATAAGAAAGTGTCTCTCCCC 600
Db |||||||
61 GCTTAGATCTACAGAGATCATATAATTTGATACAAATAAGAAAGTGTCTCTCCCC 2
Qy |||||||
601 T 601
Db 1 T 1

RESULT 2
LOCUS CB958894 800 bp mRNA linear EST 29-APR-2003
DEFINITION AGNCOURT_13785021 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30352338 5', mRNA sequence.
ACCESSION CB958894
VERSION CB958894.1 GI:30215010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM151 row: e column: 19
High quality sequence stop: 488.
Location/Qualifiers
1..800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352338"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
note="Organ: Fooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattagggc); Site_2: Sfil (ggccctcgccg);
Library is oligo-dr primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGCCGAGCGCCGACATG-CT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38

FEATURES
source

ORIGIN

Query Match 37.6%; Score 268.2; DB 6; Length 800;
Best Local Similarity 98.9%; Pred. No. 2.5e-50;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 AATATATCATCTATTATCATTAATCAATAATGATTTCTTTTATTCCTCAATCAATTTGGG 60
Db |||||||
251 AATATATCATCTATTATCATTAATCAATAATGATTTCTTTTATTCCTCAATCAATTTGGG 310
Qy |||||||
61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTCACTATTATTATT 120
Db |||||||
311 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTCACTATTATTATT 370
Qy |||||||
121 GTTGTATGTGAAGCTATTTCGAGATCCAAATTCAGGAAGCAACACATTTGGAGAATGGCTA 180
Db |||||||
371 GTTGTATGTGAAGCTATTTCGAGATCCAAATTCAGGAAGCAACACATTTGGAGAATGGCTA 430
Qy |||||||
181 CTTTCTATCAGAATAAAGAGAACCCACAGTCACCCACACATCATCTTTAGAGACAG 240
Db |||||||
431 CTTTCTATCAGAATAAAGAGAACCCACAGTCACCCACACATCATCTTTAGAGACAG 490
Qy |||||||
241 TGTGACTCTACCAAGGCTGTCAAAACACACAGG 273
Db |||||||
491 TGTGACTCTACCAAGGCTGTCAAAACACACAGG 523

RESULT 3

AZ121459/c

LOCUS AZ121459 663 bp DNA linear GSS 12-MAY-2000

DEFINITION RPCI-23-30A15-TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,

genomic survey sequence.

ACCESSION AZ121459

VERSION AZ121459.1 GI:7788387

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 663)

AUTHORS Zhao,S., Niekman,W., Feldblyum,T., Malek,J., Shatsman,S.,

Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de

Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-30A15.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@jong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html

Plate: 30 row: A column: 15

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..663

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-30A15"

kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

/clone.lib="HTB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 16.8%; Score 120; DB 1; Length 673;
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Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGGAAGCAACACATTTGGAGATGGCTACTTCTATCAAGAAATAAGAGAACACAGTCA 60
|||||

QY 214 ACCACACAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACACAGG 273
|||||

DB 61 ACCACACAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACACAGG 120
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RESULT 6

CB420818 582 bp mRNA linear EST 25-MAR-2003
LOCUS

DEFINITION 593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB420818
VERSION CB420818.1 GI:29187264
KEYWORDS EST.

SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE 1 (bases 1 to 582)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.

TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.

Plate: FOY8014 row: B column: 7
Seq primer: GTAATACGACTCACTATAGG.

FEATURES

source Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site_1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 14.7%; Score 104.8; DB 6; Length 582;
Best Local Similarity 84.3%; Pred. No. 2.8e-13;
Matches 118; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 134 GCTATTTGGAGATCCATTCAGGAGCAACACATTTGGAGATGGCTACTTCTATCAAGA 193
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DB 244 GGTATTTGGAGATCCATTCAGGAGCAACACCTTTGAAGAGTGACAGTTTCCATCAAGA 303
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QY 194 AATAAGAGAACACACAGTCAACCCACACAATCATCTTTAGAGACAGTGTGACTCTCTACC 253
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DB 304 AATAAGACACACAGAGTCAACCCACACAATCATCTTTAGAGATAGTGTGATACCTACC 363
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QY 254 AAAGCTGTCAAAACACACAGG 273
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Db 364 AAGGCTCTCACGACCACAGG 383
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RESULT 7

BY547544
LOCUS

DEFINITION 363 bp mRNA linear EST 14-DEC-2002

ACCESSION BY547544

VERSION BY547544.1 GI:26881923

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 363)

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maita,K., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,W.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Whitlested,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Aizawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source Location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="F730119008"
 /cell_type="B6-derived CD11 +ve dendritic cells"
 /clone_lib="RIKEN full-length enriched, B6-derived CD11
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ORIGIN

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 Best Local Similarity 69.8%; Pred. No. 6.9e-07;
 Matches 132; Conservative 0; Mismatches 54; Indels 3; Gaps 2;

QY 1 AATATATCATCTATTATCATTAATCAATTAATGTTATCT-TTATTCCTAATACATTGG 59
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 Db 175 AACATACAGTTTATTATCAATTAACCATAGGCATCCCTATATATGTCCTAATAAATGA 234
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 QY 60 GTTTCGGATTTTAATTTCAACACAGCAGATGACAT--TTTTCCTGTCATTATTT 117
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 Db 235 GTGCTGGCATTTCCATTTTAAACACAGCAGATGACTTCTTTCTGTCATTATGCT 294
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 QY 118 ATTTGTTGGTATGTAAGCTATTTGGAGATCCATTCAGGAAGCAACACATGGAGATGG 177
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 QY 178 CTACTTCTT 186
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 Db 355 CCACTTCTCT 363

RESULT 8

BY536666
 LOCUS
 DEFINITION
 BY536666 RIKEN full-length enriched, NOD-derived CD11c +ve
 dendritic cells Mus musculus cDNA clone F630311P20 3', mRNA
 sequence.

ACCESSION

VERSION
 BY536666.1 GI:26871045

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 419)
 Nikaido, I., Furuno, M., Sasakawa, T., Adachi, J., Bono, H., Kondo, S.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojbori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
 Chothia, C., Cousin, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, I.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
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 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1..419
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NOD"
 /db_xref="taxon:10090"
 /clone="F630311P20"
 /cell_type="NOD-derived CD11c +ve dendritic cells"
 /clone_lib="RIKEN full-length enriched, NOD-derived CD11c
 +ve dendritic cells"

ORIGIN

Query Match 10.7%; Score 76.6; DB 5; Length 419;
 Best Local Similarity 69.8%; Pred. No. 6.9e-07;
 Matches 132; Conservative 0; Mismatches 54; Indels 3; Gaps 2;
 QY 1 AATATATCATCTATTATTCATTAATCAATTAATGTTATCT-TTATTCCTAATACATTGG 59
 |||||
 Db 231 AACATACAGTTTATTATCAATTAACCATAGGCATCCCTATATATGTCCTAATAAATGA 290
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Db 752 TWRDDDDDRAGTAGKRRRTWKRRDRTRDDADADTDARDRRRGDDGADAK 693
QY 374 TTGTAAATTTAAGGCAATATACATATTAGTATACCTTAGTGTAAATGATCCCTGTCAT 433
Db 692 GKKTGKRRRRDRATWDRTDAAWAAWTTTDTDDDDKRRRRKRGARRRRRTARAA 633
QY 434 ATATACAATAAGGTGAATTAAGATACCTATGCAAGTGGCTGGGACAGTCTCAATTCG 493
Db 632 WDWTTWKAWDKWAKWDRADRDWRWAADTTWDARXADRDWAKARAWRARRRRARARAD 573
QY 494 ACTTTTAATTTTAAATTCAGTAATCTGATTTATCACTGGCTATGCTAGTATGATCATCA 553
Db 572 RWTTKGKTATTATTTWAARAAWAAWAAWATTTATTTTWTWTWTWTWTWTWTWT 513
QY 554 GGAGATCATATATTTGATACAAATTAAGAAAGTGTCTCTCCCTCTACAGAAATGAC 613
Db 512 AWWAAWMTATWAAATTAAGAAWAAWAAWATTTTWTWTWTWTWTWTWTWTWTWT 453
QY 614 ATTTTAAATCGCATAGTATAGTAAGAAATGACATTAAGAAAGAAAT 666
Db 452 WTTTWWAAATTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 400
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LOCUS T7 end of clone AW0AA009H09 of library AW0AA from strain CLIB 89 of
DEFINITION Yarrowia lipolytica, genomic survey sequence.
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ACCESSION AL411257.1 GI:12180512
VERSION 1
KEYWORDS GSS.
SOURCE Yarrowia lipolytica
ORGANISM Yarrowia lipolytica
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REFERENCE 1 (bases 1 to 759)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,P., Durrens,P., Lepingle,A., Illorente,B.,
Malpartuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
Yeast species for molecular evolution studies
```

```
FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711
11152876
REFERENCE 2 (bases 1 to 759)
AUTHORS Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynerol,C.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
lipolytica
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FEBS Lett. 487 (1), 95-100 (2000)
PUBMED 20584727
11152892
REFERENCE 3 (bases 1 to 759)
AUTHORS Genoscope.
Direct Submission
```

```
TITLE Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
JOURNAL 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
MEDLINE seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
PUBMED This GSS is part of a random genomic sequencing program of thirteen
REFERENCE yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
AUTHORS exiguus, Saccharomyces servazzii, Zygoaccharomyces rouxii,
JOURNAL Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
MEDLINE lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
PUBMED angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
REFERENCE Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
AUTHORS 5 kb were prepared and both extremities were sequenced. See
JOURNAL keywords for description of this sequence and for the sequence of
TITLE the other extremity of this insert.
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COMMENT Location/Qualifiers
FEATURES
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QY 348 TAAAGAAAACACTAGATTCATGATTCATATACAAATGCGTAAATTAAGTAC-CCTAT 466
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QY 408 ACCTTAGTGTATGTATCCCTGTCTATATATACAAATGCGTAAATTAAGTAC-CCTAT 466
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QY 467 GCAGTTGGCTGGACAGCTCTAAATGCGACTTTTAAATTTTAAATTCAGTACTGATTT 526
Db 123 TTAMATTTTATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 182
QY 527 ATCACTGGCTATGTGTTAGATCTACAGGAGATCATATTTTGTACAAATTAAGTAA 586
Db 183 WMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 242
QY 587 AGTGTCTCTCCCTTTACAGAATTGCATTTTAAATGCGATACAGTTAGAAATGAGAA 646
Db 243 AAMWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 302
QY 647 TGACATTAGAAAGGAAGATGACAGGAGAGAAAGGAAGGAAGGAAGGAAGGAAGGA 706
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QY 707 AAAAAA 712
Db 363 AAAAAA 368
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DEFINITION BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit
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ACCESSION AL071063
VERSION AL071063.1 GI:4951105
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
JOURNAL Ephydroidea; Drosophilidae; Drosophila.
MEDLINE 1 (bases 1 to 996)
PUBMED Genoscope.
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REFERENCE Direct Submission
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
```

```
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Herkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pictet de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
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ACCESSION AL103735
VERSION AL103735.1 GI:5615346
SOURCE GSS.
ORGANISM Drosophila melanogaster (fruit fly)
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          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1043)
AUTHORS Direct Submission
TITLE Determination of this BAC-end sequence was carried out as part of a
JOURNAL collaboration with the European Drosophila Genome Project (EDGP) -
          http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
          library (Dros BAC) was made by Alain Billaud at CEPH (Centre
          d'Etude du Polymorphisme Humain) with funding provided by a MRC
          project grant. The DNA was prepared from embryos by Alain Bucheton
          and Genevieve Payan. It has been constructed in the vector
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QY 366 TTCAATGATTGTAATTTAAGGCAATACACATATTAGTATTACCTTAGTGTAATGATC 425
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Db 786 TTTTATATATATATATATATATATATATATATATATATATATATATATATATAT 727
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QY 606 GAATTCACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGACATTTAGAAAGGAGAA 665
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DEFINITION 082E19 of library G from Tetraodon nigroviridis, genomic survey
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ACCESSION AL274417
VERSION AL274417.1 GI:7996692
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
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REFERENCE 1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
          Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
          Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
          using tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
          Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
          Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
          freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 583)
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr]
COMMENT - Web : www.genoscope.cns.fr)
          This sequence is a single read and was generated as part of a large
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          genome. For more information, please take a look at
          http://www.genoscope.cns.fr/Tetraodon.
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Db 331 KTTTTTTATTTTWTATATTTTWTDTWMDTADDDWWWTTTAAAAAAGAAAAA 390
QY 556 AGATCATATATTTGATACAAATAAAGAAAGAGTGTCTCTCCCTTACAGATTGACAT 615
Db 391 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 450
QY 616 TTTTAATGCGATACAGTTAGAAATATGACATTAGAAAGGAAAGAAATGACAGGAG 675
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2004, 04:19:53 ; Search time 3044 Seconds
(without alignments)
1398.184 Million cell updates/sec

Title: US-09-989-293A-377

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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	462	100.0	713	6	AX055452 Sequence
3	462	100.0	713	6	AX403489 Sequence
4	462	100.0	713	6	AX464340 Sequence

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6	462	100.0	165414	9	AC024224	AC024224 Homo sapi
7	369	79.9	240864	2	AC006510	AC006510 Homo sapi
8	247.5	53.6	625	9	AF400597	AF400597 Homo sapi
9	247.5	53.6	741	6	E21012	E21012 Novel membr
10	247.5	53.6	744	9	AF400595	AF400595 Homo sapi
11	247.5	53.6	744	9	AY026769	AY026769 Homo sapi
12	247.5	53.6	787	9	AF400601	AF400601 Homo sapi
13	247.5	53.6	1018	6	BD136999	BD136999 Isolated
14	247.5	53.6	1153	6	AX664609	AX664609 Sequence
15	247.5	53.6	1153	9	HSA312373	AJ312373 Homo sapi
16	247.5	53.6	1606	6	CQ779237	CQ779237 Sequence
17	247.5	53.6	1606	9	AF313468	AF313468 Homo sapi
18	245	53.0	881	9	AF400602	AF400602 Homo sapi
19	236	51.1	534	6	E21014	E21014 Novel membr
20	217.5	47.1	744	9	AF508729	AF508729 Macaca mu
21	208	45.0	221471	2	AC138620	AC138620 Mus muscu
22	184.5	39.9	273867	2	AC112033	AC112033 Rattus no
23	143.5	31.1	735	10	AY534909	AY534909 Mus muscu
24	143.5	31.1	2298	6	CQ779241	CQ779241 Sequence
25	143.5	31.1	2298	6	BD056525	BD056525 Uniqe de
26	143.5	31.1	2298	10	AF262985	AF262985 Mus muscu
27	139.5	30.2	528	6	BD056528	BD056528 Unique de
28	136.5	29.5	1329	10	BC027742	BC027742 Mus muscu
29	122	26.4	85	6	AX912349	AX912349 Sequence
30	122	26.4	85	6	BD047882	BD047882 Sequence
31	86.5	18.7	211342	2	AC113877	AC113877 Rattus no
32	86.5	18.7	220557	2	AC111741	AC111741 Rattus no
33	85	18.4	227031	2	AC128368	AC128368 Rattus no
34	85	18.4	235295	2	AC126817	AC126817 Rattus no
35	83	18.0	110041	2	AC141026	AC141026 Rattus no
36	83	18.0	231264	2	AC095739	AC095739 Rattus no
37	83	18.0	244024	2	AC133293	AC133293 Rattus no
38	82.5	17.9	233440	2	AC094560	AC094560 Rattus no
39	81.5	17.6	10255	1	AB009926	AB009926 Pyrobacul
40	81	17.5	254951	2	AC122999	AC122999 Rattus no
41	80	17.3	11193	1	AE010087	AE010087 Streptoco
42	80	17.3	43106	7	AY050245	AY050245 Streptoco
43	80	17.3	51908	1	AE014160	AE014160 Streptoco
44	80	17.3	164584	2	AC116727	AC116727 Mus muscu
45	80	17.3	244024	2	AC133293	AC133293 Rattus no
46	80	17.3	288358	2	AC106121	AC106121 Rattus no
47	80	17.3	310950	1	AF005143	AF005143 Streptoco
48	79	17.1	182777	10	AC115928	AC115928 Mus muscu
49	79	17.1	216754	10	AC124770	AC124770 Mus muscu
50	78.5	17.0	1336	3	AY030362	AY030362 Biophala
51	78.5	17.0	3951	10	AF304853	AF304853 Rattus no
52	78.5	17.0	137965	2	AC103669	AC103669 Mus muscu
53	78.5	17.0	230391	2	AC136337	AC136337 Mus muscu
54	78.5	17.0	238585	10	AC129539	AC129539 Mus muscu
55	78	16.9	7662	7	AF020798	AF020798 Streptoco
56	78	16.9	158990	2	AL591702	AL591702 Homo sapi
57	78	16.9	168577	2	AC133893	AC133893 Mus muscu
58	78	16.9	176794	10	AC127756	AC127756 Rattus no
59	78	16.9	179706	2	AC128045	AC128045 Rattus no
60	78	16.9	189004	2	AC142489	AC142489 Rattus no
61	78	16.9	197786	9	AL450326	AL450326 Human DNA
62	78	16.9	241563	2	AC096383	AC096383 Rattus no
63	78	16.9	245489	2	AC105665	AC105665 Rattus no
64	78	16.9	267971	2	AC128995	AC128995 Rattus no
65	77.5	16.8	98653	10	AL731664	AL731664 Mouse DNA
66	77.5	16.8	276034	1	AE017015	AE017015 Bacillus
67	77	16.7	2453	8	BBR581912	BBR581912 Botryococ
68	77	16.7	6318	10	AX122348	AX122348 Mus muscu
69	77	16.7	8141	7	BSF121105	BSF121105 Streptoco
70	77	16.7	40739	7	AF115103	AF115103 Streptoco
71	77	16.7	148654	10	AC132245	AC132245 Mus muscu
72	77	16.7	184202	2	AC150292	AC150292 Callithri
73	77	16.7	200727	10	AC123954	AC123954 Mus muscu
74	77	16.7	250147	10	AC123191	AC123191 Mus muscu
75	76.5	16.6	131484	9	AC016595	AC016595 Homo sapi
76	76.5	16.6	140743	2	AC010496	AC010496 Homo sapi
77	76.5	16.6	157177	9	AC148711	AC148711 Macaca mu

78	76.5	16.6	162579	9	AL390039	Human DNA	151	74	16.0	187416	10	AC121959	AC121959 Mus muscu
79	76.5	16.6	171260	9	AC026743	Homo sapi	152	74	16.0	232211	2	AC097595	AC097595 Rattus no
80	76.5	16.6	174172	9	AC148674	Macaca mu	153	74	16.0	236060	2	AC130954	AC130954 Rattus no
81	76.5	16.6	174926	9	AC093847	Homo sapi	154	74	16.0	241363	2	AC106298	AC106298 Rattus no
82	76	16.5	162769	2	AC136144	AC136144 Pan trogl	155	74	16.0	261352	2	EX957311	EX957311 Danio rer
83	76	16.5	220873	2	AC120258	AC120258 Rattus no	156	74	16.0	303855	1	AE017230	AE017230 Mycobacte
84	76	16.5	225493	2	AC097214	AC097214 Rattus no	157	73.5	15.9	64164	2	AC100248	AC100248 Mus muscu
85	75.5	16.3	100547	9	AC008637	Homo sapi	158	73.5	15.9	132008	2	AC128151	AC128151 Rattus no
86	75.5	16.3	110000	1	AE017355_50	Continuation (51 o	159	73.5	15.9	138471	2	AC147285	AC147285 Pan trogl
87	75.5	16.3	110000	1	AE017355_51	Continuation (52 o	160	73.5	15.9	159190	2	AC150376	AC150376 Canis fam
88	75.5	16.3	110000	2	AC148656_2	Continuation (3 of	161	73.5	15.9	164026	9	AC058791	AC058791 Homo sapi
89	75.5	16.3	141007	2	AC057674	AC057674 Homo sapi	162	73.5	15.9	168119	2	AC068686	AC068686 Homo sapi
90	75.5	16.3	156997	9	AC011465	AC011465 Homo sapi	163	73.5	15.9	168542	2	AC116849	AC116849 Mus muscu
91	75.5	16.3	183599	2	AC073501	AC073501 Homo sapi	164	73.5	15.9	170980	2	AF277371	AF277371 Homo sapi
92	75.5	16.3	215064	2	AC104918	AC104918 Mus muscu	165	73.5	15.9	175047	9	AC013280	AC013280 Homo sapi
93	75.5	16.3	215150	9	AC026689	AC026689 Homo sapi	166	73.5	15.9	175047	9	AC013280	AC013280 Homo sapi
94	75.5	16.3	219379	10	AL627083	AL627083 Mouse DNA	167	73.5	15.9	178506	2	AC141937	AC141937 Rattus no
95	75.5	16.3	227578	2	AC106500	AC106500 Rattus no	168	73.5	15.9	181880	9	BS000198	BS000198 Pan trogl
96	75	16.2	227578	2	AC106500	AC106500 Rattus no	169	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
97	75	16.2	227578	2	AC106500	AC106500 Rattus no	170	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
98	75	16.2	227578	2	AC106500	AC106500 Rattus no	171	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
99	75	16.2	227578	2	AC106500	AC106500 Rattus no	172	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
100	75	16.2	227578	2	AC106500	AC106500 Rattus no	173	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
101	75	16.2	227578	2	AC106500	AC106500 Rattus no	174	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
102	75	16.2	227578	2	AC106500	AC106500 Rattus no	175	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
103	75	16.2	227578	2	AC106500	AC106500 Rattus no	176	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
104	75	16.2	227578	2	AC106500	AC106500 Rattus no	177	73.5	15.9	186773	10	AC135356	AC135356 Mus muscu
105	75	16.2	227578	2	AC106500	AC106500 Rattus no	178	73	15.8	1890	5	BC075881	BC075881 Rattus no
106	75	16.2	227578	2	AC106500	AC106500 Rattus no	179	73	15.8	1890	5	BC075881	BC075881 Rattus no
107	75	16.2	227578	2	AC106500	AC106500 Rattus no	180	73	15.8	1890	5	BC075881	BC075881 Rattus no
108	75	16.2	227578	2	AC106500	AC106500 Rattus no	181	73	15.8	1890	5	BC075881	BC075881 Rattus no
109	75	16.2	227578	2	AC106500	AC106500 Rattus no	182	73	15.8	1890	5	BC075881	BC075881 Rattus no
110	75	16.2	227578	2	AC106500	AC106500 Rattus no	183	73	15.8	1890	5	BC075881	BC075881 Rattus no
111	75	16.2	227578	2	AC106500	AC106500 Rattus no	184	73	15.8	1890	5	BC075881	BC075881 Rattus no
112	75	16.2	227578	2	AC106500	AC106500 Rattus no	185	73	15.8	1890	5	BC075881	BC075881 Rattus no
113	75	16.2	227578	2	AC106500	AC106500 Rattus no	186	73	15.8	1890	5	BC075881	BC075881 Rattus no
114	75	16.2	227578	2	AC106500	AC106500 Rattus no	187	73	15.8	1890	5	BC075881	BC075881 Rattus no
115	75	16.2	227578	2	AC106500	AC106500 Rattus no	188	73	15.8	1890	5	BC075881	BC075881 Rattus no
116	75	16.2	227578	2	AC106500	AC106500 Rattus no	189	73	15.8	1890	5	BC075881	BC075881 Rattus no
117	75	16.2	227578	2	AC106500	AC106500 Rattus no	190	73	15.8	1890	5	BC075881	BC075881 Rattus no
118	75	16.2	227578	2	AC106500	AC106500 Rattus no	191	73	15.8	1890	5	BC075881	BC075881 Rattus no
119	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	192	73	15.8	1890	5	BC075881	BC075881 Rattus no
120	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	193	73	15.8	1890	5	BC075881	BC075881 Rattus no
121	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	194	73	15.8	1890	5	BC075881	BC075881 Rattus no
122	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	195	73	15.8	1890	5	BC075881	BC075881 Rattus no
123	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	196	73	15.8	1890	5	BC075881	BC075881 Rattus no
124	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	197	73	15.8	1890	5	BC075881	BC075881 Rattus no
125	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	198	73	15.8	1890	5	BC075881	BC075881 Rattus no
126	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	199	73	15.8	1890	5	BC075881	BC075881 Rattus no
127	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	200	73	15.8	1890	5	BC075881	BC075881 Rattus no
128	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	201	73	15.8	1890	5	BC075881	BC075881 Rattus no
129	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	202	73	15.8	1890	5	BC075881	BC075881 Rattus no
130	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	203	73	15.8	1890	5	BC075881	BC075881 Rattus no
131	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	204	72.5	15.7	323	5	U96808	U96808 Micropechis
132	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	205	72.5	15.7	323	5	U96808	U96808 Micropechis
133	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	206	72.5	15.7	323	5	U96808	U96808 Micropechis
134	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	207	72.5	15.7	323	5	U96808	U96808 Micropechis
135	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	208	72.5	15.7	323	5	U96808	U96808 Micropechis
136	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	209	72.5	15.7	323	5	U96808	U96808 Micropechis
137	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	210	72.5	15.7	323	5	U96808	U96808 Micropechis
138	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	211	72.5	15.7	323	5	U96808	U96808 Micropechis
139	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	212	72.5	15.7	323	5	U96808	U96808 Micropechis
140	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	213	72.5	15.7	323	5	U96808	U96808 Micropechis
141	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	214	72.5	15.7	323	5	U96808	U96808 Micropechis
142	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	215	72.5	15.7	323	5	U96808	U96808 Micropechis
143	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	216	72.5	15.7	323	5	U96808	U96808 Micropechis
144	74.5	16.1	2082	1	PSEAMP	AC126431 Mus muscu	217	72.5	15.7	323	5	U96808	U96808 Micropechis
145	74	16.0	2226	3	AY145662	AY145662 Homo sapi	218	72.5	15.7	323	5	U96808	U96808 Micropechis
146	74	16.0	2226	3	AY145662	AY145662 Homo sapi	219	72.5	15.7	323	5	U96808	U96808 Micropechis
147	74	16.0	2226	3	AY145662	AY145662 Homo sapi	220	72.5	15.7	323	5	U96808	U96808 Micropechis
148	74	16.0	2226	3	AY145662	AY145662 Homo sapi	221	72.5	15.7	323	5	U96808	U96808 Micropechis
149	74	16.0	2226	3	AY145662	AY145662 Homo sapi	222	72.5	15.7	323	5	U96808	U96808 Micropechis
150	74	16.0	2226	3	AY145662	AY145662 Homo sapi	223	72.5	15.7	323	5	U96808	U96808 Micropechis

C 224	72.5	15.7	230130	10	AC112633	AC112633 Rattus no	297	71	15.4	178649	10	AC127300	AC127300 Mus muscu
C 225	72.5	15.7	234290	2	AC096033	AC096033 Rattus no	298	71	15.4	180053	2	AP002506	AP002506 Homo sapi
C 226	72.5	15.7	235053	2	AC120621	AC120621 Rattus no	299	71	15.4	181892	2	AC128847	AC128847 Rattus no
C 227	72.5	15.7	241480	2	AC128363	AC128363 Rattus no	300	71	15.4	183040	2	AC113988	AC113988 Mus muscu
C 228	72.5	15.7	242618	2	AC103444	AC103444 Rattus no	C 301	71	15.4	183541	9	AL606534	AL606534 Human DNA
C 229	72.5	15.7	244079	2	AC099081	AC099081 Rattus no	302	71	15.4	185919	9	AP001831	AP001831 Homo sapi
C 230	72.5	15.7	246523	2	AC097874	AC097874 Rattus no	C 303	71	15.4	190611	5	AL157700	AL157700 Human DNA
C 231	72.5	15.7	249044	2	AC103086	AC103086 Rattus no	C 304	71	15.4	190981	5	AL845369	AL845369 Zebrafish
C 232	72.5	15.7	253973	2	AC094544	AC094544 Rattus no	305	71	15.4	192814	10	AC127417	AC127417 Mus muscu
C 233	72.5	15.7	264450	2	AC111593	AC111593 Rattus no	306	71	15.4	196755	9	AC023826	AC023826 Homo sapi
C 234	72.5	15.7	268158	2	AC137193	AC137193 Rattus no	C 307	71	15.4	214961	2	AC130723	AC130723 Mus muscu
C 235	72.5	15.7	320285	2	AC106178	AC106178 Rattus no	C 308	71	15.4	215788	9	AC007308	AC007308 Homo sapi
C 236	72.5	15.7	333629	2	AC114833	AC114833 Rattus no	C 309	71	15.4	223085	2	AC111419	AC111419 Rattus no
C 237	72	15.6	24453	9	HS404P13	AL035069 Human DNA	C 310	71	15.4	226809	2	AC109563	AC109563 Rattus no
C 238	72	15.6	77350	8	ATT25B15	AL132972 Arabidops	311	71	15.4	227065	2	AC105477	AC105477 Rattus no
C 239	72	15.6	105665	2	AC149780	AC149780 Bos tauru	312	71	15.4	233349	2	AC146637	AC146637 Ocolemur
C 240	72	15.6	110000	8	CR382131_37	Continuation (38 o	C 313	71	15.4	235335	9	AC002470	AC002470 Rattus no
C 241	72	15.6	136814	9	AC064826	AC064826 Homo sapi	314	71	15.4	239308	2	AC112290	AC112290 Rattus no
C 242	72	15.6	154856	2	AC119792	AC119792 Rattus no	315	71	15.4	245967	2	AC112091	AC112091 Rattus no
C 243	72	15.6	159602	9	CNS01DRH	AC117209 Human chr	316	71	15.4	248140	2	EX901898	EX901898 Danio rer
C 244	72	15.6	168582	2	AC079534	AC079534 Mus muscu	317	71	15.4	253152	2	AC114621	AC114621 Mus muscu
C 245	72	15.6	179154	2	AC141487	AC141487 Rattus no	C 318	71	15.4	253189	2	AC094461	AC094461 Rattus no
C 246	72	15.6	182807	2	AC026544	AC026544 Homo sapi	319	71	15.4	254650	2	AC128790	AC128790 Rattus no
C 247	72	15.6	186670	9	AC080188	AC080188 Homo sapi	C 320	71	15.4	348642	1	EX640446	EX640446 Bordetell
C 248	72	15.6	194640	10	AC108415	AC108415 Mus muscu	C 321	70.5	15.3	1799	6	AR070567	AR070567 Sequence
C 249	72	15.6	195740	2	AC118806	AC118806 Rattus no	C 322	70.5	15.3	1799	8	PSU34744	PSU34744 Phalaenopsi
C 250	72	15.6	198838	2	AC093647	AC093647 Homo sapi	C 323	70.5	15.3	93426	9	AL359732	AL359732 Human DNA
C 251	72	15.6	202365	10	AL732627	AL732627 Mouse DNA	C 324	70.5	15.3	95241	9	HS39819	HS39819 Human DNA
C 252	72	15.6	210856	2	AC091274	AC091274 Mus muscu	325	70.5	15.3	110000	2	AC114902_1	Continuation (2 of
C 253	72	15.6	224268	2	AC097185	AC097185 Rattus no	C 326	70.5	15.3	110000	2	EX649482_1	Continuation (2 of
C 254	72	15.6	272168	2	AC079561	AC079561 Mus muscu	C 327	70.5	15.3	110000	2	EX649482_2	Continuation (3 of
C 255	72	15.6	275036	2	AC150059	AC150059 Gallus ga	C 328	70.5	15.3	112057	2	AP004065	AP004065 Oryza sat
C 256	72	15.6	321848	2	AC133831	AC133831 Rattus no	C 329	70.5	15.3	126470	8	AP004065	AP004065 Oryza sat
C 257	71.5	15.5	482	1	PSEAMPV2	M33942 P.stutzeri	C 330	70.5	15.3	149079	9	AP004654	AP004654 Oryza sat
C 258	71.5	15.5	101619	2	BS669799_3	Continuation (4 of	C 331	70.5	15.3	154980	10	AC134840	AC134840 Mus muscu
C 259	71.5	15.5	110000	2	EX569799_1	Continuation (2 of	C 332	70.5	15.3	157630	9	AC135012	AC135012 Homo sapi
C 260	71.5	15.5	110340	2	AC138259	AC138259 Mus muscu	C 333	70.5	15.3	160681	10	AL844140	AL844140 Mouse DNA
C 261	71.5	15.5	149022	8	CNS08C90	AL732377 Oryza sat	C 334	70.5	15.3	169870	5	AC025977	AC025977 Homo sapi
C 262	71.5	15.5	160669	2	AC023586	AC023586 Homo sapi	C 335	70.5	15.3	170998	5	EX284674	EX284674 Zebrafish
C 263	71.5	15.5	167587	8	AP002914	AP002914 Oryza sat	C 336	70.5	15.3	172876	2	AL144370	AL144370 Bos tauru
C 264	71.5	15.5	174588	9	AC011841	AC011841 Homo sapi	C 337	70.5	15.3	181144	9	AL365444	AL365444 Human DNA
C 265	71.5	15.5	175072	8	AP001633	AP001633 Oryza sat	C 338	70.5	15.3	187203	2	AP000832	AP000832 Homo sapi
C 266	71.5	15.5	180186	8	AP003104	AP003104 Oryza sat	C 339	70.5	15.3	191204	9	AP000843	AP000843 Homo sapi
C 267	71.5	15.5	187360	2	AC129938	AC129938 Mus muscu	C 340	70.5	15.3	202505	2	AP000912	AP000912 Homo sapi
C 268	71.5	15.5	196776	10	AC100708	AC100708 Mus muscu	C 341	70.5	15.3	204096	2	AC027704	AC027704 Homo sapi
C 269	71.5	15.5	212737	2	AC147207	AC147207 Xenopus t	C 342	70.5	15.3	213180	2	AC150531	AC150531 Bos tauru
C 270	71.5	15.5	213669	2	EX470245	EX470245 Danio rer	C 343	70.5	15.3	216044	10	AC114824	AC114824 Mus muscu
C 271	71.5	15.5	218508	10	AC113497	AC113497 Mus muscu	C 344	70.5	15.3	223130	10	AC098882	AC098882 Mus muscu
C 272	71.5	15.5	223274	2	AC112443	AC112443 Rattus no	C 345	70.5	15.3	226537	2	AC121503	AC121503 Rattus no
C 273	71.5	15.5	235302	2	AC073784	AC073784 Mus muscu	C 346	70.5	15.3	239370	2	AC096076	AC096076 Rattus no
C 274	71.5	15.5	237222	2	AC121742	AC121742 Rattus no	C 347	70.5	15.3	250812	2	AC093271	AC093271 Rattus no
C 275	71.5	15.5	249987	2	AC098279	AC098279 Rattus no	C 348	70.5	15.3	259850	1	AP005949	AP005949 Bradyrhiz
C 276	71.5	15.5	253814	2	AC148731	AC148731 Ocolemur	C 349	70.5	15.2	4780	6	CQ517551	CQ517551 Sequence
C 277	71.5	15.5	274050	1	AL627276	AL627276 Salmonell	350	70	15.2	684	8	AF057754	AF057754 Gossypium r
C 278	71.5	15.5	301311	1	AE016843	AE016843 Salmonell	351	70	15.2	686	8	AF057755	AF057755 Gossypium
C 279	71	15.4	810	8	MSA248329	AY248329 Biomphago	352	70	15.2	686	8	AF057755	AF057755 Gossypium
C 280	71	15.4	1339	3	AY030402	AY030402 Biophala	353	70	15.2	771	6	AX413504	AX413504 Sequence
C 281	71	15.4	9289	6	AE007381	AE007381 Sequence	354	70	15.2	771	6	AX413504	AX413504 Sequence
C 282	71	15.4	13242	1	AE000858	AE000858 Methanoba	355	70	15.2	1438	1	AF406546	AF406546 Unculture
C 283	71	15.4	118211	8	CNS08CE1	BX000511 Oryza sat	356	70	15.2	1440	1	AF468306	AF468306 Unculture
C 284	71	15.4	131676	9	AC139749	AC139749 Homo sapi	357	70	15.2	2075	8	AK068351	AK068351 Oryza sat
C 285	71	15.4	132952	2	AC150396	AC150396 Branchios	358	70	15.2	2202	6	CQ597699	CQ597699 Sequence
C 286	71	15.4	138070	2	AC109783	AC109783 Homo sapi	359	70	15.2	2473	3	AX113259	AX113259 Drosophil
C 287	71	15.4	150594	2	AP000728	AP000728 Homo sapi	C 360	70	15.2	4367	6	CQ597698	CQ597698 Sequence
C 288	71	15.4	155355	9	AC092782	AC092782 Homo sapi	C 361	70	15.2	4485	6	CQ598607	CQ598607 Sequence
C 289	71	15.4	155461	9	AC007493	AC007493 Homo sapi	C 362	70	15.2	4880	2	AC017170	AC017170 Drosophil
C 290	71	15.4	157090	2	AC144497	AC144497 Takifugu	363	70	15.2	6380	1	AE012122	AE012122 Xanthomon
C 291	71	15.4	158425	2	EX950223	EX950223 Danio rer	364	70	15.2	10301	1	AE012122	AE012122 Xanthomon
C 292	71	15.4	161371	2	AC096972	AC096972 Homo sapi	365	70	15.2	48980	2	AC107668	AC107668 Mus muscu
C 293	71	15.4	164832	10	AL158142	AL158142 Homo sapi	366	70	15.2	69620	2	AC103359	AC103359 Mus muscu
C 294	71	15.4	175392	2	AL928635	AL928635 Mouse DNA	C 367	70	15.2	85781	9	AL663074	AL663074 Human DNA
C 295	71	15.4	177788	9	AC007342	AC007342 Homo sapi	C 368	70	15.2	106433	9	BX511012	BX511012 Human DNA
C 296	71	15.4	177872	10	AC093371	AC093371 Genomic s	C 369	70	15.2	110994	9	AF165144	AF165144 Homo sapi

370	70	15.2	118837	9	AC021183	AC021183 Homo sapi	443	69.5	15.0	2189	9	AK074963	AK074963 Homo sapi
371	70	15.2	140484	10	AL929230	AL929230 Mouse DNA	444	69.5	15.0	2192	9	BC020875	BC020875 Homo sapi
372	70	15.2	140777	8	AP005783	AP005783 Oryza sat	445	69.5	15.0	2198	6	AX083424	AX083424 Sequence
373	70	15.2	142803	10	BX470127	BX470127 Mouse DNA	446	69.5	15.0	2271	6	BD193137	BD193137 207 human
374	70	15.2	143792	5	BX957270	BX957270 Zebrafish	447	69.5	15.0	2271	6	CQ822133	CQ822133 Sequence
375	70	15.2	147164	2	AP003834	AP003834 Oryza sat	448	69.5	15.0	2276	6	BD193088	BD193088 207 human
376	70	15.2	150434	2	AL138784	AL138784 Human DNA	449	69.5	15.0	2376	6	CQ822084	CQ822084 Sequence
377	70	15.2	150690	2	AC148543	AC148543 Otolomur	450	69.5	15.0	2371	9	AF226055	AF226055 Homo sapi
378	70	15.2	151349	2	AL353647	AL353647 Homo sapi	451	69.5	15.0	2520	9	BC011725	BC011725 Homo sapi
379	70	15.2	151441	2	AC149687	AC149687 Bos tauru	452	69.5	15.0	38384	7	AY459533	AY459533 Lactobaci
380	70	15.2	151829	9	AC008164	AC008164 Homo sapi	453	69.5	15.0	60892	10	AL672130	AL672130 Mouse DNA
381	70	15.2	155332	2	AL365439	AL365439 Homo sapi	454	69.5	15.0	103030	8	AP004302	AP004302 Oryza sat
382	70	15.2	155819	9	AL358372	AL358372 Human DNA	455	69.5	15.0	103030	8	AL672130	AL672130 Mouse DNA
383	70	15.2	156168	9	AC124917	AC124917 Homo sapi	456	69.5	15.0	109757	9	AP162379	AP162379 Human sapi
384	70	15.2	158091	9	AC018904	AC018904 Homo sapi	457	69.5	15.0	116924	9	AL104394	AL104394 Human DNA
385	70	15.2	160511	2	AC022786	AC022786 Homo sapi	458	69.5	15.0	127905	9	AL513550	AL513550 Human DNA
386	70	15.2	160511	2	AC022786	AC022786 Homo sapi	459	69.5	15.0	136713	9	AL112255	AL112255 Homo sapi
387	70	15.2	161601	3	AC007594	AC007594 Drosophil	460	69.5	15.0	144167	2	AC148140	AC148140 Bos tauru
388	70	15.2	165385	2	AC103649	AC103649 Mus muscu	461	69.5	15.0	147651	8	AC099774	AC099774 Oryza sat
389	70	15.2	165932	2	AC115857	AC115857 Mus muscu	462	69.5	15.0	149797	8	AP004998	AP004998 Oryza sat
390	70	15.2	166863	3	AC009741	AC009741 Drosophil	463	69.5	15.0	154084	9	AC022311	AC022311 Homo sapi
391	70	15.2	168205	2	AC056819	AC056819 Homo sapi	464	69.5	15.0	159251	2	AC139922	AC139922 Rattus no
392	70	15.2	174651	2	CR361546	CR361546 Danio rer	465	69.5	15.0	159466	10	AL691435	AL691435 Mus muscu
393	70	15.2	174928	10	AC121975	AC121975 Mus muscu	466	69.5	15.0	163675	9	AC115873	AC115873 Mouse DNA
394	70	15.2	180542	2	BX927066	BX927066 Danio rer	467	69.5	15.0	163675	9	AC115873	AC115873 Mouse DNA
395	70	15.2	181259	9	AC063951	AC063951 Homo sapi	468	69.5	15.0	169699	2	AC110275	AC110275 Mus muscu
396	70	15.2	181322	8	CNS08CE2	CNS08CE2 Oryza sat	469	69.5	15.0	178418	2	AC027576	AC027576 Homo sapi
397	70	15.2	181567	9	AL354811	AL354811 Human DNA	470	69.5	15.0	179554	10	AC077555	AC077555 Mus muscu
398	70	15.2	182927	2	CR376825	CR376825 Danio rer	471	69.5	15.0	183727	2	AC117802	AC117802 Homo sapi
399	70	15.2	190728	2	AC150155	AC150155 Gallus ga	472	69.5	15.0	184599	2	AC121359	AC121359 Mus muscu
400	70	15.2	191288	2	AC128123	AC128123 Rattus no	473	69.5	15.0	185624	2	AC103364	AC103364 Mus muscu
401	70	15.2	195129	10	AL627069	AL627069 Mouse DNA	474	69.5	15.0	185846	2	AC027783	AC027783 Homo sapi
402	70	15.2	200078	10	AL591064	AL591064 Mouse DNA	475	69.5	15.0	188582	2	AC013720	AC013720 Homo sapi
403	70	15.2	207324	2	AC111759	AC111759 Rattus no	476	69.5	15.0	190269	5	AX088720	AX088720 Zebrafish
404	70	15.2	213275	2	AC105638	AC105638 Rattus no	477	69.5	15.0	190544	9	AC005768	AC005768 Homo sapi
405	70	15.2	217636	10	AC127411	AC127411 Mus muscu	478	69.5	15.0	190624	2	AC013811	AC013811 Homo sapi
406	70	15.2	218326	2	AC141339	AC141339 Rattus no	479	69.5	15.0	192125	2	AC141152	AC141152 Rattus no
407	70	15.2	225655	3	AE003695	AE003695 Drosophil	480	69.5	15.0	192125	2	AC102581	AC102581 Mus muscu
408	70	15.2	227182	2	AC099283	AC099283 Rattus no	481	69.5	15.0	192152	2	AC134173	AC134173 Bos tauru
409	70	15.2	230052	2	AC115255	AC115255 Rattus no	482	69.5	15.0	195534	2	AC120071	AC120071 Rattus no
410	70	15.2	230569	2	AC108250	AC108250 Rattus no	483	69.5	15.0	196878	2	AL833804	AL833804 Mouse DNA
411	70	15.2	232610	2	AC123157	AC123157 Rattus no	484	69.5	15.0	200521	10	AL833804	AL833804 Mouse DNA
412	70	15.2	237392	2	AC098560	AC098560 Rattus no	485	69.5	15.0	203431	10	AC130533	AC130533 Mus muscu
413	70	15.2	243073	2	AC108537	AC108537 Rattus no	486	69.5	15.0	204482	10	AC147227	AC147227 Mus muscu
414	70	15.2	247473	2	AC096376	AC096376 Rattus no	487	69.5	15.0	204910	2	AC131077	AC131077 Mus muscu
415	70	15.2	248050	1	AL596172	AL596172 Listeria	488	69.5	15.0	205638	9	AC009634	AC009634 Homo sapi
416	70	15.2	252129	2	AC133975	AC133975 Rattus no	489	69.5	15.0	216556	2	AC102468	AC102468 Mus muscu
417	70	15.2	261929	2	CR382370	CR382370 Danio rer	490	69.5	15.0	220718	2	AC102264	AC102264 Mus muscu
418	70	15.2	265699	5	BX088533	BX088533 Zebrafish	491	69.5	15.0	220998	2	AC102965	AC102965 Rattus no
419	70	15.2	271652	2	AC119329	AC119329 Rattus no	492	69.5	15.0	222066	10	AC115120	AC115120 Mus muscu
420	70	15.2	275702	2	AC125862	AC125862 Rattus no	493	69.5	15.0	223066	10	AC107740	AC107740 Mus muscu
421	70	15.2	282148	2	AC097022	AC097022 Rattus no	494	69.5	15.0	224936	2	AC149249	AC149249 Otolomur
422	70	15.2	306722	2	AC094245	AC094245 Rattus no	495	69.5	15.0	225465	2	AC126882	AC126882 Rattus no
423	70	15.2	311994	2	AC110556	AC110556 Mus muscu	496	69.5	15.0	230361	2	AC126860	AC126860 Rattus no
424	70	15.2	347894	1	BX640431	BX640431 Bordetell	497	69.5	15.0	240484	2	AC125745	AC125745 Rattus no
425	70	15.2	349980	6	AX413018	AX413018 Sequence	498	69.5	15.0	242366	2	AC121386	AC121386 Rattus no
426	70	15.2	349980	6	AX417047	AX417047 Sequence	499	69.5	15.0	249871	2	AC118143	AC118143 Rattus no
427	69.5	15.0	257	8	AY323463	AY323463 Chlorella	500	69.5	15.0	250519	2	AC094894	AC094894 Rattus no
428	69.5	15.0	673	8	AP513878	AP513878 Maurandya	501	69.5	15.0	252526	2	AC108639	AC108639 Rattus no
429	69.5	15.0	720	5	BX935460	BX935460 Gallus ga	502	69.5	15.0	255981	2	AC094627	AC094627 Rattus no
430	69.5	15.0	795	6	CO780335	CO780335 Sequence	503	69.5	15.0	262432	2	AC132281	AC132281 Mus muscu
431	69.5	15.0	798	6	CO780335	CO780335 Sequence	504	69.5	15.0	275878	2	AC107519	AC107519 Rattus no
432	69.5	15.0	923	6	CO780335	CO780335 Sequence	505	69.5	15.0	295970	8	AC128907	AC128907 Rattus no
433	69.5	15.0	923	6	CO781832	CO781832 Sequence	506	69.5	15.0	300029	8	AB017076	AB017076 Oryza sat
434	69.5	15.0	923	6	BD125044	BD125044 Primer fo	507	69.5	15.0	302289	1	AB017204	AB017204 Lactobaci
435	69.5	15.0	923	6	BD125044	BD125044 Primer fo	508	69.5	15.0	305806	10	AY363102S1	AY363102 Mus muscu
436	69.5	15.0	923	6	BD125044	BD125044 Primer fo	509	69.5	15.0	309506	10	AY363102S1	AY363102 Mus muscu
437	69.5	15.0	958	9	AV157581	AV157581 Homo sapi	510	69.5	15.0	341128	2	AC114690	AC114690 Rattus no
438	69.5	15.0	1073	5	BX932657	BX932657 Gallus ga	511	69.5	15.0	349980	6	AX926715	AX926715 Sequence
439	69.5	15.0	1098	5	CR407491	CR407491 Gallus ga	512	69	14.9	1426	8	SORPL1	AX926716 Sequence
440	69.5	15.0	1554	10	BC023938	BC023938 Mus muscu	513	69	14.9	6276	5	BC068015	BC068015 Danio rer
441	69.5	15.0	2189	6	CQ782931	CQ782931 Sequence	514	69	14.9	6496	14	CTLVFP	D16681 Citrus tatt
442	69.5	15.0	2189	6	BD127386	BD127386 Primer fo	515	69	14.9	13733	5	AY656698	AY656698 Ctenophar

C 516	69	14.9	42872	9	AC000395	AC000395 Genomic s	589	69	14.9	305225	2	AC130763	AC130763 Rattus no
517	69	14.9	62276	10	AL929148	AL929148 Mouse DNA	C 590	69	14.9	332000	9	HS229041	HS229041 Homo sapi
518	69	14.9	72933	9	AC016217	AC016217 Homo sapi	591	69	14.9	335593	14	AF204951	AF204951 Ectocarpus
519	69	14.9	92705	2	AC006327	AC006327 Homo sapi	592	69	14.9	340000	9	HS21C068	HS21C068 Homo sapi
520	69	14.9	100986	8	AC105363	AC105363 Oryza sat	593	68.5	14.8	852	11	BT064351	BT064351 S212P6031
C 521	69	14.9	100986	2	AC096695	AC096695 Rattus no	C 594	68.5	14.8	864	6	CQ720474	CQ720474 Sequence
C 522	69	14.9	105065	2	AC069132	AC069132 Homo sapi	C 595	68.5	14.8	921	9	BC066346	BC066346 Homo sapi
523	69	14.9	110000	2	AC091229_04	Continuation (5 of	C 596	68.5	14.8	986	6	CQ741453	CQ741453 Sequence
524	69	14.9	110000	2	AC091242_5	Continuation (5 of	C 597	68.5	14.8	1011	6	AX033037	AX033037 Sequence
525	69	14.9	110000	2	AC091347_3	Continuation (4 of	C 598	68.5	14.8	1041	6	E50536	E50536 Polyptide
C 526	69	14.9	110000	2	AC091347_3	Continuation (4 of	C 599	68.5	14.8	1041	9	BT007417	BT007417 Homo sapi
C 527	69	14.9	110000	2	LMF1CHR15_04	Continuation (5 of	C 600	68.5	14.8	1041	12	BT007697	BT007697 Synthetic
C 528	69	14.9	110000	2	LMF1CHR31_07	Continuation (8 of	C 601	68.5	14.8	1245	1	AY098910	AY098910 unculture
C 529	69	14.9	111603	2	AC150871	AC150871 Bos tauru	602	68.5	14.8	1351	3	AY030388	AY030388 Biomphala
C 530	69	14.9	123733	2	AC140837	AC140837 Homo sapi	603	68.5	14.8	1352	3	AY030387	AY030387 Biomphala
C 531	69	14.9	130491	9	AC003977	AC003977 Homo sapi	604	68.5	14.8	1859	9	AK124100	AK124100 Homo sapi
C 532	69	14.9	132003	9	AC138779	AC138779 Homo sapi	C 605	68.5	14.8	1921	6	BD249584	BD249584 Homo sapi
C 533	69	14.9	132003	9	AC008496	AC008496 Homo sapi	C 606	68.5	14.8	2530	6	CQ722266	CQ722266 Sequence
C 534	69	14.9	135434	9	AC012172	AC012172 Homo sapi	C 607	68.5	14.8	2539	6	AX879837	AX879837 Sequence
C 535	69	14.9	136803	9	AC007314	AC007314 Homo sapi	C 608	68.5	14.8	2539	6	BD158052	BD158052 Primer fo
C 536	69	14.9	139049	8	AC018929	AC018929 Oryza sat	C 609	68.5	14.8	2539	9	AF035586	AF035586 Homo sapi
C 537	69	14.9	143961	8	AC037436	AC037436 Homo sapi	C 610	68.5	14.8	2574	6	AX883082	AX883082 Sequence
C 538	69	14.9	144440	2	AC149542	AC149542 Populus b	C 611	68.5	14.8	2574	6	BD160114	BD160114 Primer fo
C 539	69	14.9	147946	2	AC091432	AC091432 Homo sapi	C 612	68.5	14.8	2574	9	AK023646	AK023646 Homo sapi
C 540	69	14.9	149964	2	AC104686	AC104686 Homo sapi	C 613	68.5	14.8	2593	9	BC001036	BC001036 Homo sapi
C 541	69	14.9	151684	2	AC146305	AC146305 Homo sapi	C 614	68.5	14.8	2693	8	AK121646	AK121646 Oryza sat
C 542	69	14.9	152863	9	AL162417	AL162417 Human DNA	C 615	68.5	14.8	3018	9	AK124498	AK124498 Homo sapi
C 543	69	14.9	154309	2	AC140820	AC140820 Homo sapi	C 616	68.5	14.8	3018	10	RAT7RFR	M58040 Rat transfe
C 544	69	14.9	154628	2	AC147469	AC147469 Canis fam	C 617	68.5	14.8	3413	9	AK126706	AK126706 Homo sapi
C 545	69	14.9	154963	2	AC008911	AC008911 Homo sapi	C 618	68.5	14.8	3670	9	AK126706	AK126706 Sequence
C 546	69	14.9	154978	2	AC073952	AC073952 Homo sapi	C 619	68.5	14.8	3810	6	CQ580127	CQ580127 Sequence
C 547	69	14.9	156988	8	AP004730	AP004730 Oryza sat	C 620	68.5	14.8	3813	6	CQ612536	CQ612536 Sequence
C 548	69	14.9	163404	2	AC009614	AC009614 Homo sapi	C 621	68.5	14.8	5875	6	CQ607532	CQ607532 Sequence
C 549	69	14.9	164084	2	AC026580	AC026580 Homo sapi	C 622	68.5	14.8	6240	6	CQ595571	CQ595571 Sequence
C 550	69	14.9	164824	2	AC023887	AC023887 Homo sapi	C 623	68.5	14.8	12276	2	AC013930	AC013930 Drosophil
C 551	69	14.9	165675	9	AC022163	AC022163 Homo sapi	C 624	68.5	14.8	23104	9	AY607842	AY607842 Homo sapi
C 552	69	14.9	166244	9	AL365222	AL365222 Human DNA	C 625	68.5	14.8	51150	9	HS0913G4	HS0913G4 Human DNA
C 553	69	14.9	170798	9	AC113415	AC113415 Homo sapi	C 626	68.5	14.8	52777	3	AC004723	AC004723 Drosophil
C 554	69	14.9	172307	9	AL590609	AL590609 Human DNA	C 627	68.5	14.8	55431	2	AC009748	AC009748 Drosophil
C 555	69	14.9	173695	9	AC138305	AC138305 Homo sapi	C 628	68.5	14.8	57893	2	AC095868_3	Continuation (4 of
C 556	69	14.9	174666	2	AC027778	AC027778 Homo sapi	C 629	68.5	14.8	75079	2	AC015047	AC015047 Drosophil
C 557	69	14.9	179378	2	AC141011	AC141011 Rattus no	C 630	68.5	14.8	85662	9	AC114812	AC114812 Homo sapi
C 558	69	14.9	179544	9	AF015720	AF015720 Homo sapi	C 631	68.5	14.8	89677	9	AC026704	AC026704 Homo sapi
C 559	69	14.9	183152	10	AC123877	AC123877 Mus muscu	C 632	68.5	14.8	101830	2	AC146350	AC146350 Homo sapi
C 560	69	14.9	184908	10	AC121981	AC121981 Mus muscu	C 633	68.5	14.8	106438	9	AL365445	AL365445 Human DNA
C 561	69	14.9	185413	10	AC068905	AC068905 Mus muscu	C 634	68.5	14.8	110000	2	AC095868_2	Continuation (3 of
C 562	69	14.9	189402	9	AC083829	AC083829 Homo sapi	C 635	68.5	14.8	110000	2	AC117030_0	Continuation (3 of
C 563	69	14.9	194103	2	AC101986	AC101986 Mus muscu	C 636	68.5	14.8	110000	2	AC055726_2	Continuation (3 of
C 564	69	14.9	194326	10	AC125542	AC125542 Mus muscu	C 637	68.5	14.8	113448	2	AC146304	AC146304 Homo sapi
C 565	69	14.9	198017	9	AC012314	AC012314 Homo sapi	C 638	68.5	14.8	115046	8	AC148775	AC148775 Medicago
C 566	69	14.9	203788	2	AC105965	AC105965 Mus muscu	C 639	68.5	14.8	115297	2	U82207	U82207 Homo sapien
C 567	69	14.9	203864	2	AC109900	AC109900 Rattus no	C 640	68.5	14.8	115778	8	AC126013	AC126013 Medicago
C 568	69	14.9	205307	9	AC009968	AC009968 Homo sapi	C 641	68.5	14.8	118969	8	H0212802	AL442007 Oryza sat
C 569	69	14.9	206163	2	AC099519	AC099519 Homo sapi	C 642	68.5	14.8	121721	9	AC090195	AC090195 Homo sapi
C 570	69	14.9	206865	2	AC027027	AC027027 Homo sapi	C 643	68.5	14.8	122056	1	D90902	D90902 Synchocyst
C 571	69	14.9	207875	2	AC130657	AC130657 Mus muscu	C 644	68.5	14.8	122213	2	AC138526	AC138526 Medicago
C 572	69	14.9	216375	2	AC112266	AC112266 Mus muscu	C 645	68.5	14.8	129226	2	AC008185	AC008185 Drosophil
C 573	69	14.9	216540	2	AC134138	AC134138 Rattus no	C 646	68.5	14.8	135638	1	SVCSLRG	AL022166 Human DNA
C 574	69	14.9	216812	10	AL672073	AL672073 Mouse DNA	C 647	68.5	14.8	137139	9	HSBB455A7	D64005 Synchocyst
C 575	69	14.9	220710	2	AC125304	AC125304 Rattus no	C 648	68.5	14.8	139969	8	AC130811	AC130811 Medicago
C 576	69	14.9	220823	2	AC150438	AC150438 Saimiri s	C 649	68.5	14.8	141281	2	AC018955	AC018955 Mus muscu
C 577	69	14.9	221050	2	AC096854	AC096854 Canis fam	C 650	68.5	14.8	142203	2	AC079521	AC079521 Mus muscu
C 578	69	14.9	230447	2	AC098142	AC098142 Rattus no	C 651	68.5	14.8	145101	2	AC127682	AC127682 Mus muscu
C 579	69	14.9	230801	2	AC094996	AC094996 Rattus no	C 652	68.5	14.8	146776	8	AP007223	AP007223 Oryza sat
C 580	69	14.9	236349	2	AC094998	AC094998 Rattus no	C 653	68.5	14.8	148555	2	AP007223	AP007223 Oryza sat
C 581	69	14.9	246203	2	AC111705	AC111705 Rattus no	C 654	68.5	14.8	149453	10	AC084109	AC126921 Bos tauru
C 582	69	14.9	247212	2	AC115439	AC115439 Rattus no	C 655	68.5	14.8	151467	8	AP005003	AC084109 Mus muscu
C 583	69	14.9	247964	2	AC137320	AC137320 Rattus no	C 656	68.5	14.8	151684	2	AC146305	AP005003 Oryza sat
C 584	69	14.9	258193	2	AC094475	AC094475 Rattus no	C 657	68.5	14.8	151684	2	AC146305	AC146305 Homo sapi
C 585	69	14.9	260560	2	AC137180	AC137180 Rattus no	C 658	68.5	14.8	151813	2	AC026737	AC026737 Homo sapi
C 586	69	14.9	264122	2	AC094651	AC094651 Rattus no	C 659	68.5	14.8	153595	2	AP004239	AP004239 Oryza sat
C 587	69	14.9	267797	2	AC106356	AC106356 Rattus no	C 660	68.5	14.8	161742	2	AC068100	AC068100 Homo sapi
C 588	69	14.9	300029	8	AE017122	AE017122 Oryza sat	C 661	68.5	14.8	163126	9	AC110012	AC110012 Homo sapi

662	68.5	14.8	163536	2	AC129199	AC129199 Mus muscu	735	68	14.7	10872	1	AE011387	AE011387 Leptospir
c 663	68.5	14.8	163899	2	AC140822	AC140822 Homo sapi	c 736	68	14.7	10901	1	AE004297	AE004297 Vibrio ch
c 664	68.5	14.8	165745	8	OSJN00105	AL606692 Oryza sat	c 737	68	14.7	36736	8	SPCC645	AL049498 S.pombe c
c 665	68.5	14.8	165958	9	AC106774	AC106774 Homo sapi	c 738	68	14.7	36797	2	AC149405	AC149405 Phakopsor
c 666	68.5	14.8	167213	2	AC141765	AC141765 Apis mell	c 739	68	14.7	45289	3	CBRG39N24	AC084576 Caenorhab
c 667	68.5	14.8	168360	2	AC041048	AC041048 Homo sapi	c 740	68	14.7	55588	9	AC073841	AC073841 Homo sapi
c 668	68.5	14.8	169047	9	AL357935	AL357935 Human DNA	c 741	68	14.7	63701	9	AL353693	AL353693 Human DNA
c 669	68.5	14.8	169310	10	AC119259	AC119259 Mus muscu	c 742	68	14.7	71871	9	AC111163	AC111163 Homo sapi
c 670	68.5	14.8	172633	3	AC008329	AC008329 Drosophil	c 743	68	14.7	83122	8	ATT20010	AL163816 Arabidops
c 671	68.5	14.8	172656	10	AC117254	AC117254 Mus muscu	c 744	68	14.7	104969	2	AC135795	AC135795 Medicago
c 672	68.5	14.8	173149	2	AL391218	AL391218 Homo sapi	c 745	68	14.7	110000	1	AE017225	Continuation (5 of
c 673	68.5	14.8	173231	2	AC141770	AC141770 Apis mell	c 746	68	14.7	110000	1	AE017334	Continuation (5 of
c 674	68.5	14.8	174776	9	AL592546	AL592546 Human DNA	c 747	68	14.7	110000	1	AE017355	Continuation (5 of
c 675	68.5	14.8	175361	2	AL390843	AL390843 Homo sapi	c 748	68	14.7	110000	2	AC127605	Continuation (4 of
c 676	68.5	14.8	175708	9	AC090196	AC090196 Homo sapi	c 749	68	14.7	110000	2	AC127605	Continuation (4 of
c 677	68.5	14.8	176507	2	AC025790	AC025790 Homo sapi	c 750	68	14.7	110526	9	HSJ811H24	AL109945 Human DNA
c 678	68.5	14.8	181132	3	AC008206	AC008206 Drosophil	c 751	68	14.7	121632	9	AC117403	AL117403 Homo sapi
c 679	68.5	14.8	183494	2	AC091977	AC091977 Homo sapi	c 752	68	14.7	121804	2	AC140771	AC140771 Canis fam
c 680	68.5	14.8	183912	2	AC021240	AC021240 Homo sapi	c 753	68	14.7	124281	10	AL645976	AL645976 Mouse DNA
c 681	68.5	14.8	184760	8	AP005532	AP005532 Oryza sat	c 754	68	14.7	125756	9	AL590369	AL590369 Human DNA
c 682	68.5	14.8	185365	10	AC069559	AC069559 Mus muscu	c 755	68	14.7	125756	9	AC118283	AC118283 Homo sapi
c 683	68.5	14.8	186864	9	AC023050	AC023050 Homo sapi	c 756	68	14.7	130805	2	AC118432	AC118432 Homo sapi
c 684	68.5	14.8	188108	2	AC118207	AC118207 Mus muscu	c 757	68	14.7	145105	2	AC011121	AC011121 Homo sapi
c 685	68.5	14.8	188559	2	AC134961	AC134961 Bos tauru	c 758	68	14.7	172574	2	AC011121	AC011121 Homo sapi
c 686	68.5	14.8	188677	10	AC126256	AC126256 Mus muscu	c 759	68	14.7	173572	2	AC135112	AC135112 Mus muscu
c 687	68.5	14.8	189760	9	AC093155	AC093155 Homo sapi	c 760	68	14.7	183657	2	AC145263	AC145263 Zea mays
c 688	68.5	14.8	189953	2	AP004844	AP004844 Oryza sat	c 761	68	14.7	183776	2	AC131780	AC131780 Mus muscu
c 689	68.5	14.8	189958	10	AL672029	AL672029 Mouse DNA	c 762	68	14.7	184943	10	BX294183	BX294183 Mouse DNA
c 690	68.5	14.8	190587	10	AC079130	AC079130 Mus muscu	c 763	68	14.7	185422	10	AL731650	AL731650 Mouse DNA
c 691	68.5	14.8	190971	10	AC149868	AC149868 Mus muscu	c 764	68	14.7	185511	2	AC007779	AC007779 Homo sapi
c 692	68.5	14.8	193271	2	AC099643	AC099643 Mus muscu	c 765	68	14.7	187731	10	AC140307	AC140307 Mus muscu
c 693	68.5	14.8	198872	9	AF297093	AF297093 Homo sapi	c 766	68	14.7	187880	2	AC102850	AC102850 Mus muscu
c 694	68.5	14.8	201162	10	AC069561	AC069561 Mus muscu	c 767	68	14.7	191117	2	AC102291	AC102291 Mus muscu
c 695	68.5	14.8	201404	9	AC020728	AC020728 Homo sapi	c 768	68	14.7	191950	2	AC022307	AC022307 Homo sapi
c 696	68.5	14.8	202270	10	AC102341	AC102341 Mus muscu	c 769	68	14.7	193860	10	BX119959	BX119959 Mouse DNA
c 697	68.5	14.8	203422	2	AC107857	AC107857 Mus muscu	c 770	68	14.7	195749	10	AL671891	AL671891 Mouse DNA
c 698	68.5	14.8	204394	9	AL590128	AL590128 Human DNA	c 771	68	14.7	196859	9	AC096740	AC096740 Homo sapi
c 699	68.5	14.8	206011	2	AC118214	AC118214 Mus muscu	c 772	68	14.7	203301	3	AB159445	AB159445 Bombyx mo
c 700	68.5	14.8	206302	2	AC133125	AC133125 Homo sapi	c 773	68	14.7	205107	2	AB159445	AB159445 Bombyx mo
c 701	68.5	14.8	207411	2	AC084746	AC084746 Mus muscu	c 774	68	14.7	205129	2	AC148031	AC148031 Homo sapi
c 702	68.5	14.8	207575	2	AC124528	AC124528 Mus muscu	c 775	68	14.7	205129	2	AC148031	AC148031 Homo sapi
c 703	68.5	14.8	207822	2	AC131040	AC131040 Mus muscu	c 776	68	14.7	213629	2	AC115870	AC115870 Mus muscu
c 704	68.5	14.8	209508	10	AC117202	AC117202 Mus muscu	c 777	68	14.7	214370	10	AL683828	AL683828 Mouse DNA
c 705	68.5	14.8	211029	2	AC126840	AC126840 Rattus no	c 778	68	14.7	215819	2	AC099288	AC099288 Zebrafish
c 706	68.5	14.8	213846	2	AC140254	AC140254 Mus muscu	c 779	68	14.7	219550	2	AC135904	AC135904 Rattus no
c 707	68.5	14.8	215497	2	AC141564	AC141564 Mus muscu	c 780	68	14.7	219550	2	AC135904	AC135904 Rattus no
c 708	68.5	14.8	215711	3	AC008205	AC008205 Drosophil	c 781	68	14.7	221468	10	AC122813	AC122813 Mus muscu
c 709	68.5	14.8	216572	2	AC149295	AC149295 Sus scrof	c 782	68	14.7	223146	2	AC150608	AC150608 Callithri
c 710	68.5	14.8	222503	10	AC112686	AC112686 Mus muscu	c 783	68	14.7	224922	2	AC106531	AC106531 Rattus no
c 711	68.5	14.8	228433	3	AE003749	AE003749 Drosophil	c 784	68	14.7	227056	9	AC087382	AC087382 Homo sapi
c 712	68.5	14.8	231629	2	AC118319	AC118319 Rattus no	c 785	68	14.7	227632	2	AC109833	AC109833 Rattus no
c 713	68.5	14.8	231991	2	AC129392	AC129392 Rattus no	c 786	68	14.7	232023	2	AC097860	AC097860 Rattus no
c 714	68.5	14.8	239553	2	AC098659	AC098659 Rattus no	c 787	68	14.7	242902	2	AC122589	AC122589 Rattus no
c 715	68.5	14.8	240339	2	AC109949	AC109949 Rattus no	c 788	68	14.7	242902	2	AC096172	AC096172 Rattus no
c 716	68.5	14.8	248594	2	AC106590	AC106590 Rattus no	c 789	68	14.7	246951	2	AC133058	AC133058 Rattus no
c 717	68.5	14.8	252153	2	AC128765	AC128765 Rattus no	c 790	68	14.7	258756	2	AC103526	AC103526 Rattus no
c 718	68.5	14.8	255562	2	AC096387	AC096387 Rattus no	c 791	68	14.7	262958	2	AC112880	AC112880 Rattus no
c 719	68.5	14.8	262555	2	AC117825	AC117825 Mus muscu	c 792	68	14.7	262958	2	AC112880	AC112880 Rattus no
c 720	68.5	14.8	262755	2	AC1033281	AC1033281 Rattus no	c 793	68	14.7	262822	2	AC117779	AC117779 Rattus no
c 721	68.5	14.8	266574	2	AC087129	AC087129 Mus muscu	c 794	68	14.7	271979	1	AE017025	AE017025 Bacillus
c 722	68.5	14.8	273812	2	AC106441	AC106441 Rattus no	c 795	68	14.7	290714	1	AE017294	AE017294 Leptospir
c 723	68.5	14.8	273994	2	AC099625	AC099625 Mus muscu	c 796	68	14.7	300207	1	AP005371	AP005371 Thermosyn
c 724	68.5	14.8	289516	3	AE003619	AE003619 Drosophil	c 797	68	14.7	300450	1	AP005371	AP005371 Thermosyn
c 725	68.5	14.8	300350	1	BX294145	BX294145 Pirellula	c 798	68	14.7	300802	2	AC128393	AC128393 Rattus no
c 726	68	14.7	600	8	AF077899	AF077899 Levistichu	c 799	68	14.7	308710	2	AC130999	AC130999 Rattus no
c 727	68	14.7	653	11	BV073364	BV073364 S212P6016	c 800	67.5	14.6	409	5	AY293931	AY293931 Trimeresu
c 728	68	14.7	1279	8	BT000315	BT000315 Arabidops	c 801	67.5	14.6	594	1	AY269016	AY269016 Lactobaci
c 729	68	14.7	1362	8	AX747578	AX747578 Arabidops	c 802	67.5	14.6	652	1	AY113834	AY113834 Unculture
c 730	68	14.7	1990	6	AK092513	AK092513 Homo sapi	c 803	67.5	14.6	849	6	AR347288	AR347288 Sequence
c 731	68	14.7	1990	9	AK092513	AK092513 Homo sapi	c 804	67.5	14.6	1398	6	C0490342	C0490342 Sequence
c 732	68	14.7	2413	4	AF416763	AF416763 Sus scrof	c 805	67.5	14.6	1422	6	C0726646	C0726646 Sequence
c 733	68	14.7	2625	8	AV281374	AV281374 Hypocrea	c 806	67.5	14.6	1680	8	AY087662	AY087662 Arabidops
c 734	68	14.7	2742	3	U00240	U00240 Caenorhabdi	c 807	67.5	14.6	1695	9	BC010545	BC010545 Homo sapi
							c 808	67.5	14.6	1702	9	AY046059	AY046059 Homo sapi
							c 809	67.5	14.6	1710	9	BC008752	BC008752 Homo sapi

954	67	14.5	153458	9	AC110761	AC110761 Homo sapi	c1027	67	14.5	229482	2	AC074149	AC074149 Mus muscu
955	67	14.5	153656	2	CR339059	Danio rer	1028	67	14.5	234224	10	AC131577	AC131577 Mus muscu
c 956	67	14.5	156404	2	AC122772	Mus muscu	c1029	67	14.5	235276	10	AC110234	AC110234 Mus muscu
957	67	14.5	157137	2	AC141006	Rattus no	c1030	67	14.5	237985	2	AC113789	AC113789 Rattus no
958	67	14.5	157763	2	AC026952	Homo sapi	1031	67	14.5	238081	2	AC098599	AC098599 Rattus no
959	67	14.5	158231	9	AC142296	AL627206 Mouse DNA	c1032	67	14.5	238439	2	AC133693	AC133693 Rattus no
c 960	67	14.5	158781	10	AL627206	Mouse DNA	c1033	67	14.5	238831	2	AC107158	AC107158 Rattus no
c 961	67	14.5	160728	10	AC124432	AC124432 Mus muscu	1034	67	14.5	239075	10	AC147992	AC147992 Mus muscu
962	67	14.5	161093	3	AC024664	Homo sapi	c1035	67	14.5	242121	2	AC096371	AC096371 Rattus no
963	67	14.5	162434	8	AC121364	AC121364 Oryza sat	1036	67	14.5	245132	2	AC127912	AC127912 Rattus no
c 964	67	14.5	162554	2	CR626901	CR626901 Danio rer	1037	67	14.5	246101	2	AC135646	AC135646 Rattus no
c 965	67	14.5	162709	10	AL607237	AL607237 Mouse DNA	1038	67	14.5	246177	10	AC132957	AC132957 Mus muscu
966	67	14.5	163553	2	AC102717	Mus muscu	1039	67	14.5	247655	10	AC145549	AC145549 Mus muscu
967	67	14.5	163969	10	AC114605	AC114605 Mus muscu	c1040	67	14.5	249173	2	AC135886	AC135886 Rattus no
968	67	14.5	164878	2	AC148648	Dasyypus n	c1041	67	14.5	249413	2	AC095008	AC095008 Rattus no
969	67	14.5	165650	2	AC063978	Homo sapi	1042	67	14.5	250456	2	AC106547	AC106547 Rattus no
970	67	14.5	165743	3	AC095016	AC095016 Drosophil	1043	67	14.5	251958	2	AC095249	AC095249 Rattus no
c 971	67	14.5	166913	9	HSBA19D2	AL080248 Human DNA	1044	67	14.5	253322	2	AC110626	AC110626 Rattus no
972	67	14.5	167794	2	AC146591	AC146591 Callithri	1045	67	14.5	257245	2	AC097396	AC097396 Rattus no
c 973	67	14.5	168318	2	AC024042	AC024042 Homo sapi	1046	67	14.5	258789	2	AC113921	AC113921 Rattus no
974	67	14.5	169760	2	AC073619	AC073619 Homo sapi	1047	67	14.5	259631	2	AC095168	AC095168 Rattus no
975	67	14.5	170048	9	AC079062	AC079062 Homo sapi	1048	67	14.5	259831	2	AC121476	AC121476 Rattus no
976	67	14.5	171039	2	AC135249	AC135249 Rattus no	c1049	67	14.5	260495	2	AC097667	AC097667 Rattus no
c 977	67	14.5	171168	2	AC093540	AC093540 Pan trogl	1050	67	14.5	269735	2	AC124925	AC124925 Rattus no
c 978	67	14.5	172359	2	AC119217	AC119217 Mus muscu	1051	67	14.5	281092	2	AC098047	AC098047 Rattus no
c 979	67	14.5	172810	9	AC123981	AC123981 Pan trogl	1052	67	14.5	289526	2	AC118964	AC118964 Rattus no
980	67	14.5	174123	3	AC008225	AC008225 Drosophil	1053	67	14.5	301047	1	AE016967	AE016967 Mycoplasm
c 981	67	14.5	175194	2	AC121128	AC121128 Mus muscu	c1054	67	14.5	301392	1	AE003672	AE003672 Drosophil
982	67	14.5	175772	10	AC111122	AC111122 Mus muscu	c1055	67	14.5	306550	1	EX294155	EX294155 Pirellula
c 983	67	14.5	178015	2	AC094993	AC094993 Rattus no	c1056	67	14.5	315507	2	AC125935	AC125935 Rattus no
984	67	14.5	178789	2	AC124108	AC124108 Mus muscu	1057	67	14.5	346865	2	AC097921	AC097921 Rattus no
c 985	67	14.5	179934	2	AC128793	AC128793 Rattus no	c1058	66.5	14.4	396	11	BV208286	BV208286 sqm22605
986	67	14.5	184383	2	AC099632	AC099632 Mus muscu	1059	66.5	14.4	684	8	AF539938	AF539938 Munnozia
c 987	67	14.5	185260	2	AC149084	AC149084 Mus muscu	c1060	66.5	14.4	1164	8	BT014493	BT014493 Lycopersi
988	67	14.5	185419	2	EX465223	EX465223 Danio rer	c1061	66.5	14.4	1364	8	AF218210	AF218210 Cryphonect
c 989	67	14.5	185456	2	AC091379	AC091379 Mus muscu	c1062	66.5	14.4	2000	6	AX656195	AX656195 Sequence
c 990	67	14.5	186729	2	AC113271	AC113271 Mus muscu	1063	66.5	14.4	2616	5	BC077474	BC077474 Xenopus 1
c 991	67	14.5	187456	2	AC036130	AC036130 Homo sapi	1064	66.5	14.4	2835	8	AF136425	AF136425 Porphyra
992	67	14.5	187568	10	AC124348	AC124348 Homo sapi	1065	66.5	14.4	2848	9	HS0803481	HS0803481 Xenopus 1
993	67	14.5	188433	2	EX927400	EX927400 Danio rer	1066	66.5	14.4	3819	5	BC076831	BC076831 Xenopus 1
994	67	14.5	191077	2	AC139231	AC139231 Mus muscu	c1067	66.5	14.4	5108	3	AY634229	AY634229 Oikopleur
c 995	67	14.5	195651	10	AC127313	AC127313 Mus muscu	c1068	66.5	14.4	10029	1	AE011598	AE011598 Leptospir
c 996	67	14.5	195755	9	AC122747	AC122747 Mus muscu	c1069	66.5	14.4	11063	1	AE004909	AE004909 Pseudomon
997	67	14.5	195782	2	AC074389	AC074389 Homo sapi	c1070	66.5	14.4	12020	1	AE011831	AE011831 Xanthomon
998	67	14.5	198624	2	AC109626	AC109626 Mus muscu	c1071	66.5	14.4	29625	3	CER09D1	CER09D1 Caenorhabdi
1000	67	14.5	198761	10	AL607041	AL607041 Mouse DNA	1072	66.5	14.4	32446	9	HS306A4	HS306A4 Human DNA
1001	67	14.5	199109	2	AC091465	AC091465 Mus muscu	c1073	66.5	14.4	40958	2	HS317C6	HS317C6 Homo sapien
1002	67	14.5	204588	10	AC074146	AC074146 Mus muscu	c1074	66.5	14.4	60971	2	AC100008	AC100008 Mus muscu
c1003	67	14.5	204668	2	AC124550	AC124550 Mus muscu	c1075	66.5	14.4	68018	2	AC103668	AC103668 Mus muscu
1004	67	14.5	204798	2	AC118444	AC118444 Rattus no	1076	66.5	14.4	72321	2	AC101399	AC101399 Mus muscu
c1005	67	14.5	206967	10	AC109255	AC109255 Mus muscu	1077	66.5	14.4	84056	10	AC002121	AC002121 Genomic S
1006	67	14.5	207512	2	AC120464	AC120464 Rattus no	c1078	66.5	14.4	89464	2	AC138543	AC138543 Magnapor
1007	67	14.5	209403	2	AC107147	AC107147 Rattus no	1079	66.5	14.4	97120	9	AP004147	AP004147 Homo sapi
1008	67	14.5	210306	10	AL683880	AL683880 Mouse DNA	c1080	66.5	14.4	98889	9	AL590863	AL590863 Homo sapi
1009	67	14.5	211350	9	AC073912	AC073912 Homo sapi	c1081	66.5	14.4	100000	9	AP000082	AP000082 Homo sapi
c1010	67	14.5	213303	9	AC073912	AC073912 Mouse DNA	1082	66.5	14.4	109381	9	AP002350	AP002350 Homo sapi
c1011	67	14.5	214178	5	EX640577	EX640577 Zebrafish	1083	66.5	14.4	110000	2	AC115472	AC115472 Rattus no
1012	67	14.5	216937	2	AC022061	AC022061 Mus muscu	c1084	66.5	14.4	110000	2	AC139940	AC139940 Continuation (3 of
1013	67	14.5	217530	10	AC121845	AC121845 Mus muscu	c1085	66.5	14.4	110000	2	AC129250	AC129250 Continuation (2 of
c1014	67	14.5	218771	10	AC129773	AC129773 Mus muscu	c1086	66.5	14.4	110000	2	AC141459	AC141459 Homo sapi
c1015	67	14.5	219423	2	AC126093	AC126093 Rattus no	c1087	66.5	14.4	110000	2	EX890580	EX890580 Mus muscu
1016	67	14.5	219944	2	AC106194	AC106194 Rattus no	1088	66.5	14.4	110000	8	CR380959	CR380959 Continuation (4 of
c1017	67	14.5	221352	10	AC126682	AC126682 Mus muscu	c1089	66.5	14.4	110000	8	CR382123	CR382123 Continuation (16 o
1018	67	14.5	222351	2	AC127870	AC127870 Rattus no	1090	66.5	14.4	110000	8	CR382123_16	CR382123_16 Continuation (17 o
c1019	67	14.5	223385	2	AL392187	AL392187 Homo sapi	c1091	66.5	14.4	115483	2	AC108079	AC108079 Homo sapi
1020	67	14.5	223885	2	AC107604	AC107604 Rattus no	c1092	66.5	14.4	116018	2	AC127424	AC127424 Magnapor
c1021	67	14.5	225611	10	AC131724	AC131724 Mus muscu	c1093	66.5	14.4	116236	9	AC099677	AC099677 Homo sapi
1022	67	14.5	225612	2	AC097081	AC097081 Rattus no	1094	66.5	14.4	120515	9	HSJ744124	HSJ744124 Human DNA
c1023	67	14.5	226346	2	AC140747	AC140747 Rattus no	c1095	66.5	14.4	121591	8	OSTN00120	OSTN00120 Oryza sat
c1024	67	14.5	226438	2	AC132793	AC132793 Rattus no	1096	66.5	14.4	125893	2	H0124E07	H0124E07 Oryza sat
1025	67	14.5	227242	10	AC093925	AC093925 Genomic S	c1097	66.5	14.4	127176	10	CR536609	CR536609 Mouse DNA
1026	67	14.5	227263	2	AC124121	AC124121 Mus muscu	c1098	66.5	14.4	130642	2	AC147870	AC147870 Monodelph
							c1099	66.5	14.4	132151	8	AC144491	AC144491 Oryza sat

1100	66.5	14.4	132718	9	AC107908	Homo sapi
1101	66.5	14.4	136886	9	AL138889	Human DNA
1102	66.5	14.4	141036	2	AC023807	Mus muscu
1103	66.5	14.4	141264	2	AC129628	Rattus no
1104	66.5	14.4	142098	2	AC129577	Mus muscu
1105	66.5	14.4	143903	2	CR391976	Danio rer
1106	66.5	14.4	143908	8	AP005255	Oryza sat
1107	66.5	14.4	144294	8	AP004663	Oryza sat
1108	66.5	14.4	147821	9	AC104241	Homo sapi
1109	66.5	14.4	147859	2	AC011079	Homo sapi
1110	66.5	14.4	149787	9	AC0116229	Homo sapi
1111	66.5	14.4	151277	2	BS000300	Pan trogl
1112	66.5	14.4	151710	10	AC142267	Mus muscu
1113	66.5	14.4	152363	2	AC135813	Rattus no
1114	66.5	14.4	152659	9	AL591503	Human DNA
1115	66.5	14.4	153205	10	AL844905	Mouse DNA
1116	66.5	14.4	153328	9	AC118585	Pan trogl
1117	66.5	14.4	153493	9	AP006252	Homo sapi
1118	66.5	14.4	154416	8	AP005389	Oryza sat
1119	66.5	14.4	154616	2	AC067772	Homo sapi
1120	66.5	14.4	154935	2	AC150680	Monodelph
1121	66.5	14.4	155770	2	AC092381	Homo sapi
1122	66.5	14.4	157122	2	AC087109	Homo sapi
1123	66.5	14.4	157951	9	AC092670	Homo sapi
1124	66.5	14.4	159867	9	AL450303	Human DNA
1125	66.5	14.4	160066	2	AC150679	Monodelph
1126	66.5	14.4	161183	9	AL138715	Human DNA
1127	66.5	14.4	161619	2	CR388403	Danio rer
1128	66.5	14.4	162189	9	AL592295	Human DNA
1129	66.5	14.4	165281	10	BX546505	Mouse DNA
1130	66.5	14.4	167158	2	AC134991	Homo sapi
1131	66.5	14.4	167278	2	AP001536	Homo sapi
1132	66.5	14.4	167416	2	AC022752	Homo sapi
1133	66.5	14.4	167878	8	AP006244	Homo sapi
1134	66.5	14.4	168430	8	AC126221	Oryza sat
1135	66.5	14.4	169401	9	AP006524	Homo sapi
1136	66.5	14.4	170736	5	BX004962	Zebraphis
1137	66.5	14.4	170778	10	BX950196	Mouse DNA
1138	66.5	14.4	172380	10	AC126252	Mus muscu
1139	66.5	14.4	173943	2	AC022717	Homo sapi
1140	66.5	14.4	174124	2	AC115895	Mus muscu
1141	66.5	14.4	174479	2	AC115824	Mus muscu
1142	66.5	14.4	174544	2	AC117782	Mus muscu
1143	66.5	14.4	176025	2	AC124734	Mus muscu
1144	66.5	14.4	176125	2	AC102858	Mus muscu
1145	66.5	14.4	176498	9	AC003035	Homo sapi
1146	66.5	14.4	176541	10	AC127367	Mus muscu
1147	66.5	14.4	177260	9	AC131206	Homo sapi
1148	66.5	14.4	177326	2	AC114235	Rattus no
1149	66.5	14.4	178465	2	AP001901	Homo sapi
1150	66.5	14.4	180418	2	AC102419	Mus muscu
1151	66.5	14.4	180532	9	AC124149	Pan trogl
1152	66.5	14.4	180532	9	AC124149	Pan trogl
1153	66.5	14.4	181174	9	AC020634	Homo sapi
1154	66.5	14.4	181499	2	AC150454	Callithri
1155	66.5	14.4	182418	2	AC150817	Callithri
1156	66.5	14.4	184168	10	AL683877	Mouse DNA
1157	66.5	14.4	185250	9	AC124073	Homo sapi
1158	66.5	14.4	186370	9	AC093671	Homo sapi
1159	66.5	14.4	187413	2	AC141871	Mus muscu
1160	66.5	14.4	189418	2	AC110041	Mus muscu
1161	66.5	14.4	189866	2	AC137848	Mus muscu
1162	66.5	14.4	191111	9	AC006080	Homo sapi
1163	66.5	14.4	192235	2	AC122897	Mus muscu
1164	66.5	14.4	192472	5	BX545915	Zebraphis
1165	66.5	14.4	193182	9	AL365361	Human DNA
1166	66.5	14.4	194050	9	AC138774	Homo sapi
1167	66.5	14.4	195216	10	BX001066	Mouse DNA
1168	66.5	14.4	195354	2	AC122282	Mus muscu
1169	66.5	14.4	195993	2	AL606507	Mus muscu
1170	66.5	14.4	196097	9	AC122175	Pan trogl
1171	66.5	14.4	197161	10	AC122253	Mus muscu
1172	66.5	14.4	198642	9	AC124290	Homo sapi
	66.5	14.4	199345	2	AC084102	Mus muscu

66.5	14.4	201076	2	AC150594	Gasterost
66.5	14.4	201331	10	AC127361	Mus muscu
66.5	14.4	203071	10	AL606522	Mouse DNA
66.5	14.4	203635	9	AC148310	Pan trogl
66.5	14.4	205633	9	AL591496	Mouse DNA
66.5	14.4	206348	5	BX649327	Zebraphis
66.5	14.4	206924	10	AC087780	Mus muscu
66.5	14.4	208284	2	BX649387	Danio rer
66.5	14.4	208503	10	AC144715	Mus muscu
66.5	14.4	211866	2	AC120101	Rattus no
66.5	14.4	212421	2	AC109591	Homo sapi
66.5	14.4	212636	10	AL646097	Mouse DNA
66.5	14.4	212645	2	AC098135	Rattus no
66.5	14.4	215800	2	AC137947	Mus muscu
66.5	14.4	218348	10	AC121537	Mus muscu
66.5	14.4	218730	2	AC110971	Rattus no
66.5	14.4	219349	2	AC145551	Mus muscu
66.5	14.4	220688	2	AC134741	Rattus no
66.5	14.4	220719	2	AC114042	Rattus no
66.5	14.4	221357	2	AP004246	Homo sapi
66.5	14.4	221449	2	AC098759	Rattus no
66.5	14.4	223699	10	BX322590	Mouse DNA
66.5	14.4	224065	2	AC125200	Mus muscu
66.5	14.4	225644	2	AC103598	Rattus no
66.5	14.4	229259	2	AC096212	Danio rer
66.5	14.4	231124	2	CR376824	Rattus no
66.5	14.4	232298	2	AC109842	Rattus no
66.5	14.4	236142	2	AC073936	Mus muscu
66.5	14.4	236824	2	AC122632	Rattus no
66.5	14.4	241290	2	AC110415	Rattus no
66.5	14.4	242577	2	AC121694	Rattus no
66.5	14.4	242701	9	AC122596	Rattus no
66.5	14.4	242913	9	AC115994	Homo sapi
66.5	14.4	245900	2	AC097727	Rattus no
66.5	14.4	246259	2	AC128274	Rattus no
66.5	14.4	247950	2	AC110126	Rattus no
66.5	14.4	250242	2	AC095683	Rattus no
66.5	14.4	253045	2	AC099374	Rattus no
66.5	14.4	258312	2	AC122313	Mus muscu
66.5	14.4	259562	2	AC094499	Rattus no
66.5	14.4	278911	9	AE006465	Homo sapi
66.5	14.4	280335	2	AC105705	Rattus no
66.5	14.4	281122	2	AC140430	Mus muscu
66.5	14.4	300029	8	AE016887	Bremothec
66.5	14.4	303250	1	BX294143	Pirellula
66.5	14.4	306003	2	AC129941	Mus muscu
66.5	14.4	348950	1	MLPRTN7	Mycobacte
66.5	14.3	435	6	AX822034	Sequence
66.5	14.3	435	14	INA458267	Influenza
66.5	14.3	435	14	INA458271	Influenza
66.5	14.3	436	14	INA458268	Influenza
66.5	14.3	436	14	INA458269	Influenza
66.5	14.3	436	14	INA458270	Influenza
66.5	14.3	529	6	CQ526927	Sequence
66.5	14.3	572	10	WMU403170	M. musculu
66.5	14.3	783	14	AF400756	Influenza
66.5	14.3	830	9	HS4338914	Homo sapi
66.5	14.3	1179	8	BD006847	Transform
66.5	14.3	1179	8	CUURA3	C. utillis UR
66.5	14.3	1237	1	AY098911	Arabidops
66.5	14.3	1285	8	AY150425	Arabidops
66.5	14.3	1374	5	CR406539	Gallus ga
66.5	14.3	1394	6	AX250403	Sequence
66.5	14.3	1416	1	AY145601	Unculture
66.5	14.3	1477	14	AF400755	Influenza
66.5	14.3	1477	14	AF400757	Influenza
66.5	14.3	1494	14	AB126624	Influenza
66.5	14.3	1494	14	AB126632	Influenza
66.5	14.3	1497	14	AF038258	Influenza
66.5	14.3	1497	14	AF038259	Influenza
66.5	14.3	1497	14	AF225534	Influenza

1246	66	14.3	1497	14	AF225535	AF225535 Influenza	1319	66	14.3	155124	2	AL356112	AL356112 Homo sapi
1247	66	14.3	1497	14	AF225536	AF225536 Influenza	1320	66	14.3	155742	2	CNS01DWG	AL137190 Human chr
1248	66	14.3	1497	14	AF225537	AF225537 Influenza	1321	66	14.3	157898	2	CR391921	CR391921 Danio rer
1249	66	14.3	1497	14	AF483604	AF483604 Influenza	1322	66	14.3	158543	2	CR376746	CR376746 Danio rer
1250	66	14.3	1497	14	IAU71144	U71144 Influenza A	1323	66	14.3	159320	2	AC148214	AC148214 Monodelph
1251	66	14.3	1520	14	INA307071	AC307071 Influenza	1324	66	14.3	160039	9	AC106804	AC106804 Homo sapi
1252	66	14.3	1550	14	AB019359	AB019359 Influenza	1325	66	14.3	160972	3	AC007723	AC007723 Drosophil
1253	66	14.3	1550	14	AB019360	AB019360 Influenza	1326	66	14.3	162701	10	AC131800	AC131800 Mus muscu
1254	66	14.3	1565	14	AF255749	AF255749 Influenza	1327	66	14.3	162805	2	AC020565	AC020565 Homo sapi
1255	66	14.3	1565	14	INA458276	AJ458276 Influenza	1328	66	14.3	163514	3	AC091227	AC091227 Drosophil
1256	66	14.3	1701	8	AF370285	AF370285 Arabidops	1329	66	14.3	163778	2	AC010868	AC010868 Homo sapi
1257	66	14.3	1867	3	AY102653	AY102653 Drosophil	1330	66	14.3	164167	2	AC090104	AC090104 Homo sapi
1258	66	14.3	1963	5	AF365970	AF365970 Oryzias 1	1331	66	14.3	164223	10	AC127228	AC127228 Mus muscu
1259	66	14.3	2065	6	QM614432	QM614432 Sequence	1332	66	14.3	164325	10	AL845558	AL845558 Mouse DNA
1260	66	14.3	3680	9	HUMTPOC	M17755 Homo sapien	1333	66	14.3	164947	2	AC113673	AC113673 Rattus no
1261	66	14.3	4900	3	PLI495767	AJ495767 Paracentr	1334	66	14.3	165049	9	CNS01DRF	AL117190 Human chr
1262	66	14.3	4936	10	AK129428	AK129428 Mus muscu	1335	66	14.3	165563	2	AC083752	AC083752 Mus muscu
1263	66	14.3	7524	2	AC020533	AC020533 Drosophil	1336	66	14.3	165563	2	AC083752	AC083752 Mus muscu
1264	66	14.3	10029	1	AE007903	AE007903 Agrobacte	1337	66	14.3	167014	3	AGA439353	AJ439353 Anopheles
1265	66	14.3	10804	2	AC017920	AC017920 Drosophil	1338	66	14.3	167913	2	CR352227	CR352227 Danio rer
1266	66	14.3	1265	1	AE008956	AE008956 Agrobacte	1339	66	14.3	168651	2	CR352227	CR352227 Danio rer
1267	66	14.3	11178	1	AF298116	AF298116 Mus muscu	1340	66	14.3	170096	2	AC084314	AC084314 Mus muscu
1268	66	14.3	13978	8	AB013613	AB013613 Oryza sat	1341	66	14.3	171089	9	AC006368	AC006368 Homo sapi
1269	66	14.3	16184	3	AL356653	AL356653 Human DNA	1342	66	14.3	171978	10	AC125138	AC125138 Mus muscu
1270	66	14.3	22363	3	U41544	U41544 Caenorhabdi	1343	66	14.3	172137	2	AC139921	AC139921 Rattus no
1271	66	14.3	32276	3	LMFL8342	LMFL8342 Leishmani	1344	66	14.3	172982	2	AC146434	AC146434 Pan trogl
1272	66	14.3	32649	9	AL359839	AL359839 Human DNA	1345	66	14.3	173669	2	AC017110	AL590103 Human DNA
1273	66	14.3	38759	9	BX470187	BX470187 Human DNA	1346	66	14.3	175162	9	AL590103	AL590103 Human DNA
1274	66	14.3	38989	10	AL953849	AL953849 Mouse DNA	1347	66	14.3	175927	2	AC100733	AC100733 Mus muscu
1275	66	14.3	50944	5	AC091298	AC091298 Danio rer	1348	66	14.3	176874	2	AC147456	AC147456 Atelelix
1276	66	14.3	53204	2	AC005087	AC005087 Homo sapi	1349	66	14.3	177031	9	AP002840	AP002840 Homo sapi
1277	66	14.3	67027	2	AC135342	AC135342 Homo sapi	1350	66	14.3	177754	10	AL591584	AL591584 Mouse DNA
1278	66	14.3	69541	2	AC019785	AC019785 Drosophil	1351	66	14.3	179203	9	AC009194	AC009194 Homo sapi
1279	66	14.3	71236	2	AC146781	AC146781 Sminthops	1352	66	14.3	179454	3	AC007646	AC007646 Drosophil
1280	66	14.3	72508	2	AC101589	AC101589 Mus muscu	1353	66	14.3	179547	10	AL928806	AL928806 Mouse DNA
1281	66	14.3	73132	9	HS833B2	AL023800 Human DNA	1354	66	14.3	182041	2	AC136153	AC136153 Rattus no
1282	66	14.3	82875	8	AC013482	AC013482 Genomic s	1355	66	14.3	183272	2	AC150298	AC150298 Callithri
1283	66	14.3	93271	8	AP005763	AP005763 Oryza sat	1356	66	14.3	183905	10	AC022682	AC022682 Mus muscu
1284	66	14.3	95078	8	AF466931	AF466931 Zea mays	1357	66	14.3	184015	10	AC125458	AC125458 Mus muscu
1285	66	14.3	95422	8	AC073108	AC073108 Homo sapi	1358	66	14.3	185931	2	AL133554	AL133554 Homo sapi
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1290	66	14.3	110867	2	AC118208	AC118208 Mus muscu	1363	66	14.3	189486	9	AC008733	AC008733 Homo sapi
1291	66	14.3	110000	2	AC11021	AC11021 Mus muscu	1364	66	14.3	190168	10	AC145303	AC145303 Mus muscu
1292	66	14.3	110000	2	AC148613	AC148613 Homo sapi	1365	66	14.3	191011	2	AC105294	AC105294 Sus scrof
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1295	66	14.3	110980	8	ATF9K21	AL138657 Arabidops	1368	66	14.3	192826	9	AC113266	AC113266 Papio anu
1296	66	14.3	111255	8	AC125478	AC125478 Medicago	1369	66	14.3	194576	2	AC147953	AC147953 Canis fam
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1300	66	14.3	120990	2	AC149833	AC149833 Zea mays	1373	66	14.3	203160	2	AC139959	AC139959 Rattus no
1301	66	14.3	121995	2	AC091512	AC091512 Leishmani	1374	66	14.3	205499	2	AC023352	AC023352 Homo sapi
1302	66	14.3	125528	2	AC027389	AC027389 Homo sapi	1375	66	14.3	206252	10	AC113498	AC113498 Mus muscu
1303	66	14.3	127682	9	AL137861	AL137861 Human DNA	1376	66	14.3	208368	3	AE003701	AE003701 Drosophil
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1306	66	14.3	135267	2	AC021434	AC021434 Mus muscu	1379	66	14.3	210385	2	AC009627	AC009627 Homo sapi
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1317	66	14.3	153627	9	AC147054	AC147054 Pan trogl	1390	66	14.3	223948	2	AC113730	AC113730 Rattus no
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1393	66	14.3	227882	2	AC122603	2	AC122603 Rattus no	14.2	51761	2	AC068574	AC068574 Homo sapi
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1404	66	14.3	236551	2	AC125831	2	AC125831 Rattus no	14.2	107914	2	AP003949	AC091566 Homo sapi
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ALIGNMENTS

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DEFINITION	AR252626				
ACCESSION	AR252626.1	GI:27300534			
VERSION	AR252626.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 713)				
AUTHORS	Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.				
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects				
JOURNAL	Patent: US 6478825-A 376 12-NOV-2002;				
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US-09-989-293A-377 (1-90) x AR252626 (1-713)					
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QY      61  GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
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RESULT 2
AX055452
LOCUS      AX055452
DEFINITION Sequence 82 from Patent WO0073452.
ACCESSION AX055452
VERSION    AX055452.1 GI:12228719
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE      Compositions and methods for the treatment of immune related
            diseases
JOURNAL
Patent: WO 0073452-A 82 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
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      212  CAACCCACACATCATCTTTAGAGACAGTGTGACTCTACCAAGCTGTCAAAACCACA 271
QY      61  GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
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QY      81  AlaTrpGlyArgGlyValLysLysAsnThr 90
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RESULT 3
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LOCUS      AX403489
DEFINITION Sequence 376 from Patent WO0073454.
ACCESSION AX403489
VERSION    AX403489.1 GI:21436980
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL
Patent: WO 0073454-A 376 07-DEC-2000;
Genentech Inc. (US)
FEATURES
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QY      1  MetThrPheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
      92  ATGACATTTTCTGTCACATATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAAT 151
QY      21  SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
      152  TCAGGAAGCAACACATTTAGAGACAGTGTGACTCTTCTATCAAGAAATAAAGAACCCACAGT 211
QY      41  GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
      212  CAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGCTGTCAAAACCACA 271
QY      61  GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
      272  GGCAGGGCAGATAGTTAAAGACCGGAATCTTGACTCAAGAGGGTTAAATTCCTGGTCTGAA 331
QY      81  AlaTrpGlyArgGlyValLysLysAsnThr 90
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Db
RESULT 4
AX464340
LOCUS      AX464340
DEFINITION Sequence 473 from Patent WO0140466.
ACCESSION AX464340
VERSION    AX464340.1 GI:21899186
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,

```

Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding same

JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;
Genentech Inc. (US)

FEATURES
source Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
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Pred. NO.: 462.00 Matches: 90
Score: 100.00% Conservativeness: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-989-293A-377 (1-90) x AX464340 (1-713)
Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
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Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACACAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACACA 271
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Db 332 GCCTGGGCGAGGGGTGTAAGAAAAACACT 361

RESULT 5
AY358685
LOCUS Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.
DEFINITION
ACCESSION
AY358685.1 GI:37182491
VERSION
KEYWORDS
FLI_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiesand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309

JOURNAL
PUBMED 2 (bases 1 to 713)
REFERENCE
AUTHORS
Clark, H.F.
TITLE
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
source Location/Qualifiers
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/clone="DNA60627"

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ORIGIN
Alignment Scores: 7.44e-44 Length: 713
Pred. NO.: 462.00 Matches: 90
Score: 100.00% Conservativeness: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
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US-09-989-293A-377 (1-90) x AY358685 (1-713)
Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
Db 92 ATGACATTTTCTGTCATATTATTGTTGGTATGTGAGCTATTGGAGATCCAA 151
Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACACAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACACA 271
Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGlu 80
Db 272 GCGAAGGCGCATAGTTAAAGGACGGAATCTTGACTCAGAGGGTTAATTCITGGTGCTGAA 331
Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
Db 332 GCCTGGGCGAGGGGTGTAAGAAAAACACT 361

RESULT 6
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LOCUS Homo sapiens 12 BAC RP11-133114 (Roswell Park Cancer Institute
DEFINITION
AC024224
Human BAC Library) complete sequence.
ACCESSION
AC024224.33 GI:21240476
VERSION
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Murny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T., Barbacia, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homei, P., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieut, C., Liu, J., Liu, W., Lounsged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mathew, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Mettaker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kuchelapati, R., Weinstein, G., and Gibbs, R.

TITLE

REFERENCE

AUTHORS

JOURNAL

JOURNAL

REFERENCE

AUTHORS

JOURNAL

JOURNAL

REFERENCE

AUTHORS

JOURNAL

JOURNAL

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence

continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

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	/clone="RP11-133L14"
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misc_feature	754..774
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repeat_region	778..814
repeat_region	/rpt_family="(CA)n"
repeat_region	/complement(2040..2134)
repeat_region	/rpt_family="MIR"
repeat_region	/complement(2987..3137)
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repeat_region	/complement(4558..4629)
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repeat_region	4859..4941
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repeat_region	7137..7184
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repeat_region	/complement(9745..10034)
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ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

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18102..18318
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Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x AC024224 (1-165414)

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Qy	21	SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer	40
Db	117268	TCAGGAAGCAACACATTCGAGATGGCTACTTCTTATCAAGAAATAAAGAGAACACACAGT	117209
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Qy	61	GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu	80
Db	117148	GGCAGGGGATAGTTAAAGACGGATCTTGACTCAAGAGGGTTAATCTTGTGCTGTGAA	117089
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Db	117088	GCCTGGGGCAGGGGTGTAAAGAAACAACT	117059
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LOCUS			
DEFINITION	Homo sapiens clone RP11-13C13, RP11-656E20, *** SEQUENCING IN		
PROGRESS	***, 16 unordered pieces.		
AC006510			
AC006510			
AC006510.8	GI:10122018		
KEYWORDS	HTG; HTGS PHASE1.		
SOURCE	Homo sapiens (human)		

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Unpublished
2 (bases 1 to 240864)
Worley,K.C.
Direct Submission
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2000 this sequence version replaced gi:10086352.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: J-33
Center clone name: RP11-13C13, RP11-656E20
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71594 bases at least Q40
Consensus quality: 93014 bases at least Q30
Consensus quality: 110702 bases at least Q20
Estimated insert size: 229041; sum-of-contigs estimation
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Quality coverage: 0.6x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

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QY 60 ThrGly 61
Db 337 ACAGGG 342

RESULT 9
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LOCUS 741 bp DNA linear PAT 18-JUN-2001
DEFINITION Novel membrane protein and DNA thereof.
ACCESSION E21012
VERSION E21012.1 GI:13023572
KEYWORDS JP 1999001497-A/2.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 741)
AUTHORS Shuji,H., Shoji,F., Kazunori,N. and Yasushi,A.
TITLE Novel membrane protein and DNA thereof
JOURNAL Patent: JP 1999001497-A 2 06-JAN-1999;
TAKEDA CHEM IND LTD
COMMENT OS Unidentified
PN JP 1999001497-A/2
PD 06-JAN-1999
PF 13-JUN-1997 JP 1997156376
PI SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, YASUSHI ARAYA PC
C07K14/47, A61K38/00, A61K38/00, A61K38/00, A61K38/00, PC
A61K38/395, C07K16/28, C12N1/21, C12N15/09, C12P21/02, C12Q1/68, PC
G01N33/53//
PC (C12N1/21, C12R1:19), (C12N15/09, C12R1:91), A61K37/02, A61K37/02,
PC A61K37/02,
PC A61K37/02, A61K37/02, C12N15/00, C12R1:91) CC
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CC Topology: Linear;
FH Key Location/Qualifiers
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Pred. No.: 4.79e-19 Length: 741
Score: 247.50 Matches: 50
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Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 6 Gaps: 1

US-09-989-293A-377 (1-90) x E21012 (1-741)
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QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 217 AATTCAGGAGCAACATCTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCC 276
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 277 AGTCAACCCACAAATCATCTTTAGAAGACAGTGTGACTCTTACCAAGCTGTCAAACC 336
QY 60 ThrGly 61
Db 337 ACAGGG 342
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RESULT 10
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LOCUS 744 bp mRNA linear PRI 19-NOV-2001
DEFINITION Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete
cds, alternatively spliced.
ACCESSION AF400595
VERSION AF400595.1 GI:15986699
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Characterization of the human beta -glucan receptor and its
alternatively spliced isoforms
JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
MEDLINE 21570237
PubMed 11567029
REFERENCE 2 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 4.81e-19 Length: 744
Score: 247.50 Matches: 50
Percent Similarity: 87.10% Conservative: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x AF400595 (1-744)
QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19
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Db 277 AGTCAACCCACAAATCATCTTTAGAAGACAGTGTGACTCTTACCAAGCTGTCAAACC 336
QY 60 ThrGly 61
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Db 277 AGTCAACCCACACATCATCTTTTAGAAGACAGTGTGACTCTCTACCAAGCTGTCAAACCC 336
QY 60 ThrGly 61
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Db 337 ACAGGG 342

RESULT 13
LOCUS BD136999 1018 bp DNA linear PAT 18-SEP-2002
DEFINITION Isolated mammalian membrane protein gene and reagent relating
SOURCE BD136999
ACCESSION BD136999
VERSION 1 GI:23231944
KEYWORDS JP 2002506645-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1018)
AUTHORS Chalus,L., Quan,A., Bates,E.E.M., Gorman,D.M., Saeland,S.,
Lebecque,S.J.E. and Jr,J.H.P.
TITLE Isolated mammalian membrane protein gene and reagent relating
JOURNAL Patent: JP 2002506645-A 3 05-MAR-2002;
COMMENT SCHERING CORP
OS Homo sapiens (human)
PN JP 2002506645-A/3
PD 05-MAR-2002
PF 16-MAR-1999 JP 2000536856
PR 17-MAR-1998 US 09/040111
PI LIONEL CHALUS, AHN QUAN, ELIZABETH ESTHER MARY BATES, DANIEL M
PI GORMAN,
PI SEM SAELAND, SERGE J E LEBECQUE, JOSEPH H PHILLIPS JR PC
PI C12N15/09, A61K31/70, A61K38/00, A61K39/395, A61P35/00, PC
PI A61P37/02,
PC A61P43/00, C07K14/705, C07K16/28, C12N1/19, C12N1/21, C12N5/10, PC
C12Q1/68,
PC G01N33/68, C12N15/00, A61K37/02, C12N5/00
CC Isolated mammalian membrane protein gene and reagent relating
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PH Key Location/Qualifiers
FT CDS (160)..(900).

FEATURES
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Query Match: 53.57% Indels: 5
DB: 6 Gaps: 1

US-09-989-293A-377 (1-90) x BD136999 (1-1018)
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QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
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Db 376 AATTCAGGAAGCAACACATTGGAGAATGGCTACTTCTATCAAGAAATAAAGAGAACCAC 435
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QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
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QY 60 ThrGly 61
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Db 496 ACAGGG 501
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RESULT 14
LOCUS AX664609 1153 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 7 from Patent WO20077216.
ACCESSION AX664609
VERSION AX664609.1 GI:29164442
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS de Martin,R., Hofer,E., Hofer-Warbinek,R., Kalthoff,F.S.,
Lipp,H.J., Mechtcheriakova,D., Schmid,J. and Sobanov,Y.
TITLE Ikk2 variant, dino gene, lectin-like receptor gene, and proteins
encoded thereby
JOURNAL Patent: WO 02077216-A 7 03-OCT-2002;
Novartis AG (CH); Novartis Erfindungen Verwaltungsgesellschaft
M.B.H. (AT)
FEATURES
source
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Percent Similarity: 87.10% Conservative: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 6 Gaps: 1

US-09-989-293A-377 (1-90) x AX664609 (1-1153)
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QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
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Db 372 AATTCAGGAAGCAACACATTGGAGAATGGCTACTTCTATCAAGAAATAAAGAGAACCAC 431
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QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
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Db 432 AGTCAACCCACACAATCATCTTTTAGAAGACAGTGTGACTCTCTACCAAGCTGTCAAACCC 491
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QY 60 ThrGly 61
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Db 492 ACAGGG 497

RESULT 15
LOCUS HSA312373 1153 bp mRNA linear PRI 03-JUL-2001
DEFINITION Homo sapiens mRNA for DECTIN-1 receptor, splice variant 2.
ACCESSION AJ312373.1 GI:14599395
VERSION AJ312373.1
KEYWORDS alternative splicing; C-type lectin-1; DECTIN-1 gene; DECTIN-1
receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Sobanov,Y., Bernreiter,A., Derdak,S., Mechtcheriakova,D.,
Dueschler,M., Kalthoff,F. and Hofer,E.
TITLE A novel cluster of lectin-like receptor genes expressed in
monocytic, dendritic and endothelial cells maps close to the NK
receptor genes in the human NK gene complex
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1153)
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AUTHORS Sobanov, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2001) Vascular Biology and Thrombosis Research,
 University of Vienna, Brunnerstrasse 59, Vienna A-1235, Austria
 COMMENT Alternative splicing: See also AU312372.
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Location/Qualifiers
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CDS
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ORIGIN

Alignment Scores:
 Pred. No.: 7 63e-19 Length: 1153
 Score: 247.50 Matches: 50
 Percent Similarity: 87.10% Conservative: 4
 Best Local Similarity: 80.65% Mismatches: 3
 Query Match: 53.57% Indels: 5
 DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x HSA312373 (1-1153)

QY 5 LeuSerLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19
 Db 312 CTATGCTGGTAATACTGGTGATAGCTGTGGTCCCTGGGTACCATGGCTATTGGAGATCC 371
 QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
 Db 372 AATTGAGGAGCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAC 431
 QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrIysAlaValLysThr 59
 Db 432 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACC 491
 QY 60 ThrGly 61
 Db 492 ACAGGG 497

Search completed: December 2, 2004, 07:22:58
 Job time : 3307 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - nucleic search, using frame plus.p2n model
Run on: December 2, 2004, 05:01:29 ; Search time 378 Seconds
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1249,862 Million cell updates/sec

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Searched: 413486 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
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Maximum Match 0%
Post-processing: Minimum Match 10%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1						
ID	AAc91481	standard;	cDNA;	712 BP.		
DE	Human PRO1159	cDNA.				
PN	WO2000073452-A2.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
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ID	AAZ65094	standard;	cDNA;	713 BP.		
DE	Membrane-bound protein PRO1159	encoding cDNA.				
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
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ID	AAC58634	standard;	cDNA;	713 BP.		
DE	Human PRO1159	protein UNQ589	encoding cDNA	SEQ ID NO:272.		
PN	WO200053758-A2.					
PD	14-SEP-2000.					

PA	(GETH) GENENTECH INC.					
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Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
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ID	AAS21480	standard;	cDNA;	713 BP.		
DE	Human cDNA	sequence encoding for	PRO1159	polypeptide.		
PN	WO200140466-A2.					
PD	07-JUN-2001.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 5						
ID	AAF44240	standard;	cDNA;	713 BP.		
DE	Human PRO1159	(UNQ589) nucleotide	sequence	SEQ ID NO:376.		
PN	WO2000073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
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ID	ACA64409	standard;	cDNA;	713 BP.		
DE	Novel human	secreted and transmembrane	protein	PRO1159	cDNA.	
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 7						
ID	ACA03839	standard;	cDNA;	713 BP.		
DE	CNA	encoding human	PRO	polypeptide	#237.	
PN	US2003036180-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
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ID	ABX89377	standard;	cDNA;	713 BP.		
DE	DNA	encoding novel	secreted and transmembrane	protein	PRO1159.	
PN	US2003017563-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 9						
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DE	Human	secreted/transmembrane	protein	cDNA, #154.		
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
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Query Match:	100.00%				Indels:	0
RESULT 10						
ID	ACD44377	standard;	cDNA;	713 BP.		
DE	cDNA	encoding human	PRO1159	polypeptide.		
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 11						
ID	ACD42031	standard;	cDNA;	713 BP.		
DE	Human	secreted/transmembrane	protein	(PRO) cDNA	#237.	
PN	US2003036179-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Percent Similarity:	100.00%				Conservative:	0

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Query Match: 100.00% Indels: 0
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ID ABX79548 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 13
ID ACA93569 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 14
ID ABX81251 standard; DNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA04260 standard; cDNA; 713 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 473.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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PA (GETH ) GENENTECH INC.
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ID ACA68006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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ID ACA88455 standard; cDNA; 713 BP.
DE Human secreted and transmembrane polypeptide PRO1159 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 20
ID AC081962 standard; cDNA; 713 BP.
DE Human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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ID ADA5992 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 22
ID ADA76423 standard; cDNA; 713 BP.
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PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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DE Homo sapiens.
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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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ID ADB19481 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
RESULT 26
ID ADB28022 standard; cDNA; 713 BP.
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PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00% Indels: 0
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DE Human PRO polynucleotide #237.
PN US2003087350-A1.
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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 29
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DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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ID ADA47851 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 32
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PN US2003059831-A1.
PD 27-MAR-2003.
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 33
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00%
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Indels: 0
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PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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ID ADA17904 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 37
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DE Human PRO polynucleotide #237.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 38
ID ADA79465 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 39
ID ADA87604 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 40
ID ADB16806 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 41
ID ADA28012 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 42
ID ADA91898 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 43
ID ADB14961 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 44
ID ADB18922 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 45
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ID ADA94137 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 46
ID ADB20033 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 47
ID ADB13345 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 48
ID ACD98660 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 49
ID ADA94592 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 50
ID ADA74599 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 51
ID ADB24832 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 52
ID ADA82356 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 53
ID ADA75319 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.

PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 54
ID ADA85397 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 55
ID ADA84845 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 56
ID ADB30101 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 57
ID ADA80629 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 58
ID ADA75871 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 59
ID ADA38817 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 60
ID ADA47096 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 61
ID ADB25392 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307715-A1.
PD 24-APR-2003.


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Query Match: 100.00% Indels: 0
RESULT 78
ID ADB28574 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADB29126 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ACH65523 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003044806-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADA77078 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADA22499 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1159.
PN US2003040473-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADA88708 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADA97713 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADB27470 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US200302239-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ADB22403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ACD39513 standard; cDNA; 713 BP.
DE Human cDNA encoding PRO1124.
PN US2003017982-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADA06665 standard; cDNA; 713 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #118.
PN US2003049638-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADA39358 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059782-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADA67094 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003058793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADB22955 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ADB3728 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ADA92450 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ADB15513 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 95
ID ADB38765 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 96
ID ADB96384 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 97
ID ADB38213 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 98
ID ADB66685 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 99
ID ADB89765 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 100
ID ADB90497 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 101
ID ADB39598 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 102
ID ADB47221 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 103
ID ADB46641 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 104
ID ADB77433 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 105
ID ADB34590 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 106
ID ADB35694 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 107
ID ADB34038 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 108
ID ADB35142 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 109
ID ADB36246 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 110
ID ADB46641 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 111
ID ADC57856 standard; cDNA; 713 BP.
```

DE Human PRO polynucleotide #118.
PN US2003027754-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 112
ID ADC55220 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003045463-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 113
ID ADC12087 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003049681-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 114
ID ADC56509 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003064375-A1.
PD 03-APR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 115
ID ADC07564 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003068647-A1.
PD 10-APR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 116
ID ADC11554 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003069403-A1.
PD 10-APR-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 117
ID ADC50514 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 118
ID ADC72061 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 119
ID ADC60040 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 120
ID ADC53047 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 121
ID ADC57401 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 122
ID ADC60592 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 123
ID ADC51067 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 124
ID ADC65594 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 125
ID ADC54692 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 126
ID ADC53653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 127
ID ADC59176 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 128
ID ADC59176 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

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ID ADC56054 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ADC58624 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADC14676 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADD08208 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADD03298 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADC90290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADC82033 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADC69709 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADC48598 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADD10127 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADD07675 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADD04702 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADC82566 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ADC80658 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADD11165 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ADC48046 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ADD08746 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 145
ID ADC80106 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 146
ID ADD06995 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 147
ID ADD09575 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 148
ID ADC83242 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 149
ID ADD41288 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 150
ID ADD52427 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 151
ID ADD53167 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 152
ID ADD53719 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 153
ID ADD91503 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 154
ID ADD56307 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 155
ID ADD51875 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 156
ID ADD02674 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 157
ID ADD02108 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 158
ID ADD54290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 159
ID ADD54745 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 160
ID ADD92607 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 161
ID ADD91503 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199055-A1.
```



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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 162
ID ADE04117 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 163
ID ADE04117 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 164
ID ADE26899 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 165
ID ADE32414 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 166
ID ADE22346 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 167
ID ADD79570 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 168
ID ADE17923 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 169
ID ADD92055 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 170
ID ADE33518 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 171
ID ADE34070 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 172
ID ADD80122 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 173
ID ADD93159 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 174
ID ADE19579 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 175
ID ADE19027 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 176
ID ADE43223 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 177
ID ADD96012 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 178
ID ADD92055 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
```


ID ADH55403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 195
ID ADH55955 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 196
ID ADI3557 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 197
ID ADI64174 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 198
ID ADI65123 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 199
ID ADI63622 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 200
ID ADH82036 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 201
ID ADI00050 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 202
ID ADH81484 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207377-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 203
ID ABX77952 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 204
ID ABX80364 standard; cDNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 205
ID ACA69270 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 206
ID ACD24089 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 207
ID ABX90341 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 208
ID ABX64187 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 209
ID ACA67230 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 210
ID ADM82653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Conservative: 0


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RESULT 227
ID ADE94804 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 228
ID ADE91215 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 229
ID ADF35502 standard; cDNA; 713 BP.
DE CDNA encoding human PRO1159 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 230
ID ADE93566 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 231
ID ADE93466 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 232
ID ADF35047 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 233
ID ADE92362 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 234
ID ADE90663 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 235
ID ADE91810 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 236
ID ADG11752 standard; cDNA; 713 BP.
DE CDNA encoding human PRO1159 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 237
ID ADG02389 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 238
ID ADG22175 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 239
ID ADG20245 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 240
ID ADF98151 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 241
ID ADG24368 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 242
ID ADF98722 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE ADE93466 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE ADE93566 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE ADE92362 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE ADE90663 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
DE ADE91810 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

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PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 244
ID ADF99274 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 245
ID ADG16859 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 246
ID ADG05318 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 247
ID ADG19585 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 248
ID ADG13422 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 249
ID ADG08479 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 250
ID ADG15649 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 251
ID ADF97047 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207371-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 252
ID ADG06232 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 253
ID ADG23816 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 254
ID ADG04105 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 255
ID ADG25006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 256
ID ADG07303 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 257
ID ADG07855 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 258
ID ADG55350 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 259
ID ADG61014 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.


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Query Match: 100.00% Indels: 0
RESULT 276
ID ADG81215 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 277
ID ADG56454 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 278
ID ADH12720 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 279
ID ADH21115 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 280
ID ADG61566 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 281
ID ADH20155 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 282
ID ADH28653 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 283
ID ADG54798 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 284
ID ADJ77579 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 285
ID ADI181262 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 286
ID ADG10005 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 287
ID ADI15476 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 288
ID ADG09353 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 289
ID ADI14808 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 290
ID ADI18403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 291
ID ADJ63684 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 292
ID ADJ77579 standard; cDNA; 713 BP.
```



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DE Human PRO polynucleotide #237.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 293
ID ADJ65701 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 294
ID ADM27837 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 295
ID ADM42561 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 296
ID ADM28423 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 297
ID AAK81282 standard; DNA; 5709 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 298
ID AAX01260 standard; cDNA; 741 BP.
DE Human DC3' protein coding sequence.
PN JP11001497-A.
PD 06-JAN-1999.
PA (TAKG ) TAKEDA CHEM IND LTD.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 299
ID AA207533 standard; cDNA; 1018 BP.
DE Human SDCMP4 polypeptide encoding cDNA.
PN WO9947673-A2.
PD 23-SEP-1999.
PA (SCHE ) SCHERING CORP.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 300
ID ADF60937 standard; cDNA; 1018 BP.
DE Human long Schering dendritic cell membrane protein 4 (SDCMP4) cDNA.
PN US2003162955-A1.
PD 28-AUG-2003.
PA (CHAL/) CHALUS L.
PA (QUAN/) QUAN A B.
PA (BATE/) BATES E E M.
PA (GORM/) GORMAN D M.
PA (SAEL/) SAELAND S.
PA (LEBE/) LEBECQUE S J E.
PA (PHIL/) PHILLIPS J H.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 301
ID ABV73351 standard; cDNA; 1153 BP.
DE LIR-J24-2 polypeptide encoding cDNA.
PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS ) NOVARTIS AG.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 302
ID AAS31409 standard; cDNA; 1281 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 223.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 303
ID ABQ66733 standard; cDNA; 1281 BP.
DE Human polynucleotide SEQ ID NO 223.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 304
ID ADC10755 standard; cDNA; 1281 BP.
DE Human cDNA from extracellular matrix gene 66 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 305
ID ABZ24041 standard; DNA; 1606 BP.
DE Human Dectin-1 polypeptide encoding DNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Percent Similarity: 87.10%
Best Local Similarity: 80.65%
Query Match: 53.57%
Indels: 5
Conservative: 4
Mismatch: 3
RESULT 306
ID ABV73363 standard; cDNA; 138 BP.
DE LIR-J24-stalk peptide encoding cDNA.
PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS ) NOVARTIS AG.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 50.65%
Indels: 0
Conservative: 0
Mismatch: 0
RESULT 307
ID AAK81284 standard; DNA; 336 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36096.
```

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 39.83%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 308
ID AAV42548 standard; cDNA; 2298 BP.
DE Mouse dectin-1 cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 74.47%
Best Local Similarity: 61.70%
Query Match: 31.06%
Indels: 1
Conservative: 6
Mismatch: 11
Indels: 1
RESULT 309
ID ABZ24043 standard; DNA; 2298 BP.
DE Mouse dectin-1 polypeptide encoding DNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Percent Similarity: 74.47%
Best Local Similarity: 61.70%
Query Match: 31.06%
Indels: 1
Conservative: 6
Mismatch: 11
Indels: 1
RESULT 310
ID AAV42551 standard; cDNA; 528 BP.
DE Mouse dectin-1 extracellular domain cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 75.56%
Best Local Similarity: 62.22%
Query Match: 30.13%
Indels: 1
Conservative: 6
Mismatch: 10
Indels: 1
RESULT 311
ID AAC24137 standard; cDNA; 85 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 28212.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 26.41%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 312
ID AAS25954 standard; cDNA; 1737 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 133.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.16%
Best Local Similarity: 30.39%
Query Match: 16.56%
Indels: 26
Conservative: 12
Mismatch: 33
Indels: 26
RESULT 313
ID ABX73295 standard; DNA; 1737 BP.
DE Human novel polynucleotide #123.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 42.16%
Best Local Similarity: 30.39%
Query Match: 16.56%
Indels: 26
Conservative: 12
Mismatch: 33
Indels: 26
RESULT 314
ID AAI18833 standard; DNA; 595 BP.
DE Probe #8766 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 315
ID ABA63831 standard; DNA; 595 BP.

DE Human foetal liver single exon nucleic acid probe #12136.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 316
ID AAI43956 standard; DNA; 595 BP.
DE Probe #12642 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 317
ID ABA31012 standard; DNA; 595 BP.
DE Probe #9478 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 318
ID AAK38061 standard; DNA; 595 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 12618.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 319
ID AAK12342 standard; DNA; 595 BP.
DE Human brain expressed single exon probe SEQ ID NO: 12333.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 320
ID ABS37680 standard; DNA; 595 BP.
DE Human liver single exon probe, SEQ ID No 12670.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 321
ID ABS12068 standard; DNA; 595 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 12059.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.12%
Best Local Similarity: 30.39%
Query Match: 16.23%
Indels: 24
Conservative: 14
Mismatch: 33
Indels: 24
RESULT 322
ID AAS98258 standard; cDNA; 825 BP.
DE DNA encoding novel human diagnostic protein #24062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.66%
Best Local Similarity: 29.58%
Query Match: 16.13%
Indels: 5
Conservative: 10
Mismatch: 35
Indels: 5
RESULT 323
ID AAS74556 standard; cDNA; 825 BP.
DE DNA encoding novel human diagnostic protein #10360.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 43.66%
Percent Similarity: 43.66%
Best Local Similarity: 29.58%
Query Match: 16.13%
Indels: 5
RESULT 324
ID ADE84033 standard; DNA; 9289 BP.
DE 5' regulatory region of human gene RBL2.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 48.28%
Best Local Similarity: 29.31%
Query Match: 15.37%
Indels: 0
RESULT 325
ID AAX55600 standard; DNA; 1799 BP.
DE Clone 040 ovule-specific gene encoding a cytochrome P450 monooxygenase.
PN U85907082-A.
PD 25-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 43.21%
Best Local Similarity: 29.63%
Query Match: 15.26%
Indels: 15
RESULT 326
ID ABV49399 standard; cDNA; 478 BP.
DE Human prostate expression marker cDNA 49390.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNium PREDICTIVE MEDICINE INC.
Percent Similarity: 46.67%
Best Local Similarity: 29.33%
Query Match: 15.15%
Indels: 3
RESULT 327
ID AAP11530 standard; cDNA; 629 BP.
DE Aspergillus niger EST SEQ ID NO:4053.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 50.85%
Best Local Similarity: 27.12%
Query Match: 15.15%
Indels: 2
RESULT 328
ID ABQ67682 standard; DNA; 771 BP.
DE Listeria innocua DNA sequence #484.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 47.06%
Best Local Similarity: 31.37%
Query Match: 15.15%
Indels: 14
RESULT 329
ID ABO69702 standard; DNA; 771 BP.
DE Listeria innocua DNA sequence #1141.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 47.06%
Best Local Similarity: 31.37%
Query Match: 15.15%
Indels: 14
RESULT 330
ID ABL18811 standard; DNA; 2202 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7906.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 50.79%
Best Local Similarity: 31.75%
Query Match: 15.15%
Indels: 8
RESULT 331

ID ABL18810 standard; DNA; 4367 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7903.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 50.79%
Best Local Similarity: 31.75%
Query Match: 15.15%
Indels: 8
RESULT 332
ID ABL19416 standard; DNA; 4485 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9721.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 50.79%
Best Local Similarity: 31.75%
Query Match: 15.15%
Indels: 8
RESULT 333
ID ABO67196 standard; DNA; 684707 BP.
DE Listeria innocua contig DNA sequence #9.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 47.06%
Best Local Similarity: 31.37%
Query Match: 15.15%
Indels: 14
RESULT 334
Percent Similarity: 47.06%
Best Local Similarity: 31.37%
Query Match: 15.15%
Indels: 8
RESULT 335
ID ADL08119 standard; DNA; 158091 BP.
DE Human gene associated with low HDL-C LIPC #1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Percent Similarity: 39.77%
Best Local Similarity: 27.27%
Query Match: 15.15%
Indels: 32
RESULT 336
ID ADF69677 standard; DNA; 181257 BP.
DE Human SLC5A8 gene SEQ ID NO:2.
PN WO2003104427-A2.
PD 18-DEC-2003.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Percent Similarity: 42.65%
Best Local Similarity: 30.88%
Query Match: 15.15%
Indels: 10
RESULT 337
ID ADE60145 standard; DNA; 415 BP.
DE Rat gene AA893569, SEQ ID NO 6045.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Percent Similarity: 42.19%
Best Local Similarity: 34.38%
Query Match: 15.04%
Indels: 15
RESULT 338
ID ABX63474 standard; cDNA; 771 BP.
DE Human cDNA #474 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Indels: 9
RESULT 339
ID AAF94482 standard; cDNA; 795 BP.
DE Human hydrophobic domain containing protein clone HP10715 cDNA #106.
PN WO200112660-A2.
PD 22-FEB-2001.

PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 340
ID AAK93512 standard; cDNA; 923 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 1972.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 341
ID AAK92015 standard; cDNA; 923 BP.
DE Human cDNA 5'-end sequence, SEQ ID NO: 475.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 342
ID ADL28442 standard; cDNA; 923 BP.
DE 5' end of a human cDNA molecule SeqID 475.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 343
ID ADL29939 standard; cDNA; 923 BP.
DE 5' end of a representative human cDNA cluster SeqID 1972.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 344
ID ABQ99325 standard; cDNA; 971 BP.
DE Human coding sequence SEQ ID 58.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 345
ID AAS81553 standard; cDNA; 1045 BP.
DE DNA encoding novel human diagnostic protein #17357.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 57.14%
Best Local Similarity: 34.69%
Query Match: 15.04%
Conservative: 11
Mismatches: 16
Indels: 5
RESULT 346
ID AAF74861 standard; cDNA; 1999 BP.
DE Human hTGN48-iso nucleotide sequence SEQ ID NO:6.
PN CN1272541-A.
PD 08-NOV-2000.
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 347
ID AAK94357 standard; cDNA; 2189 BP.
DE Human full-length cDNA, SEQ ID NO: 3071.
PN EPI130094-A2.
PD 05-SEP-2001.

PA (HELI-) HELIX RES INST.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 348
ID ADL31038 standard; cDNA; 2189 BP.
DE Full length human cDNA clone SeqID 3071.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 349
ID AAF94492 standard; cDNA; 2198 BP.
DE Human hydrophobic domain containing protein clone HP10715 cDNA #116.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 350
ID AAV84632 standard; DNA; 2271 BP.
DE Human secreted protein gene 173 clone H8MG65.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 351
ID ABA83426 standard; cDNA; 2271 BP.
DE Human secreted protein gene 173 SEQ ID NO:243.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 352
ID ACH04927 standard; cDNA; 2271 BP.
DE Novel human secreted protein #233 cDNA.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 353
ID ACD44737 standard; cDNA; 2271 BP.
DE Human cDNA from novel secreted protein gene 173 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 354
ID AAV84583 standard; DNA; 2276 BP.
DE Human secreted protein gene 173 clone H8MG65.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Conservative: 14
Mismatches: 22
Indels: 9
RESULT 355
ID ABA83366 standard; cDNA; 2276 BP.
DE Human secreted protein gene 173 SEQ ID NO:183.
PN WO200162891-A2.
PD 30-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Indels: 9
Conservative: 14
Mismatches: 22

RESULT 356
ID ACH04867 standard; cDNA; 2276 BP.
DE Novel human secreted protein #173 cDNA.
FN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Indels: 9
Conservative: 14
Mismatches: 22

RESULT 357
ID ACD44677 standard; cDNA; 2276 BP.
DE Human cDNA from novel secreted protein gene 173.
FN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.03%
Best Local Similarity: 31.82%
Query Match: 15.04%
Indels: 9
Conservative: 14
Mismatches: 22

RESULT 358
ID ABZ51143 standard; cDNA; 657 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 256.
FN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Percent Similarity: 44.30%
Best Local Similarity: 27.85%
Query Match: 14.94%
Indels: 8
Conservative: 13
Mismatches: 36

RESULT 360
ID AAS32620 standard; cDNA; 14637 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 574.
FN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.20%
Best Local Similarity: 24.72%
Query Match: 14.94%
Indels: 32
Conservative: 12
Mismatches: 23

RESULT 361
ID ABQ72537 standard; cDNA; 1011 BP.
DE Human MDTT encoding cDNA SEQ ID NO 89.
FN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 64.86%
Best Local Similarity: 45.95%
Query Match: 14.83%
Indels: 1
Conservative: 7
Mismatches: 12

RESULT 362
ID AAL64368 standard; cDNA; 1041 BP.
DE Human coding sequence #1.
FN JP2001161366-A.
PD 19-JUN-2001.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
Percent Similarity: 51.61%
Best Local Similarity: 30.65%
Query Match: 14.83%
Indels: 5
Conservative: 13
Mismatches: 25

RESULT 363
ID AAS26396 standard; cDNA; 1742 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 575.
FN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.27%
Best Local Similarity: 30.77%
Query Match: 14.83%
Indels: 25
Conservative: 13
Mismatches: 24

Query Match: 14.83%
Indels: 29

RESULT 364
ID ABX73737 standard; cDNA; 1742 BP.
DE Human novel polynucleotide #565.
FN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 43.27%
Best Local Similarity: 30.77%
Query Match: 14.83%
Indels: 29
Conservative: 13
Mismatches: 25

RESULT 365
ID AAZ93151 standard; cDNA; 1921 BP.
DE Sequence encoding DNA replication and repair associated protein.
FN WO200008156-A2.
PD 17-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 51.61%
Best Local Similarity: 30.65%
Query Match: 14.83%
Indels: 5
Conservative: 13
Mismatches: 25

RESULT 366
ID AAH16060 standard; cDNA; 2539 BP.
DE Human cDNA sequence SEQ ID NO:14742.
FN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.61%
Best Local Similarity: 30.65%
Query Match: 14.83%
Indels: 5
Conservative: 13
Mismatches: 25

RESULT 367
ID AAH18122 standard; cDNA; 2574 BP.
DE Human cDNA sequence SEQ ID NO:17987.
FN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.61%
Best Local Similarity: 30.65%
Query Match: 14.83%
Indels: 5
Conservative: 13
Mismatches: 25

RESULT 368
ID ABZ22564 standard; cDNA; 3413 BP.
DE Rat CD71 encoding cDNA SEQ ID NO:27.
FN WO2002100336-A2.
PD 19-DEC-2002.
PA (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Percent Similarity: 47.37%
Best Local Similarity: 27.63%
Query Match: 14.83%
Indels: 17
Conservative: 15
Mismatches: 23

RESULT 369
ID ABT41778 standard; cDNA; 3413 BP.
DE Toxicity modelling related rat gene SEQ ID NO 1480.
FN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 47.37%
Best Local Similarity: 27.63%
Query Match: 14.83%
Indels: 17
Conservative: 15
Mismatches: 23

RESULT 370
ID ABL07096 standard; cDNA; 3810 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15770.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 45.56%
Best Local Similarity: 28.89%
Query Match: 14.83%
Indels: 25
Conservative: 15
Mismatches: 24

RESULT 371
ID ABL28702 standard; cDNA; 3813 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37579.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 45.56%
Indels: 15
Conservative: 15

Best Local Similarity: 28.89% Mismatches: 24
 Query Match: 14.83% Indels: 25
 RESULT 372
 ID ABL25366 standard; DNA; 5875 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27571.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 48.98%
 Best Local Similarity: 24.49%
 Query Match: 14.83%
 Indels: 17
 RESULT 373
 ID ABL17392 standard; DNA; 6240 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3649.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 45.56%
 Best Local Similarity: 28.89%
 Query Match: 14.83%
 Indels: 25
 RESULT 374
 ID ACA53364 standard; DNA; 843 BP.
 DE Prokaryotic essential Gene #35021.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 46.84%
 Best Local Similarity: 25.33%
 Query Match: 14.72%
 Indels: 22
 RESULT 375
 ID AAS92510 standard; cDNA; 1206 BP.
 DE DNA encoding novel human diagnostic protein #28314.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 46.67%
 Best Local Similarity: 26.67%
 Query Match: 14.72%
 Indels: 1
 RESULT 376
 ID ABV75574 standard; cDNA; 1681 BP.
 DE SR protein RNFS143.01 cDNA.
 PN CN1351018-A.
 PD 29-MAY-2002.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Percent Similarity: 43.12%
 Best Local Similarity: 32.11%
 Query Match: 14.72%
 Indels: 30
 RESULT 377
 ID ADB62949 standard; cDNA; 1990 BP.
 DE Human cDNA encoding clone PLACB60175640.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 44.30%
 Best Local Similarity: 25.32%
 Query Match: 14.72%
 Indels: 10
 RESULT 378
 ID ADE07768 standard; DNA; 2346 BP.
 DE Novel coding sequence (useful for identifying genetic disorders) #934.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 40.66%
 Best Local Similarity: 28.57%
 Query Match: 14.72%
 Indels: 26
 RESULT 379
 ID ACC50044 standard; cDNA; 2625 BP.
 DE Novel beta-galactosidase BGL3 encoding sequence.
 PN WO2003027306-A2.
 PD 03-APR-2003.
 PA (GEMV) GENENCOR INT INC.
 Percent Similarity: 51.95%
 Conservative: 20

Best Local Similarity: 25.97% Mismatches: 35
 Query Match: 14.72% Indels: 2
 RESULT 380
 ID ACC50041 standard; cDNA; 2785 BP.
 DE Novel beta-galactosidase BGL3 full length encoding sequence.
 PN WO2003027306-A2.
 PD 03-APR-2003.
 PA (GEMV) GENENCOR INT INC.
 Percent Similarity: 51.95%
 Best Local Similarity: 25.97%
 Query Match: 14.72%
 Indels: 2
 RESULT 381
 ID AAK90242 standard; DNA; 5282 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35054.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.71%
 Best Local Similarity: 23.97%
 Query Match: 14.72%
 Indels: 42
 RESULT 382
 ID ADC92272 standard; DNA; 849 BP.
 DE E. faecium DNA sequence SEQ ID 1899.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 41.84%
 Best Local Similarity: 24.49%
 Query Match: 14.61%
 Indels: 28
 RESULT 383
 ID AAS78554 standard; cDNA; 1326 BP.
 DE DNA encoding novel human diagnostic protein #14358.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 41.38%
 Best Local Similarity: 27.59%
 Query Match: 14.61%
 Indels: 19
 RESULT 384
 ID ABV22216 standard; cDNA; 1398 BP.
 DE Human prostate expression marker cDNA 22207.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 43.69%
 Best Local Similarity: 31.07%
 Query Match: 14.61%
 Indels: 27
 RESULT 385
 ID ADJ56426 standard; cDNA; 1539 BP.
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 232.
 PN US2003119009-A1.
 PD 26-JUN-2003.
 PA (STUA-) STUART S G.
 PA (NUCH-) NUCHTERN J G.
 PA (PLON-) PLON S E.
 PA (SHOH-) SHOHET J M.
 Percent Similarity: 58.14%
 Best Local Similarity: 39.53%
 Query Match: 14.61%
 Indels: 3
 RESULT 386
 ID AAC40912 standard; DNA; 1682 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29979.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 38.26%
 Best Local Similarity: 24.35%
 Query Match: 14.61%
 Indels: 35
 RESULT 387
 ID ABX62946 standard; cDNA; 1699 BP.
 DE Human activated T cell cDNA #62.
 PN US2002137077-A1.
 PD 26-SEP-2002.
 PA (HOPK-) HOPKINS C M.

PA (PETE/) PETERSON D P.
PA (COCK/) COCKS B G.
PA (HAWK/) HAWKINS P R.
Percent Similarity: 43.69%
Best Local Similarity: 31.07%
Query Match: 14.61%
Conservative: 13
Mismatches: 31
Indels: 27
RESULT 388
ID AAI58122 standard; cDNA; 1700 BP.
DE Human polynucleotide SEQ ID NO 325.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.69%
Best Local Similarity: 31.07%
Query Match: 14.61%
Conservative: 13
Mismatches: 31
Indels: 27
RESULT 389
ID AAS74794 standard; cDNA; 2430 BP.
DE DNA encoding novel human diagnostic protein #10598.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.69%
Best Local Similarity: 31.07%
Query Match: 14.61%
Conservative: 13
Mismatches: 31
Indels: 27
RESULT 390
ID AAA16664 standard; cDNA; 2922 BP.
DE Human secreted protein clone bf157_16 nucleotide sequence SEQ ID NO:93.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 43.69%
Best Local Similarity: 31.07%
Query Match: 14.61%
Conservative: 13
Mismatches: 31
Indels: 27
RESULT 391
ID AAS91392 standard; cDNA; 2991 BP.
DE DNA encoding novel human diagnostic protein #27796.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.53%
Best Local Similarity: 26.44%
Query Match: 14.61%
Conservative: 14
Mismatches: 42
Indels: 8
RESULT 392
ID AAS73660 standard; cDNA; 2991 BP.
DE DNA encoding novel human diagnostic protein #9464.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.53%
Best Local Similarity: 26.44%
Query Match: 14.61%
Conservative: 14
Mismatches: 42
Indels: 8
RESULT 393
ID AAC41257 standard; cDNA; 1418 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 31226.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.94%
Best Local Similarity: 27.93%
Query Match: 14.50%
Conservative: 10
Mismatches: 42
Indels: 28
RESULT 394
ID AAT08603 standard; DNA; 2330 BP.
DE URA3 gene.
PN WO9532289-A1.
PD 30-NOV-1995.
PA (KIRI) KIRIN BEER KK.
Percent Similarity: 43.02%
Best Local Similarity: 32.56%
Query Match: 14.50%
Conservative: 9
Mismatches: 41
Indels: 9
RESULT 395
ID AAV31505 standard; DNA; 2330 BP.
DE Base sequence of DNA fragment containing yeast URA3 gene.
PN WO9807873-A1.
PD 26-FEB-1998.

PA (KIRI) KIRIN BEER KK.
Percent Similarity: 43.02%
Best Local Similarity: 32.56%
Query Match: 14.50%
Conservative: 9
Mismatches: 41
Indels: 9
RESULT 396
ID ABQ53248 standard; DNA; 724 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39839.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 47.92%
Best Local Similarity: 43.75%
Query Match: 14.39%
Conservative: 2
Mismatches: 19
Indels: 6
RESULT 397
ID ABQ53249 standard; DNA; 724 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39840.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 47.92%
Best Local Similarity: 43.75%
Query Match: 14.39%
Conservative: 2
Mismatches: 19
Indels: 6
RESULT 398
ID ABD17716 standard; DNA; 1065 BP.
DE Pseudomonas aeruginosa polynucleotide #16320.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 41.89%
Best Local Similarity: 25.68%
Query Match: 14.39%
Conservative: 12
Mismatches: 32
Indels: 11
RESULT 399
ID ABD17357 standard; DNA; 1332 BP.
DE Pseudomonas aeruginosa polynucleotide #15961.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 41.89%
Best Local Similarity: 25.68%
Query Match: 14.39%
Conservative: 12
Mismatches: 32
Indels: 11
RESULT 400
ID ADB06105 standard; DNA; 1611 BP.
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:45.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AWHP) WRETH HOLDINGS CORP.
Percent Similarity: 43.06%
Best Local Similarity: 30.56%
Query Match: 14.39%
Conservative: 9
Mismatches: 26
Indels: 15
RESULT 401
ID ADB06107 standard; DNA; 1611 BP.
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:47.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AWHP) WRETH HOLDINGS CORP.
Percent Similarity: 43.06%
Best Local Similarity: 30.56%
Query Match: 14.39%
Conservative: 9
Mismatches: 26
Indels: 15
RESULT 402
ID ADA72740 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 6065.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 48.44%
Best Local Similarity: 40.62%
Query Match: 14.39%
Conservative: 5
Mismatches: 18
Indels: 15
RESULT 403
ID ADE61846 standard; DNA; 3636 BP.
DE Human gene M22919, SEQ ID NO 7775.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Percent Similarity: 45.16%
Best Local Similarity: 29.03%
Query Match: 14.39%
Indels: 19
Conservative: 15
Mismatches: 32

RESULT 404
ID ABX77212 standard; DNA; 75798 BP.
DE Mouse uridine diphosphoglucuronosyl transferase gene locus.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Percent Similarity: 47.54%
Best Local Similarity: 29.51%
Query Match: 14.39%
Indels: 7
Conservative: 11
Mismatches: 25

RESULT 405
ID ADB12064 standard; DNA; 1754382 BP.
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.06%
Best Local Similarity: 30.56%
Query Match: 14.39%
Indels: 15
Conservative: 9
Mismatches: 26

RESULT 406
ID ADO15235 standard; DNA; 435 BP.
DE Influenza A virus A/Moscow/10/99 (H3N2) partial nucleoprotein DNA.
PN WO2004041866-A1.
PD 21-MAY-2004.
PA (ADJU-) ADJUVANTIX LTD.
Percent Similarity: 42.86%
Best Local Similarity: 31.87%
Query Match: 14.29%
Indels: 24
Conservative: 10
Mismatches: 28

RESULT 407
ID ABV58775 standard; cDNA; 529 BP.
DE Human prostate expression marker cDNA 58766.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 42.62%
Best Local Similarity: 29.87%
Query Match: 14.29%
Indels: 17
Conservative: 9
Mismatches: 17

RESULT 408
ID AAS77275 standard; cDNA; 874 BP.
DE DNA encoding novel human diagnostic protein #13079.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.83%
Best Local Similarity: 31.94%
Query Match: 14.29%
Indels: 6
Conservative: 10
Mismatches: 33

RESULT 409
ID AAV19462 standard; DNA; 1179 BP.
DE C. utilis URA3 gene.
PN WO9814600-A1.
PD 09-APR-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Percent Similarity: 45.35%
Best Local Similarity: 32.56%
Query Match: 14.29%
Indels: 9
Conservative: 11
Mismatches: 39

RESULT 410
ID ABQ32519 standard; DNA; 1246 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 19110.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPTG-) EPIGENOMICS AG.
Percent Similarity: 52.63%
Best Local Similarity: 24.56%
Query Match: 14.29%
Indels: 0
Conservative: 16
Mismatches: 27

RESULT 411
ID ABQ32518 standard; DNA; 1246 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 19109.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 52.63%
Best Local Similarity: 24.56%
Query Match: 14.29%
Indels: 0
Conservative: 16
Mismatches: 27

Percent Similarity: 52.63%
Best Local Similarity: 24.56%
Query Match: 14.29%
Indels: 0
Conservative: 16
Mismatches: 27

RESULT 412
ID ABA01231 standard; DNA; 1394 BP.
DE T26F17.15 coding sequence.
PN FR2806095-A1.
PD 14-SEP-2001.
PA (GENT-) GENTECH SARL.
Percent Similarity: 36.89%
Best Local Similarity: 23.77%
Query Match: 14.29%
Indels: 44
Conservative: 16
Mismatches: 33

RESULT 413
ID ABT20509 standard; DNA; 1880 BP.
DE Aspergillus fumigatus essential gene #2867.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.91%
Best Local Similarity: 27.27%
Query Match: 14.29%
Indels: 10
Conservative: 9
Mismatches: 29

RESULT 414
ID ABL29966 standard; DNA; 2685 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41371.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Percent Similarity: 42.67%
Best Local Similarity: 28.00%
Query Match: 14.29%
Indels: 15
Conservative: 11
Mismatches: 28

RESULT 415
ID AAQ40728 standard; DNA; 3045 BP.
DE Human TPO gene lacking bases 2221-2247.
PN WO9303146-A1.
PD 18-FEB-1993.
PA (RAPO/) RAPOPORT B.
Percent Similarity: 46.15%
Best Local Similarity: 28.21%
Query Match: 14.29%
Indels: 14
Conservative: 14
Mismatches: 28

RESULT 416
ID AAQ37493 standard; DNA; 3072 BP.
DE Human TPO gene.
PN WO9303146-A1.
PD 18-FEB-1993.
PA (RAPO/) RAPOPORT B.
Percent Similarity: 46.15%
Best Local Similarity: 28.21%
Query Match: 14.29%
Indels: 14
Conservative: 14
Mismatches: 28

RESULT 417
ID AAS26694 standard; DNA; 3659 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1668.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.90%
Best Local Similarity: 25.00%
Query Match: 14.29%
Indels: 28
Conservative: 10
Mismatches: 25

RESULT 418
ID AAL05132 standard; DNA; 3659 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7820.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.90%
Best Local Similarity: 25.00%
Query Match: 14.29%
Indels: 28
Conservative: 10
Mismatches: 25

RESULT 419
ID ABL98023 standard; DNA; 3659 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2675.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.90%
Indels: 10
Conservative: 10

Best Local Similarity: 25.00% Mismatches: 25
Query Match: 14.29% Indels: 28
RESULT 420
ID ABE74043 standard; DNA; 3659 BP.
DE Human novel polynucleotide #871.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 36.90%
Best Local Similarity: 25.00%
Query Match: 14.29%
Indels: 28
RESULT 421
ID ABE19913 standard; DNA; 3880 BP.
DE Aspergillus fumigatus essential gene #2271.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.91%
Best Local Similarity: 27.27%
Query Match: 14.29%
Indels: 10
RESULT 422
ID ABA18087 standard; DNA; 11599 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10418.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.33%
Best Local Similarity: 28.89%
Query Match: 14.29%
Indels: 0
RESULT 423
ID AAL06991 standard; DNA; 32082 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9679.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.61%
Best Local Similarity: 26.73%
Query Match: 14.29%
Indels: 18
RESULT 424
ID AAH3516 standard; cDNA; 733 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:572.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.39%
Best Local Similarity: 29.82%
Query Match: 14.18%
Indels: 3
RESULT 425
ID ADH85055 standard; DNA; 744 BP.
DE Enterococcus faecalis polynucleotide #2940.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Percent Similarity: 44.23%
Best Local Similarity: 30.77%
Query Match: 14.18%
Indels: 15
RESULT 426
ID ADF82151 standard; DNA; 862 BP.
DE Leukaemia-related DNA sequence #2707.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 54.39%
Best Local Similarity: 29.82%
Query Match: 14.18%
Indels: 3
RESULT 427

ID AAS31096 standard; cDNA; 1106 BP.
DE Human diagnostic and therapeutic polynucleotide (DITHP) #111.
PN WO200162927-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 51.79%
Best Local Similarity: 35.71%
Query Match: 14.18%
Indels: 1
RESULT 428
ID ABD17940 standard; DNA; 1341 BP.
DE Pseudomonas aeruginosa polynucleotide #16544.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 42.37%
Best Local Similarity: 28.81%
Query Match: 14.18%
Indels: 9
RESULT 429
ID AAK78943 standard; DNA; 2052 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33755.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.39%
Best Local Similarity: 29.82%
Query Match: 14.18%
Indels: 3
RESULT 430
ID AD041689 standard; cDNA; 2482 BP.
DE Novel human polypeptide NOV20b cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASW/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWV/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Percent Similarity: 40.74%
Best Local Similarity: 28.40%
Query Match: 14.18%
Indels: 15
RESULT 431
ID ABT16044 standard; DNA; 2483 BP.
DE NOVX related polynucleotide SEQ ID No 55.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.74%
Best Local Similarity: 28.40%
Query Match: 14.18%
Indels: 15
RESULT 432
ID ABE74043 standard; DNA; 3659 BP.
DE Human novel polynucleotide #871.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 36.90%
Best Local Similarity: 25.00%
Query Match: 14.29%
Indels: 28
RESULT 433
ID ABE19913 standard; DNA; 3880 BP.
DE Aspergillus fumigatus essential gene #2271.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.91%
Best Local Similarity: 27.27%
Query Match: 14.29%
Indels: 10
RESULT 434
ID ABA18087 standard; DNA; 11599 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10418.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 53.33%
Best Local Similarity: 28.89%
Query Match: 14.29%
Indels: 0
RESULT 435
ID AAL06991 standard; DNA; 32082 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9679.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.61%
Best Local Similarity: 26.73%
Query Match: 14.29%
Indels: 18
RESULT 436
ID AAH3516 standard; cDNA; 733 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:572.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.39%
Best Local Similarity: 29.82%
Query Match: 14.18%
Indels: 3
RESULT 437
ID ADH85055 standard; DNA; 744 BP.
DE Enterococcus faecalis polynucleotide #2940.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Percent Similarity: 44.23%
Best Local Similarity: 30.77%
Query Match: 14.18%
Indels: 15
RESULT 438
ID ADF82151 standard; DNA; 862 BP.
DE Leukaemia-related DNA sequence #2707.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 54.39%
Best Local Similarity: 29.82%
Query Match: 14.18%
Indels: 3
RESULT 439

ID ABL1972 standard; cDNA; 445 BP.
DE Human ovarian cancer related CDNA clone SEQ ID NO:4950.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 57.58%
Best Local Similarity: 42.42%
Query Match: 14.07%
Conservative: 5
Mismatches: 14
Indels: 0
RESULT 438

ID AAA02682 standard; cDNA; 509 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2673.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 57.58%
Best Local Similarity: 42.42%
Query Match: 14.07%
Conservative: 5
Mismatches: 14
Indels: 0
RESULT 439

ID ABN66805 standard; DNA; 726 BP.
DE Streptococcus polynucleotide SEQ ID NO 1523.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 42.19%
Best Local Similarity: 28.12%
Query Match: 14.07%
Conservative: 9
Mismatches: 17
Indels: 20
RESULT 440

ID AAA62065 standard; DNA; 1296 BP.
DE Hydrophobic domain protein CDNA HF10670 isolated from WERI-RB cells.
PN WO20029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Percent Similarity: 57.58%
Best Local Similarity: 42.42%
Query Match: 14.07%
Conservative: 5
Mismatches: 14
Indels: 0
RESULT 441

ID ADC87324 standard; DNA; 1300 BP.
DE Human GPCR gene SEQ ID NO:1777.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Percent Similarity: 57.58%
Best Local Similarity: 42.42%
Query Match: 14.07%
Conservative: 5
Mismatches: 14
Indels: 0
RESULT 442

ID ACA46734 standard; DNA; 1359 BP.
DE Prokaryotic essential gene #28391.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 45.90%
Best Local Similarity: 29.51%
Query Match: 14.07%
Conservative: 10
Mismatches: 19
Indels: 14
RESULT 443

ID AAHS2705 standard; DNA; 1362 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:803.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 45.90%
Best Local Similarity: 29.51%
Query Match: 14.07%
Conservative: 10
Mismatches: 19
Indels: 14
RESULT 444

ID ABN91304 standard; DNA; 1386 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:767.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 45.90%
Conservative: 10

ID ABL16043 standard; DNA; 2588 BP.
DE NOVX related polynucleotide SEQ ID No 53.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.74%
Best Local Similarity: 28.40%
Query Match: 14.18%
Conservative: 10
Mismatches: 33
Indels: 15
RESULT 433

ID ADO41687 standard; cDNA; 2588 BP.
DE Novel human polypeptide NOV20a cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE-) ANDERSON D W.
PA (ZERR-) ZERHUSEN B D.
PA (LILL-) LI L.
PA (ZHON-) ZHONG M.
PA (CASM-) CASMAN S J.
PA (GERL-) GERLACH V.
PA (SHIM-) SHIMKETS R A.
PA (GORM-) GORMAN L.
PA (PENA-) PENA C E A.
PA (KEKU-) KEKUDA R.
PA (PATI-) PATTURAJAN M.
PA (SPYT-) SPYTEK K A.
PA (LEIT-) LEITE M W.
PA (RAST-) RASTELLI L.
PA (MACD-) MACDOUGALL J R.
PA (TAUP-) TAUPIER R J.
PA (GUOX-) GUO X S.
PA (MILL-) MILLER C E.
PA (SHEN-) SHENOY S G.
PA (HUAL-) HUALT T.
PA (VOSS-) VOSS B Z.
PA (BOLD-) BOLDOS F L.
PA (MALY-) MALYANKAR U M.
PA (PADI-) PADIGANKAR M.
PA (JIWW-) JI W.
PA (SMIT-) SMITHSON G.
PA (EDIN-) EDINGER S R.
PA (MILL-) MILLET I.
PA (ELLE-) ELLERMAN K.
Percent Similarity: 40.74%
Best Local Similarity: 28.40%
Query Match: 14.18%
Conservative: 10
Mismatches: 33
Indels: 15
RESULT 434

ID ABK63760 standard; cDNA; 3726 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1667.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.71%
Best Local Similarity: 26.88%
Query Match: 14.18%
Conservative: 11
Mismatches: 27
Indels: 30
RESULT 435

ID ADB58350 standard; DNA; 3726 BP.
DE Toxicity-related gene, SEQ ID 3376.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.71%
Best Local Similarity: 26.88%
Query Match: 14.18%
Conservative: 11
Mismatches: 27
Indels: 30
RESULT 436

ID ABT42014 standard; DNA; 3726 BP.
DE Toxicity modelling related rat gene SEQ ID No 1716.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.71%
Best Local Similarity: 26.88%
Query Match: 14.18%
Conservative: 11
Mismatches: 27
Indels: 30
RESULT 437

Best Local Similarity: 29.51% Mismatches: 19
 Query Match: 14.07% Indels: 14
 RESULT 445
 ID AAH44494 standard; cDNA; 1419 BP.
 DE Human UGT-isoenzyme 28 encoding cDNA.
 PN CN1297045-A.
 PD 30-MAY-2001.
 PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 446
 ID ABT08325 standard; DNA; 1463 BP.
 DE Human NOV8a gene sequence.
 PN WO200246408-A2.
 PD 13-JUN-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 447
 ID ACC46261 standard; cDNA; 1703 BP.
 DE Human dithp intracellular signalling protein-encoding cDNA.
 PN WO200297031-A2.
 PD 05-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.87% Mismatches: 26
 Query Match: 14.07% Indels: 8
 RESULT 448
 ID ABT08326 standard; DNA; 1742 BP.
 DE Human NOV8b gene sequence.
 PN WO200246408-A2.
 PD 13-JUN-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 449
 ID AAX2247 standard; DNA; 1849 BP.
 DE Human secreted protein gene 37 clone HPBET96.
 PN WO9903990-A1.
 PD 28-JAN-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.87% Mismatches: 26
 Query Match: 14.07% Indels: 8
 RESULT 450
 ID ACD40491 standard; cDNA; 1849 BP.
 DE cDNA sequence #37 encoding human secreted protein.
 PN US2003050455-A1.
 PD 13-MAR-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (FLOR/) FLORENCE K A.
 PA (HUUJ/) HU J.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (DUAN/) DUAN R D.
 PA (JANA/) JANAT F.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.87% Mismatches: 26
 Query Match: 14.07% Indels: 8
 RESULT 451
 ID ACF70595 standard; DNA; 1860 BP.
 DE Phototransducin nucleotide sequence #9062.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.
 Percent Similarity: 53.85% Conservative: 5
 Best Local Similarity: 41.03% Mismatches: 18
 Query Match: 14.07% Indels: 0
 RESULT 452
 ID ABQ91953 standard; cDNA; 1898 BP.
 DE Human NF-kB activating gene SEQ ID NO 84.
 PN WO200253737-A1.
 PD 11-JUL-2002.
 PA (ASAH) ASAHI KASEI KOGYO KK.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 453
 ID ACC42296 standard; cDNA; 1898 BP.
 DE Human MAP kinase cascade activator #15 cDNA.
 PN WO2003008589-A1.
 PD 30-JAN-2003.
 PA (ASAH) ASAHI KASEI KOGYO KK.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 454
 ID AAF93826 standard; cDNA; 1988 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0149.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 455
 ID AAV34252 standard; DNA; 2003 BP.
 DE Human secreted protein gene 41 clone HNTME13.
 PN WO9839446-A2.
 PD 11-SEP-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 456
 ID ACD08123 standard; cDNA; 2003 BP.
 DE cDNA encoding novel human secreted protein #99.
 PN US2003027132-A1.
 PD 08-FEB-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (FISC/) FISCHER C L.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D R.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN R.
 PA (HUUJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (SHIV/) SHI Y.
 Percent Similarity: 57.58% Conservative: 5
 Best Local Similarity: 42.42% Mismatches: 14
 Query Match: 14.07% Indels: 0
 RESULT 457
 ID ABQ91954 standard; cDNA; 2018 BP.
 DE Human NF-kB activating gene SEQ ID NO 86.
 PN WO200253737-A1.
 PD 11-JUL-2002.

PA (ASAH) ASahi KASEI KOGYO KK.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 458
ID AAA62075 standard; DNA; 2022 BP.
DE Hydrophobic domain protein cDNA HF10670 isolated from WERI-RB cells.
PN WO200029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 459
ID ABQ77696 standard; cDNA; 2027 BP.
DE Human transmembrane sugar transporter BioHSTR-encoding cDNA.
PN CN1293249-A.
PD 02-MAY-2001.
PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 460
ID AAH20413 standard; cDNA; 2027 BP.
DE Human BioATPase cDNA.
PN WO200130836-A1.
PD 03-MAY-2001.
PA (SHAN-) SHANGHAI BIORIGIN GENE DEV CO LTD.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 461
ID AAC59822 standard; DNA; 2051 BP.
DE Human secreted protein encoding DNA clone vo22 1.
PN WO20005375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 462
ID AAD08198 standard; cDNA; 2053 BP.
DE Human secreted protein-encoding gene 8 cDNA clone HLHDL62, SEQ ID NO:18.
PN WO200132837-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 463
ID AAV34194 standard; DNA; 2070 BP.
DE Human secreted protein gene 41 clone HNTWE13.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 464
ID ACD08065 standard; cDNA; 2070 BP.
DE cDNA encoding novel human secreted protein #41.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPP D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJU/) NI J.

PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (ERNE/) ERNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 465
ID AAD08211 standard; cDNA; 2072 BP.
DE Human secreted protein-encoding gene 8 cDNA clone HDFQB93, SEQ ID NO:31.
PN WO200132837-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 466
ID AAI59731 standard; cDNA; 2152 BP.
DE Human polynucleotide SEQ ID NO 3720.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 467
ID AAI57945 standard; cDNA; 2172 BP.
DE Human polynucleotide SEQ ID NO 148.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 468
ID ADP98650 standard; DNA; 2355 BP.
DE C. albicans specific gene, orf6.7416, DNA sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Percent Similarity: 51.72% Conservative: 9
Best Local Similarity: 36.21% Mismatches: 12
Query Match: 14.07% Indels: 16
RESULT 469
ID ADQ24665 standard; DNA; 2551 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7485.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 57.58% Conservative: 5
Best Local Similarity: 42.42% Mismatches: 14
Query Match: 14.07% Indels: 0
RESULT 470
ID ADQ23265 standard; DNA; 2555 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6085.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 471
ID ABZ35234 standard; cDNA; 3170 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 345.
PN WO200274979-A2.

PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 472
ID ADE79065 standard; DNA; 3273 BP.
DE Human protein modification and maintenance molecule (PMM) -45 gene.
PN WO2003063688-A2.
PD 07-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 473
ID ABQ54610 standard; cDNA; 3523 BP.
DE Human ovarian antigen HNTAK22 cDNA, SEQ ID NO:490.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 474
ID AAH54886 standard; DNA; 3553 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4250.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 45.90% Conservative: 10
Best Local Similarity: 29.51% Mismatches: 19
Query Match: 14.07% Indels: 14
RESULT 475
ID AAT97610 standard; cDNA; 3854 BP.
DE Human E2A-binding protein cDNA.
PN WO9733900-A1.
PD 18-SEP-1997.
PA (HARD) HARVARD COLLEGE.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 476
ID ADE79063 standard; DNA; 3872 BP.
DE Human protein modification and maintenance molecule (PMM) -43 gene.
PN WO2003063688-A2.
PD 07-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 477
ID ACH03928 standard; cDNA; 3922 BP.
DE Human cDNA differentially expressed in lung cancer #133.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASEK) LASEK A W.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 478
ID AB234770 standard; cDNA; 3935 BP.
DE Coding sequence SEQ ID 128, upregulated in osteogenesis.
PN WO200281745-A2.
PD 17-OCT-2002.
PA (AVET) AVENTIS PHARMA SA.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 479
ID ACC50076 standard; cDNA; 3935 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:1.
PN WO2003004989-A2.
PD 16-JAN-2003.

PA (MILL-) MILLENIUM PHARM INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 480
ID ADF90653 standard; DNA; 3935 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 115.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 481
ID ADE79067 standard; DNA; 4025 BP.
DE Human protein modification and maintenance molecule (PMM) -47 gene.
PN WO2003063688-A2.
PD 07-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 43.01% Conservative: 10
Best Local Similarity: 32.26% Mismatches: 42
Query Match: 14.07% Indels: 11
RESULT 482
ID AAH54715 standard; DNA; 4095 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4079.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 45.90% Conservative: 10
Best Local Similarity: 29.51% Mismatches: 19
Query Match: 14.07% Indels: 14
RESULT 483
ID ABA16110 standard; DNA; 4678 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8441.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 47.06% Conservative: 10
Best Local Similarity: 32.35% Mismatches: 30
Query Match: 14.07% Indels: 6
RESULT 484
ID ABQ54837 standard; cDNA; 5169 BP.
DE Human ovarian antigen HNOKM38 cDNA, SEQ ID NO:717.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.26% Conservative: 10
Best Local Similarity: 27.87% Mismatches: 26
Query Match: 14.07% Indels: 8
RESULT 485
ID ADF74193 standard; cDNA; 5223 BP.
DE Human novel brain/hippocampus cDNA #11.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Percent Similarity: 46.03% Conservative: 9
Best Local Similarity: 31.75% Mismatches: 33
Query Match: 14.07% Indels: 1
RESULT 486
ID AAD39115 standard; cDNA; 5387 BP.
DE Human lung-specific nucleic acid (LSNA) #22.
PN WO200240673-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 46.03% Conservative: 9
Best Local Similarity: 31.75% Mismatches: 33
Query Match: 14.07% Indels: 1
RESULT 487
ID ADL12454 standard; cDNA; 5833 BP.
DE Human steroid-induced C3A liver cell cDNA #183.
PN US6673549-B1.
PD 06-JAN-2004.

PA (INCY-) INCYTE CORP.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 488
 ID ADQ18018 standard; DNA; 5886 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 835.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 489
 ID ADD14646 standard; cDNA; 5887 BP.
 DE Human src biomarker polynucleotide SEQ ID NO:40.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 490
 ID ABV26869 standard; cDNA; 5893 BP.
 DE Human prostate expression marker cDNA 26860.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 491
 ID ABV21027 standard; cDNA; 5893 BP.
 DE Human prostate expression marker cDNA 21018.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 492
 ID ADQ2616 standard; DNA; 5903 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5436.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 44.26% Conservative: 10
 Best Local Similarity: 27.8% Mismatches: 26
 Query Match: 14.0% Indels: 8
 RESULT 493
 ID ADQ26437 standard; DNA; 9345 BP.
 DE Chicken fatty acid synthase gene.
 PN WO2004056848-A2.
 PD 08-JUL-2004.
 PA (MONS-) MONSANTO TECHNOLOGY LLC.
 Percent Similarity: 55.32% Conservative: 8
 Best Local Similarity: 38.30% Mismatches: 17
 Query Match: 14.0% Indels: 4
 RESULT 494
 ID ABS58302 standard; DNA; 12017 BP.
 DE Novel human transporter protein genomic DNA sequence.
 PN US2002137128-A1.
 PD 26-SEP-2002.
 PA (WEIM-) WEI M.
 PA (GUEG/) GUEGLER K.
 PA (BEAS-) BEASLEY E M.
 Percent Similarity: 37.93% Conservative: 9
 Best Local Similarity: 27.59% Mismatches: 29
 Query Match: 14.0% Indels: 25
 RESULT 495
 ID AAL37333 standard; DNA; 16100 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3698.
 PN WO200155367-A1.

PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 38.52% Conservative: 17
 Best Local Similarity: 24.53% Mismatches: 37
 Query Match: 14.07% Indels: 38
 RESULT 496
 ID ABX60321 standard; cDNA; 16100 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2665.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Percent Similarity: 38.52% Conservative: 17
 Best Local Similarity: 24.53% Mismatches: 37
 Query Match: 14.07% Indels: 38
 RESULT 497
 ID ADJ31071 standard; DNA; 16100 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3698.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 38.52% Conservative: 17
 Best Local Similarity: 24.53% Mismatches: 37
 Query Match: 14.07% Indels: 38
 RESULT 498
 ID AAD36071 standard; DNA; 16161 BP.
 DE Human adipocyte enhancer binding protein encoding genomic DNA.
 PN WO200224741-A2.
 PD 28-MAR-2002.
 PA (RYAN/) RYAN J W.
 Percent Similarity: 43.01% Conservative: 10
 Best Local Similarity: 32.26% Mismatches: 42
 Query Match: 14.07% Indels: 11
 RESULT 499
 ID AA668247 standard; DNA; 41708 BP.
 DE Bacteriophage 77 complete genome sequence.
 PN WO20032825-A2.
 PD 08-JUN-2000.
 PA (PHAG-) PHAGETECH INC.
 Percent Similarity: 43.55% Conservative: 10
 Best Local Similarity: 27.42% Mismatches: 15
 Query Match: 14.07% Indels: 20
 RESULT 500
 ID AAC66106 standard; cDNA; 41708 BP.
 DE Complete genome of bacteriophage 77.
 PN WO200146383-A2.
 PD 28-JUN-2001.
 PA (PHAG-) PHAGETECH INC.
 Percent Similarity: 43.55% Conservative: 10
 Best Local Similarity: 27.42% Mismatches: 15
 Query Match: 14.07% Indels: 20
 RESULT 501
 ID ADC87620 standard; DNA; 144792 BP.
 DE Human GPCR related polynucleotide SEQ ID NO:2073.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Percent Similarity: 44.44% Conservative: 8
 Best Local Similarity: 33.33% Mismatches: 20
 Query Match: 14.07% Indels: 20
 RESULT 504
 ID ADC87619 standard; DNA; 349981 BP.

DE Human GPCR related polynucleotide SEQ ID NO:2072.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Percent Similarity: 44.44%
 Best Local Similarity: 44.44%
 Mismatches: 20
 Indels: 20
 Query Match:
 RESULT 505
 ID ABX46041 standard; cDNA; 383 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #11206.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Percent Similarity: 44.62%
 Best Local Similarity: 32.31%
 Mismatches: 15
 Indels: 21
 Query Match:
 RESULT 506
 ID ABZ18469 standard; cDNA; 386 BP.
 DE Group III cDNA cancer related clone SEQ ID NO:895.
 PN WO200278516-A2.
 PD 10-OCT-2002.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 50.00%
 Best Local Similarity: 38.46%
 Mismatches: 21
 Indels: 5
 Query Match:
 RESULT 507
 ID ACD05689 standard; cDNA; 630 BP.
 DE cDNA encoding novel human polypeptide #199.
 PN WO2003023013-A2.
 PD 20-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 41.18%
 Best Local Similarity: 30.88%
 Mismatches: 33
 Indels: 7
 Query Match:
 RESULT 508
 ID ADK56099 standard; DNA; 644 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #3482.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 509
 ID ADK39802 standard; DNA; 679 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #7185.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 510
 ID ADG32540 standard; DNA; 879 BP.
 DE DNA encoding the human Claudin-23 protein.
 PN WO2003100001-A2.
 PD 04-DEC-2003.
 PA (IMMV) IMMUNEX CORP.
 Percent Similarity: 41.18%
 Best Local Similarity: 30.88%
 Mismatches: 33
 Indels: 7
 Query Match:
 RESULT 511
 ID ACA21110 standard; DNA; 1026 BP.
 DE Prokaryotic essential gene #2767.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.

Percent Similarity: 50.91%
 Best Local Similarity: 32.73%
 Mismatches: 26
 Indels: 1
 Query Match:
 RESULT 512
 ID ADA29147 standard; DNA; 1068 BP.
 DE DNA encoding Acinetobacter baumannii protein #434.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 50.91%
 Best Local Similarity: 32.73%
 Mismatches: 26
 Indels: 1
 Query Match:
 RESULT 513
 ID ACF72008 standard; DNA; 1272 BP.
 DE Photorhabdus luminescens nucleotide sequence #10475.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Percent Similarity: 47.00%
 Best Local Similarity: 26.00%
 Mismatches: 26
 Indels: 27
 Query Match:
 RESULT 514
 ID AAC51442 standard; DNA; 1347 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68538.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 515
 ID ABZ13684 standard; DNA; 1347 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1489.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 516
 ID AAC39127 standard; DNA; 1535 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23472.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 517
 ID AAF80403 standard; cDNA; 1707 BP.
 DE Nucleotide sequence of a plant transcription factor G748.
 PN WO200126459-A2.
 PD 19-APR-2001.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 PA (RATC) RATCLIFFE O.
 PA (HEAR/) HEARD J.
 PA (SAMA) SAMAHA R.
 PA (KREED) KREELMAN R.
 PA (KEDD) KEDDIE J.
 PA (JIAN) JIANG C.
 PA (REUB/) REUBER L.
 PA (RIEC/) RIECHMANN J L.
 Percent Similarity: 45.83%
 Best Local Similarity: 34.72%
 Mismatches: 26
 Indels: 13
 Query Match:
 RESULT 518
 ID AAD05834 standard; cDNA; 1707 BP.
 DE Arabidopsis thaliana transcription factor G748 cDNA.
 PN WO200136444-A1.
 PD 25-MAY-2001.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 PA (RIEC/) RIECHMANN J L.
 PA (REUB/) REUBER L.

PA (KEDD/) KEDDIE J. 45.83% Conservative: 8
PA (RATC/) RATCLIFFE O. 34.72% Mismatches: 26
PA (HEAR/) HEARD J. 13.96% Indels: 13
PA (SAMA/) SAWAHA R.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
Percent Similarity: 45.83%
Best Local Similarity: 34.72%
Query Match: 13.96%
RESULT 519
ID ABK45211 standard; cDNA; 1707 BP.
DE Arabidopsis cDNA encoding a transcription factor #63.
PN WO200215675-A1.
PD 28-FEB-2002.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (PILG/) PILGRIM M.
PA (CREE/) CREELMAN R.
PA (DUBE/) DUBELL A. J.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (KEDD/) KEDDIE J.
PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFFE O.
PA (REUB/) REUBER J. L.
PA (RIEC/) RIECHMANN J. L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O. 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 520
ID ADB30715 standard; cDNA; 1707 BP.
DE Plant yield-related polynucleotide clone G748.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Percent Similarity: 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 521
ID ADR31478 standard; cDNA; 1707 BP.
DE Plant yield related polynucleotide clone G748.
PN WO2003013228-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Percent Similarity: 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 522
ID AAD47515 standard; DNA; 1707 BP.
DE Arabidopsis thaliana G748 transcription factor DNA.
PN WO200274917-A2.
PD 26-SEP-2002.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Percent Similarity: 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 523
ID ADI41692 standard; DNA; 1707 BP.
DE Plant transcription factor polynucleotide #78.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B. K.
PA (RIEC/) RIECHMANN J. L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J. E.
PA (HAAR/) HAAKE V.
PA (CREE/) CREELMAN R. A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L. J.
PA (REUB/) REUBER T. L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P. E.

PA (PILG/) PILGRIM M. L.
PA (DUBE/) DUBELL A. N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Percent Similarity: 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 524
ID ADO02084 standard; cDNA; 1707 BP.
DE Thalecress transcription factor cDNA #249.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M. E.
PA (HEAR/) HEARD J. E.
PA (RIEC/) RIECHMANN J. L.
PA (ADAM/) ADAM L. J.
PA (BROU/) BROUN P. E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T. L.
PA (KEDD/) KEDDIE J. S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAWAHA R. S.
PA (PILG/) PILGRIM M. L.
PA (CREE/) CREELMAN R. A.
PA (DUBE/) DUBELL A. N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B. K.
Percent Similarity: 45.83% Conservative: 8
Best Local Similarity: 34.72% Mismatches: 26
Query Match: 13.96% Indels: 13
RESULT 525
ID ACA20485 standard; DNA; 1713 BP.
DE Prokaryotic essential gene #2142.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 44.59% Conservative: 14
Best Local Similarity: 25.68% Mismatches: 28
Query Match: 13.96% Indels: 13
RESULT 526
ID ADE07093 standard; DNA; 1716 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #159.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.18% Conservative: 7
Best Local Similarity: 30.88% Mismatches: 33
Query Match: 13.96% Indels: 7
RESULT 527
ID ABT16021 standard; DNA; 1719 BP.
DE NOVK related polynucleotide SEQ ID No 9.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.18% Conservative: 7
Best Local Similarity: 30.88% Mismatches: 33
Query Match: 13.96% Indels: 7
RESULT 528
ID ADO41643 standard; cDNA; 1719 BP.
DE Novel human polypeptide NOV5a cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D. W.
PA (ZERH/) ZERHUSEN B. D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S. J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R. A.
PA (GORM/) GORMAN L.


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PA (PENA/) PENNA C E A.
PA (KEKU/) KEKUDA R.
PA (PATI/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (NALI/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIMW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Percent Similarity: 41.18%
Best Local Similarity: 30.88%
Query Match: 13.96%
Conservative: 7
Mismatch: 33
Indels: 7
RESULT 529
ID ABA00966 standard; cDNA; 2052 BP.
DE CGDD-7 coding sequence, Incyte ID No. 1820882CB1.
PN WO2003008553-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.18%
Best Local Similarity: 30.88%
Query Match: 13.96%
Conservative: 7
Mismatch: 33
Indels: 7
RESULT 530
ID ADH69503 standard; DNA; 6251 BP.
DE Rat dopamine D1 receptor DNA.
PN US2003170741-A1.
PD 11-SEP-2003.
PA (PROC) PROCTER & GAMBLE CO.
Percent Similarity: 50.94%
Best Local Similarity: 37.74%
Query Match: 13.96%
Conservative: 7
Mismatch: 21
Indels: 5
RESULT 531
ID AAS30529 standard; DNA; 10812 BP.
DE DNA encoding novel prostate gland antigen, Seq ID No 387.
PN WO200155447-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.94%
Best Local Similarity: 32.65%
Query Match: 13.96%
Conservative: 7
Mismatch: 21
Indels: 5
RESULT 532
ID AAL06307 standard; DNA; 10812 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8995.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.94%
Best Local Similarity: 32.65%
Query Match: 13.96%
Conservative: 7
Mismatch: 21
Indels: 5
RESULT 533
ID ABL19002 standard; DNA; 21231 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8479.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 49.15%
Best Local Similarity: 28.81%
Query Match: 13.96%
Conservative: 12
Mismatch: 27
Indels: 3
RESULT 534
ID AAS36610 standard; DNA; 22008 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2110.
PN WO200155321-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 535
ID ABA15839 standard; DNA; 22008 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8170.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 536
ID ABZ73783 standard; DNA; 22008 BP.
DE Secreted protein gene 33 genomic fragment HBJAB02, SEQ ID NO:930.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 537
ID ADA98459 standard; DNA; 22008 BP.
DE Human secreted protein-related DNA sequence #52.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 538
ID ADC20627 standard; DNA; 22008 BP.
DE Human secreted protein-related DNA sequence #45.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 539
ID ADE47304 standard; DNA; 22008 BP.
DE Human cardiovascular system related genomic DNA #870.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 540
ID ABT16888 standard; DNA; 22008 BP.
DE Human secreted protein-related DNA sequence - SEQ ID No 242.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 541
ID ABZ67377 standard; DNA; 22008 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 900.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.31%
Best Local Similarity: 31.25%
Query Match: 13.96%
Conservative: 9
Mismatch: 18
Indels: 17
RESULT 542
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN WO200157182-A2.
PD 09-AUG-2001.
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PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 29.30% Conservative: 12
Best Local Similarity: 21.66% Mismatches: 34
Query Match: 13.96% Indels: 77
RESULT 543
ID AAKG7283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 29.30% Conservative: 12
Best Local Similarity: 21.66% Mismatches: 34
Query Match: 13.96% Indels: 77
RESULT 544
Percent Similarity: 47.00% Conservative: 21
Best Local Similarity: 26.00% Mismatches: 26
Query Match: 13.96% Indels: 27
RESULT 545
Percent Similarity: 47.00% Conservative: 21
Best Local Similarity: 26.00% Mismatches: 26
Query Match: 13.96% Indels: 27
RESULT 546
ID AAD54480 standard; DNA; 117962 BP.
DE Human CIP DNA #1.
PN WO200299055-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIX INC.
Percent Similarity: 40.22% Conservative: 13
Best Local Similarity: 28.00% Mismatches: 32
Query Match: 13.96% Indels: 23
RESULT 547
ID ADL13850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 51.72% Conservative: 23
Best Local Similarity: 25.29% Mismatches: 24
Query Match: 13.96% Indels: 18
RESULT 548
ID AEQ75562 standard; DNA; 188888 BP.
DE Human related CYP 27C1 clone RP11-30F3 SEQ ID NO:21.
PN WO200264765-A2.
PD 22-AUG-2002.
PA (CYTO-) CYTOCHROMA INC.
Percent Similarity: 45.65% Conservative: 17
Best Local Similarity: 27.17% Mismatches: 27
Query Match: 13.96% Indels: 23
RESULT 549
ID AEK84349 standard; cDNA; 222930 BP.
DE Human cDNA differentially expressed in granulocytic cells #920.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 18
Query Match: 13.96% Indels: 7
RESULT 550
ID ABX46032 standard; cDNA; 371 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11197.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Percent Similarity: 46.48% Conservative: 13
Best Local Similarity: 28.17% Mismatches: 26
Query Match: 13.85% Indels: 12
RESULT 551
ID ABV12569 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 12560.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 45.05% Conservative: 12
Best Local Similarity: 31.87% Mismatches: 26
Query Match: 13.85% Indels: 24
RESULT 552
ID ABV03400 standard; cDNA; 434 BP.
DE Human prostate expression marker cDNA 3391.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 45.05% Conservative: 12
Best Local Similarity: 31.87% Mismatches: 26
Query Match: 13.85% Indels: 24
RESULT 553
ID ABK45654 standard; cDNA; 456 BP.
DE cDNA encoding colon tumour protein, SEQ ID NO 1205.
PN WO200212328-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 46.34% Conservative: 16
Best Local Similarity: 28.83% Mismatches: 28
Query Match: 13.85% Indels: 16
RESULT 554
ID ABV33703 standard; cDNA; 461 BP.
DE Human prostate expression marker cDNA 33694.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 45.05% Conservative: 12
Best Local Similarity: 31.87% Mismatches: 26
Query Match: 13.85% Indels: 24
RESULT 555
ID ADC76835 standard; DNA; 511 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1104.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Percent Similarity: 41.98% Conservative: 13
Best Local Similarity: 25.93% Mismatches: 37
Query Match: 13.85% Indels: 10
RESULT 556
ID ADC77099 standard; DNA; 511 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2028.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Percent Similarity: 41.98% Conservative: 13
Best Local Similarity: 25.93% Mismatches: 37
Query Match: 13.85% Indels: 10
RESULT 557
ID ABV42605 standard; cDNA; 618 BP.
DE Human prostate expression marker cDNA 42596.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 45.05% Conservative: 12
Best Local Similarity: 31.87% Mismatches: 26
Query Match: 13.85% Indels: 24
RESULT 558
ID AAF08249 standard; cDNA; 625 BP.
DE Fusarium venenatum EST SEQ ID NO:772.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 43.75% Conservative: 12
Best Local Similarity: 28.75% Mismatches: 37
Query Match: 13.85% Indels: 8
RESULT 559
ID ABQ69341 standard; DNA; 774 BP.
DE Listeria innocua DNA sequence #780.
PN WO200228891-A2.

PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 45.10%
Best Local Similarity: 29.41%
Query Match: 13.85%
Indels: 14
Conservative: 8
Mismatches: 14
RESULT 560
ID ABO67685 standard; DNA; 774 BP.
DE Listeria innocua DNA sequence #497.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 45.10%
Best Local Similarity: 29.41%
Query Match: 13.85%
Indels: 14
Conservative: 8
Mismatches: 14
RESULT 561
ID ABL21165 standard; DNA; 1003 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14968.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.11%
Best Local Similarity: 32.63%
Query Match: 13.85%
Indels: 28
Conservative: 9
Mismatches: 27
RESULT 562
ID ABV28053 standard; cDNA; 1131 BP.
DE Human prostate expression marker cDNA 28044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 41.05%
Best Local Similarity: 27.37%
Query Match: 13.85%
Indels: 35
Conservative: 13
Mismatches: 21
RESULT 563
ID AAC53418 standard; DNA; 1266 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 74455.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.76%
Best Local Similarity: 24.18%
Query Match: 13.85%
Indels: 18
Conservative: 16
Mismatches: 35
RESULT 564
ID AAC32883 standard; DNA; 1364 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 996.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.76%
Best Local Similarity: 24.18%
Query Match: 13.85%
Indels: 18
Conservative: 16
Mismatches: 35
RESULT 565
ID AAA78540 standard; DNA; 2029 BP.
DE Plant SDF polynucleotide sequence SEQ List 1 NO:372.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Percent Similarity: 46.58%
Best Local Similarity: 27.40%
Query Match: 13.85%
Indels: 16
Conservative: 14
Mismatches: 23
RESULT 566
ID AAF15814 standard; cDNA; 2422 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:249.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Percent Similarity: 46.34%
Best Local Similarity: 26.83%
Query Match: 13.85%
Indels: 16
Conservative: 16
Mismatches: 28
RESULT 567
ID ADL22897 standard; DNA; 2476 BP.
DE Human MP2153 coding sequence SEQ ID NO: 17.
PN WO2004015069-A2.

PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 41.79%
Best Local Similarity: 29.85%
Query Match: 13.85%
Indels: 12
Conservative: 8
Mismatches: 27
RESULT 568
ID AAS83129 standard; cDNA; 2918 BP.
DE DNA encoding novel human diagnostic protein #18933.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 33.33%
Best Local Similarity: 24.07%
Query Match: 13.85%
Indels: 48
Conservative: 10
Mismatches: 24
RESULT 569
ID ABL21164 standard; DNA; 3003 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14965.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.11%
Best Local Similarity: 32.63%
Query Match: 13.85%
Indels: 28
Conservative: 9
Mismatches: 27
RESULT 570
ID ABA02133 standard; cDNA; 3006 BP.
DE Human zinc ion transport protein 26-encoding cDNA.
PN WO200181539-A2.
PD 01-NOV-2001.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Percent Similarity: 41.79%
Best Local Similarity: 29.85%
Query Match: 13.85%
Indels: 12
Conservative: 8
Mismatches: 27
RESULT 571
ID AAV15221 standard; DNA; 3501 BP.
DE Bacillus thuringiensis 158C2b toxin encoding DNA.
PN US5723758-A.
PD 03-MAR-1998.
PA (MYCO) MYCOGEN CORP.
Percent Similarity: 45.45%
Best Local Similarity: 29.87%
Query Match: 13.85%
Indels: 8
Conservative: 12
Mismatches: 34
RESULT 572
ID AAA89220 standard; DNA; 3501 BP.
DE Bacillus thuringiensis delta-endotoxin gene 158C2b.
PN US6150589-A.
PD 21-NOV-2000.
PA (MYCO) MYCOGEN CORP.
Percent Similarity: 45.45%
Best Local Similarity: 29.87%
Query Match: 13.85%
Indels: 8
Conservative: 12
Mismatches: 34
RESULT 573
ID AAS02474 standard; DNA; 3507 BP.
DE B. thuringiensis DNA encoding a toxic crystal protein, CryT53.
PN WO200119859-A2.
PD 22-MAR-2001.
PA (MONS) MONSANTO CO.
Percent Similarity: 45.45%
Best Local Similarity: 29.87%
Query Match: 13.85%
Indels: 8
Conservative: 12
Mismatches: 34
RESULT 574
ID ABX34815 standard; cDNA; 3666 BP.
DE Human mddt cDNA SEQ ID 376.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 49.43%
Best Local Similarity: 29.89%
Query Match: 13.85%
Indels: 13
Conservative: 17
Mismatches: 31
RESULT 575
ID ABL07926 standard; cDNA; 3991 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 18260.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Percent Similarity: 52.50%
Best Local Similarity: 40.00%
Query Match: 13.85%
Indels: 8
Conservative: 5
Mismatches: 11

RESULT 576
ID ABL18500 standard; DNA; 4063 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6973.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.11%
Best Local Similarity: 32.63%
Query Match: 13.85%
Indels: 28
Conservative: 9
Mismatches: 27

RESULT 577
ID ABN71526 standard; DNA; 4650 BP.
DE Streptococcus polynucleotide SEQ ID NO 10965.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 48.53%
Best Local Similarity: 36.76%
Query Match: 13.85%
Indels: 18
Conservative: 8
Mismatches: 17

RESULT 578
ID ABN71162 standard; DNA; 4710 BP.
DE Streptococcus polynucleotide SEQ ID NO 10237.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 48.53%
Best Local Similarity: 36.76%
Query Match: 13.85%
Indels: 18
Conservative: 8
Mismatches: 17

RESULT 579
ID ABN70525 standard; DNA; 4734 BP.
DE Streptococcus polynucleotide SEQ ID NO 8963.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 48.53%
Best Local Similarity: 36.76%
Query Match: 13.85%
Indels: 18
Conservative: 8
Mismatches: 17

RESULT 580
ID ABN69191 standard; DNA; 4770 BP.
DE Streptococcus polynucleotide SEQ ID NO 6295.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 48.53%
Best Local Similarity: 36.76%
Query Match: 13.85%
Indels: 18
Conservative: 8
Mismatches: 17

RESULT 581
ID ADD01254 standard; cDNA; 5674 BP.
DE Human nucleic acid-associated protein NAAP-35 cDNA SEQ ID NO:92.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 45.71%
Best Local Similarity: 30.00%
Query Match: 13.85%
Indels: 4
Conservative: 11
Mismatches: 34

RESULT 582
ID ABL28694 standard; DNA; 22875 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37555.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.48%
Best Local Similarity: 25.00%
Query Match: 13.85%
Indels: 18
Conservative: 13
Mismatches: 32

RESULT 583
ID ADA02615 standard; DNA; 73634 BP.

DE Mouse Fyn carcinoma associated gene, SEQ ID NO:1133.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 47.37%
Best Local Similarity: 33.33%
Query Match: 13.85%
Indels: 1
Conservative: 8
Mismatches: 29

RESULT 584
ID ADB72353 standard; DNA; 73634 BP.
DE Mouse Fyn gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 47.37%
Best Local Similarity: 33.33%
Query Match: 13.85%
Indels: 1
Conservative: 8
Mismatches: 29

RESULT 585
ID ADE95863 standard; DNA; 73634 BP.
DE Mouse Fyn gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 47.37%
Best Local Similarity: 33.33%
Query Match: 13.85%
Indels: 1
Conservative: 8
Mismatches: 29

RESULT 586
ID ABN85767 standard; cDNA; 83698 BP.
DE Arabidopsis yellow striped-like 4 encoding cDNA SEQ ID NO 9.
PN WO200240688-A2.
PD 23-MAY-2002.
PA (UYVA) UNIV YALE.
Percent Similarity: 42.17%
Best Local Similarity: 28.92%
Query Match: 13.85%
Indels: 13
Conservative: 11
Mismatches: 35

RESULT 587
ID AAX91990 standard; DNA; 1230025 BP.
DE Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Percent Similarity: 38.61%
Best Local Similarity: 24.75%
Query Match: 13.85%
Indels: 32
Conservative: 14
Mismatches: 30

RESULT 588
Percent Similarity: 48.53%
Best Local Similarity: 36.76%
Query Match: 13.85%
Indels: 18
Conservative: 8
Mismatches: 17

RESULT 589
Percent Similarity: 45.10%
Best Local Similarity: 29.41%
Query Match: 13.85%
Indels: 14
Conservative: 8
Mismatches: 14

RESULT 590
ID ABQ89245 standard; DNA; 3011208 BP.
DE Listeria innocua DNA sequence #684.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 45.10%
Best Local Similarity: 29.41%
Query Match: 13.85%
Indels: 14
Conservative: 8
Mismatches: 14

RESULT 591
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Percent Similarity: 44.62%
Best Local Similarity: 33.85%
Query Match: 13.85%
Indels: 10
Conservative: 7
Mismatches: 26

RESULT 592
ID AAC00776 standard; cDNA; 350 BP.

DE Human secreted protein 5' EST, SEQ ID NO: 774.
PN EPI033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 38.64% Conservative: 10
Best Local Similarity: 27.27% Mismatches: 30
Query Match: 13.74% Indels: 24
RESULT 593
ID AAH11120 standard; cDNA: 546 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7955.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 594
ID AAD36477 standard; cDNA: 549 BP.
DE Human phospholipase A2-like enzyme encoding cDNA #2.
PN WO200231162-A2.
PD 18-APR-2002.
PA (FARB) BAYER AG.
Percent Similarity: 38.54% Conservative: 11
Best Local Similarity: 27.08% Mismatches: 34
Query Match: 13.74% Indels: 25
RESULT 595
ID ABV48210 standard; cDNA: 551 BP.
DE Human prostate expression marker cDNA 48201.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.96% Conservative: 11
Best Local Similarity: 27.71% Mismatches: 39
Query Match: 13.74% Indels: 10
RESULT 596
ID ADK53732 standard; DNA: 587 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #1115.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Percent Similarity: 52.00% Conservative: 6
Best Local Similarity: 40.00% Mismatches: 21
Query Match: 13.74% Indels: 3
RESULT 597
ID AAS30336 standard; cDNA: 588 BP.
DE DNA encoding novel prostate gland antigen, Seq ID No 86.
PN WO200155447-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.94% Conservative: 7
Best Local Similarity: 32.65% Mismatches: 21
Query Match: 13.74% Indels: 5
RESULT 598
ID AAL02017 standard; cDNA: 588 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2018.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.94% Conservative: 7
Best Local Similarity: 32.65% Mismatches: 21
Query Match: 13.74% Indels: 5
RESULT 599
ID ABL07235 standard; cDNA: 651 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16187.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.67% Conservative: 9
Best Local Similarity: 29.17% Mismatches: 29
Query Match: 13.74% Indels: 13
RESULT 600
ID AAS80715 standard; cDNA: 795 BP.

DE DNA encoding novel human diagnostic protein #16519.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 48.33% Conservative: 11
Best Local Similarity: 30.00% Mismatches: 24
Query Match: 13.74% Indels: 7
RESULT 601
ID ABL53352 standard; DNA: 1202 BP.
DE Mushroom GPD gene.
PN KR2001011673-A.
PD 15-FEB-2001.
PA (ROKR-) ROK RURAL DEV ADMINISTRATION.
Percent Similarity: 41.98% Conservative: 13
Best Local Similarity: 25.93% Mismatches: 18
Query Match: 13.74% Indels: 29
RESULT 602
ID ABL53444 standard; DNA: 1202 BP.
DE Glycero1-3-phosphate dehydrogenase (GPD) gene.
PN KR2001011674-A.
PD 15-FEB-2001.
PA (ROKR-) ROK RURAL DEV ADMINISTRATION.
Percent Similarity: 41.98% Conservative: 13
Best Local Similarity: 25.93% Mismatches: 18
Query Match: 13.74% Indels: 29
RESULT 603
ID ADB46123 standard; cDNA: 1215 BP.
DE Bread wheat thiamine biosynthetic enzyme 1 cDNA #5.
PN US6512164-B1.
PD 28-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Percent Similarity: 45.26% Conservative: 20
Best Local Similarity: 24.21% Mismatches: 33
Query Match: 13.74% Indels: 19
RESULT 604
ID AAC5207 standard; cDNA: 1363 BP.
DE Human secreted protein gene 18 SEQ ID NO:28.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 41.38% Conservative: 14
Best Local Similarity: 25.29% Mismatches: 43
Query Match: 13.74% Indels: 8
RESULT 605
ID AAI20210 standard; DNA: 1728 BP.
DE Probe #10143 for Gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 606
ID ABA65239 standard; DNA: 1728 BP.
DE Human foetal liver single exon nucleic acid probe #13544.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 607
ID AAI45410 standard; DNA: 1728 BP.
DE Probe #14096 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 608
ID ABA47354 standard; DNA: 1728 BP.
DE Human breast cell single exon nucleic acid probe #6049.

PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 609
ID ABA32340 standard; DNA; 1728 BP.
DE Probe #10806 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 610
ID AAK39397 standard; DNA; 1728 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 13954.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 611
ID AAK13656 standard; DNA; 1728 BP.
DE Human brain expressed single exon probe SEQ ID NO: 13647.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 612
ID ABS38985 standard; DNA; 1728 BP.
DE Human liver single exon probe, SEQ ID No 13975.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 613
ID AAI05914 standard; DNA; 1728 BP.
DE Probe #5905 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 614
ID ABS13484 standard; DNA; 1728 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 13475.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 615
ID ADD18217 standard; DNA; 1800 BP.
DE Human molecule (MOL) protein MOL2c DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 616
ID ADD18215 standard; DNA; 1800 BP.
DE Human molecule (MOL) protein MOL2b DNA sequence.
PN WO2003003984-A2.

PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 617
ID ADH72315 standard; DNA; 1800 BP.
DE Human gene of the invention NOV62f SEQ ID NO:1211.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 618
ID ADH72307 standard; DNA; 1800 BP.
DE Human gene of the invention NOV62b SEQ ID NO:1203.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 619
ID ADH72309 standard; DNA; 1800 BP.
DE Human gene of the invention NOV62c SEQ ID NO:1205.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00%
Best Local Similarity: 42.59%
Query Match: 13.74%
Conservative: 4
Mismatches: 16
Indels: 11
RESULT 620
ID AAA07960 standard; DNA; 1908 BP.
DE Murine Oct4 enhancer and promoter.
PN WO200056932-A2.
PD 28-SEP-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Percent Similarity: 32.00%
Best Local Similarity: 21.33%
Query Match: 13.74%
Conservative: 16
Mismatches: 33
Indels: 69
RESULT 621
ID AAH98759 standard; cDNA; 1927 BP.
DE Human EST-derived coding sequence SEQ ID NO: 616.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 29.63%
Query Match: 13.74%
Conservative: 12
Mismatches: 28
Indels: 17
RESULT 622
ID AAH99768 standard; cDNA; 1927 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:603.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 29.63%
Query Match: 13.74%
Conservative: 12
Mismatches: 28
Indels: 17
RESULT 623
ID AAD19218 standard; DNA; 1931 BP.
DE Human CG95 (or C870) lipase DNA.
PN WO200179446-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 29.63%
Query Match: 13.74%
Conservative: 12
Mismatches: 28
Indels: 17
RESULT 624
ID ADO18176 standard; DNA; 1938 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 993.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 44.44% Conservative: 12
Best Local Similarity: 29.63% Mismatches: 28
Query Match: 13.74% Indels: 17
RESULT 625
ID ADP18657 standard; cDNA; 1939 BP.
DE Human TAT415 cDNA used to treat cancer SeqID 17.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.44% Conservative: 12
Best Local Similarity: 29.63% Mismatches: 28
Query Match: 13.74% Indels: 17
RESULT 626
ID ADN73816 standard; cDNA; 1956 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1711.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Percent Similarity: 49.15% Conservative: 6
Best Local Similarity: 38.98% Mismatches: 17
Query Match: 13.74% Indels: 13
RESULT 627
ID ADK64937 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #1548.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Percent Similarity: 36.80% Conservative: 20
Best Local Similarity: 20.80% Mismatches: 34
Query Match: 13.74% Indels: 45
RESULT 628
ID ADB63242 standard; cDNA; 2042 BP.
DE Human cDNA encoding clone TES110001570.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 37.39% Conservative: 15
Best Local Similarity: 24.35% Mismatches: 31
Query Match: 13.74% Indels: 41
RESULT 629
ID ACA35820 standard; DNA; 2286 BP.
DE Prokaryotic essential gene #17477.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.30% Conservative: 7
Best Local Similarity: 29.85% Mismatches: 29
Query Match: 13.74% Indels: 11
RESULT 630
ID AAH99075 standard; cDNA; 2361 BP.
DE Human EST-derived coding sequence SEQ ID NO: 932.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 631
ID AAD36478 standard; cDNA; 2409 BP.
DE Human phospholipase A2-like enzyme encoding cDNA #3.
PN WO200231162-A2.
PD 18-APR-2002.
PA (FARB) BAYER AG.
Percent Similarity: 38.54% Conservative: 11
Best Local Similarity: 27.08% Mismatches: 34
Query Match: 13.74% Indels: 25
RESULT 632
ID ADH72313 standard; DNA; 2469 BP.
DE Human gene of the invention NOV62a SEQ ID NO:1209.
PN WO2003102155-A2.
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 633
ID ABQ72594 standard; cDNA; 2476 BP.
DE Human MDDT encoding cDNA SEQ ID NO 146.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.39% Conservative: 15
Best Local Similarity: 24.35% Mismatches: 31
Query Match: 13.74% Indels: 41
RESULT 634
ID AAH78202 standard; DNA; 2601 BP.
DE Nucleotide sequence of a human secreted polypeptide.
PN WO20016690-A2.
PD 13-SEP-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 635
ID AAD28943 standard; cDNA; 2631 BP.
DE Human MOL2 cDNA.
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 636
ID AAD35333 standard; DNA; 2631 BP.
DE Human toll like receptor like molecule 4 (TLR-L4) DNA.
PN WO20020569-A2.
PD 14-MAR-2002.
PA (SCHE) SCHERING CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 637
ID ADD18195 standard; DNA; 2631 BP.
DE Human molecule (MOL) protein MOL2a DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 638
ID ADH72305 standard; DNA; 2631 BP.
DE Human gene of the invention NOV62a SEQ ID NO:1201.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 639
ID ACH99037 standard; DNA; 2646 BP.
DE Klebsiella pneumoniae polynucleotide seqid 4832.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.30% Conservative: 7
Best Local Similarity: 29.85% Mismatches: 29
Query Match: 13.74% Indels: 11
RESULT 640
ID ABL07234 standard; cDNA; 2651 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16184.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Percent Similarity: 41.67% Conservative: 9
Best Local Similarity: 29.17% Mismatches: 29
Query Match: 13.74% Indels: 13
RESULT 641
ID ADH72311 standard; DNA; 2654 BP.
DE Human Gene of the invention NOV62d SEQ ID NO:1207.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 642
ID AAH16115 standard; cDNA; 2739 BP.
DE Human cDNA sequence SEQ ID NO:14845.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 643
ID AAK87250 standard; DNA; 2740 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42062.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 50.98% Conservative: 6
Best Local Similarity: 39.22% Mismatches: 20
Query Match: 13.74% Indels: 5
RESULT 644
ID AAK73991 standard; DNA; 2740 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28803.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 50.98% Conservative: 6
Best Local Similarity: 39.22% Mismatches: 20
Query Match: 13.74% Indels: 5
RESULT 645
ID ACC72857 standard; cDNA; 2747 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:195.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 44.44% Conservative: 12
Best Local Similarity: 29.63% Mismatches: 28
Query Match: 13.74% Indels: 17
RESULT 646
ID ADQ22737 standard; DNA; 2789 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5557.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 44.44% Conservative: 12
Best Local Similarity: 29.63% Mismatches: 28
Query Match: 13.74% Indels: 17
RESULT 647
ID ADF82460 standard; DNA; 2796 BP.
DE Leukaemia-related DNA sequence #3016.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKE-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 648
ID ABL17391 standard; DNA; 2864 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3646.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.30% Conservative: 13
Best Local Similarity: 27.17% Mismatches: 37
Query Match: 13.74% Indels: 17
RESULT 649
ID ADB62683 standard; cDNA; 3072 BP.
DE Human cDNA encoding clone MESAN20021220.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 50.00% Conservative: 4
Best Local Similarity: 42.59% Mismatches: 16
Query Match: 13.74% Indels: 11
RESULT 650
ID ADC10173 standard; DNA; 3138 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 195.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.54% Conservative: 11
Best Local Similarity: 27.08% Mismatches: 34
Query Match: 13.74% Indels: 25
RESULT 651
ID ABA94700 standard; cDNA; 3197 BP.
DE Human lipid metabolism molecule (LMM) cDNA (ID: 7477093CB1).
PN WO200204490-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.54% Conservative: 11
Best Local Similarity: 27.08% Mismatches: 34
Query Match: 13.74% Indels: 25
RESULT 652
ID ABZ74133 standard; DNA; 3200 BP.
DE Secreted protein gene 191 genomic fragment HLYGE16, SEQ ID NO:1280.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 653
ID ABZ74132 standard; DNA; 3200 BP.
DE Secreted protein gene 191 genomic fragment HLYGE16, SEQ ID NO:1279.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 654
ID ADA98667 standard; DNA; 3200 BP.
DE Human secreted protein-related DNA sequence #260.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 655
ID ADA98668 standard; DNA; 3200 BP.
DE Human secreted protein-related DNA sequence #261.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 656
ID ABT16945 standard; DNA; 3200 BP.

DE Human secreted protein-related DNA sequence - SEQ ID NO 299.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 657
ID ABT16946 standard; DNA; 3200 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 300.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 658
ID ABZ67689 standard; DNA; 3200 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1212.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 659
ID ABZ67690 standard; DNA; 3200 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1213.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.72% Conservative: 7
Best Local Similarity: 39.66% Mismatches: 21
Query Match: 13.74% Indels: 7
RESULT 660
ID ADB61644 standard; DNA; 3587 BP.
DE Human DNA encoding 818 amino acid phospholipase A2 (PLA2) protein.
PN WO2003060132-A1.
PD 24-JUL-2003.
PA (TANA) TANABE SEIYAKU CO.
Percent Similarity: 38.54% Conservative: 11
Best Local Similarity: 27.08% Mismatches: 34
Query Match: 13.74% Indels: 25
RESULT 661
ID ADF6730 standard; cDNA; 3986 BP.
DE Novel human secreted and transmembrane protein cDNA seqID 405.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 662
ID ADP76730 standard; cDNA; 3986 BP.
DE Novel human secreted and transmembrane protein cDNA seqID 405.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 663
ID ADQ24897 standard; DNA; 4003 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7717.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 664
ID ADE31412 standard; DNA; 4013 BP.
DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID NO 167.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 665
ID ABV25850 standard; cDNA; 4688 BP.
DE Human prostate expression marker cDNA 25841.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 666
ID ABV25472 standard; cDNA; 4688 BP.
DE Human prostate expression marker cDNA 25463.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 41.18% Conservative: 15
Best Local Similarity: 23.53% Mismatches: 43
Query Match: 13.74% Indels: 7
RESULT 667
ID ABL17390 standard; DNA; 11359 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3643.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.30% Conservative: 13
Best Local Similarity: 27.17% Mismatches: 37
Query Match: 13.74% Indels: 17
RESULT 668
ID ABL03198 standard; cDNA; 11390 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4076.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.30% Conservative: 13
Best Local Similarity: 27.17% Mismatches: 37
Query Match: 13.74% Indels: 17
RESULT 669
ID AAD35032 standard; DNA; 52354 BP.
DE Human transporter protein gene.
PN US2002028773-A1.
PD 07-MAR-2002.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (KETC/) KETCHUM K. A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E. M.
Percent Similarity: 39.47% Conservative: 17
Best Local Similarity: 24.56% Mismatches: 38
Query Match: 13.74% Indels: 31
RESULT 670
ID ADA02795 standard; DNA; 52479 BP.
DE Mouse Tnfsl1 carcinoma associated gene, SEQ ID NO:1313.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 58.97% Conservative: 8
Best Local Similarity: 38.46% Mismatches: 15
Query Match: 13.74% Indels: 1
RESULT 671
ID ADB72533 standard; DNA; 52479 BP.
DE Mouse Tnfsl1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 58.97% Conservative: 8
Best Local Similarity: 38.46% Mismatches: 15
Query Match: 13.74% Indels: 1

RESULT 672
 ID ADC85275 standard; DNA; 52479 BP.
 DE Mouse Tnfsf11 genomic sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Percent Similarity: 58.97%
 Best Local Similarity: 38.46%
 Query Match: 13.74%
 RESULT 673
 ID ADM74390 standard; DNA; 52479 BP.
 DE Murine carcinoma associated (CA) nucleic acid #31.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Percent Similarity: 58.97%
 Best Local Similarity: 38.46%
 Query Match: 13.74%
 RESULT 674
 ID ADM27081 standard; DNA; 1694968 BP.
 DE Hyperthermophile Methanopyrus kandleri complete genome.
 PN WO2003076575-A2.
 PD 18-SEP-2003.
 PA (FIDE-) FIDELITY SYSTEMS INC.
 PA (MALY/) MALYKH A.
 Percent Similarity: 45.45%
 Best Local Similarity: 35.06%
 Query Match: 13.74%
 RESULT 675
 ID ADI29095 standard; DNA; 119501 BP.
 DE Human MARK3 genomic DNA.
 PN US2003232771-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Percent Similarity: 49.43%
 Best Local Similarity: 28.74%
 Query Match: 13.74%
 RESULT 676
 ID AAC89560 standard; DNA; 122186 BP.
 DE Human histone deacetylase HDAC-D coding sequence.
 PN WO2000071703-A2.
 PD 30-NOV-2000.
 PA (METH-) METHYLGENE INC.
 Percent Similarity: 46.43%
 Best Local Similarity: 33.93%
 Query Match: 13.74%
 RESULT 677
 ID ADF69167 standard; cDNA; 216215 BP.
 DE Human MP53 nucleotide sequence SEQ ID NO:25.
 PN WO2003083047-A2.
 PD 09-OCT-2003.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 50.00%
 Best Local Similarity: 42.59%
 Query Match: 13.74%
 RESULT 678
 ID ABK89296 standard; DNA; 326014 BP.
 DE Human gene for novel serine/threonine serine kinase.
 Percent Similarity: 45.78%
 Best Local Similarity: 33.73%
 Query Match: 13.74%
 RESULT 679
 ID ADQ94981 standard; DNA; 326014 BP.
 DE Human kinase genomic DNA.
 Percent Similarity: 45.78%
 Best Local Similarity: 33.73%
 Query Match: 13.74%
 RESULT 680
 ID ABZ39935 standard; DNA; 321 BP.
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4459.
 PN WO200279243-A2.
 PD 10-OCT-2002.

PA (CHIR-) CHIRON SPA.
 Percent Similarity: 39.02%
 Best Local Similarity: 25.61%
 Query Match: 13.64%
 RESULT 681
 ID ABZ39936 standard; DNA; 321 BP.
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4461.
 PN WO200279243-A2.
 PD 10-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Percent Similarity: 39.02%
 Best Local Similarity: 25.61%
 Query Match: 13.64%
 RESULT 682
 ID ABQ98868 standard; DNA; 445 BP.
 DE Human ORF675 coding sequence.
 PN US2002082206-A1.
 PD 27-JUN-2002.
 PA (LEAC/) LEACH M D.
 PA (MEHR/) MEHRABAN P.
 PA (CONL/) CONLEY P B.
 PA (TOPP/) TOPPER J N.
 PA (LAWD/) LAW D.
 Percent Similarity: 51.06%
 Best Local Similarity: 36.17%
 Query Match: 13.64%
 RESULT 683
 ID AAH53568 standard; DNA; 561 BP.
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2529.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Percent Similarity: 44.16%
 Best Local Similarity: 28.57%
 Query Match: 13.64%
 RESULT 684
 ID ABK63186 standard; cDNA; 586 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1093.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.62%
 Best Local Similarity: 26.73%
 Query Match: 13.64%
 RESULT 685
 ID ADB57405 standard; DNA; 586 BP.
 DE Toxicity-related gene, SEQ ID 2431.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.62%
 Best Local Similarity: 26.73%
 Query Match: 13.64%
 RESULT 686
 ID ABV46588 standard; cDNA; 648 BP.
 DE Human prostate expression marker cDNA 46579.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 47.37%
 Best Local Similarity: 28.07%
 Query Match: 13.64%
 RESULT 687
 ID ADQ23606 standard; DNA; 680 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6426.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 51.02%
 Best Local Similarity: 34.69%
 Query Match: 13.64%
 RESULT 688
 ID ADR02302 standard; DNA; 729 BP.

DE A. gossypii genomic DNA PAG1610UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 46.67% Conservative: 12
Best Local Similarity: 30.67% Mismatches: 28
Query Match: 13.64% Indels: 12
RESULT 689
ID AAS97141 standard; DNA; 753 BP.
DE PS-9 single chain FV DNA.
PN WO200171005-A2.
PD 27-SEP-2001.
PA (KUFE/) KUFE P.
Percent Similarity: 50.00% Conservative: 10
Best Local Similarity: 30.77% Mismatches: 22
Query Match: 13.64% Indels: 4
RESULT 690
ID ABS76754 standard; cDNA; 771 BP.
DE Frog embryonic gene sequence Q9924933.
PN US2002081610-A1.
PD 27-JUN-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Percent Similarity: 37.62% Conservative: 13
Best Local Similarity: 24.75% Mismatches: 41
Query Match: 13.64% Indels: 22
RESULT 691
ID ADC27651 standard; DNA; 872 BP.
DE Human colon specific nucleic acid (CSNA) Seq ID20.
PN WO2003020953-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 45.71% Conservative: 15
Best Local Similarity: 24.29% Mismatches: 32
Query Match: 13.64% Indels: 6
RESULT 692
ID ABN91955 standard; DNA; 948 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1418.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 44.16% Conservative: 12
Best Local Similarity: 28.57% Mismatches: 35
Query Match: 13.64% Indels: 8
RESULT 693
ID ABK68669 standard; DNA; 963 BP.
DE Human DNA for olfactory and pheromone G protein-coupled receptor #269.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.64% Indels: 32
RESULT 694
ID ADG83531 standard; DNA; 963 BP.
DE Human Olfactory and pheromone GPCR DNA #123.
PN US2003221205-A1.
PD 27-NOV-2003.
PA (VEIT/) VEITHEN A.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.64% Indels: 32
RESULT 695
ID ABS58843 standard; DNA; 977 BP.
DE Human G-protein coupled receptor (GPCR) gene #97.
PN WO200259313-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.64% Indels: 32
RESULT 696
ID ACC49343 standard; cDNA; 1097 BP.
DE Human G protein-coupled receptor GCRC-17 encoding cDNA Seq ID NO:39.
PN WO2003023009-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.64% Indels: 32
RESULT 697
ID AAC54977 standard; DNA; 1362 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79743.
PN EF1033405-A2.
PD 06-SEP-2000.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Percent Similarity: 40.66% Conservative: 15
Best Local Similarity: 24.18% Mismatches: 36
Query Match: 13.64% Indels: 18
RESULT 698
ID ADC86246 standard; DNA; 1363 BP.
DE Human GPCR gene SEQ ID NO:699.
PN EF1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.64% Indels: 32
RESULT 699
ID AAS69004 standard; cDNA; 1422 BP.
DE DNA encoding novel human diagnostic protein #4808.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 23.16% Mismatches: 31
Query Match: 13.64% Indels: 26
RESULT 700
ID AAZ37308 standard; DNA; 1499 BP.
DE Arabidopsis Abi4 coding sequence.
PN WO9955840-A1.
PD 04-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 41.94% Conservative: 15
Best Local Similarity: 25.81% Mismatches: 40
Query Match: 13.64% Indels: 14
RESULT 701
ID AAZ37307 standard; DNA; 1500 BP.
DE Arabidopsis Abi4 coding sequence.
PN WO9955840-A1.
PD 04-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 41.94% Conservative: 15
Best Local Similarity: 25.81% Mismatches: 40
Query Match: 13.64% Indels: 14
RESULT 702
ID AAD05663 standard; cDNA; 1500 BP.
DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 4, ABI4 cDNA.
PN WO200136596-A2.
PD 25-MAY-2001.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 41.94% Conservative: 15
Best Local Similarity: 25.81% Mismatches: 40
Query Match: 13.64% Indels: 14
RESULT 703
ID ADD30509 standard; cDNA; 1500 BP.
DE Plant yield-related polynucleotide clone G625.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.
Percent Similarity: 41.94% Conservative: 15
Best Local Similarity: 25.81% Mismatches: 40
Query Match: 13.64% Indels: 14
RESULT 704
ID ADI43922 standard; DNA; 1500 BP.

DE Plant transcription factor related polynucleotide #1550.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEG-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAR-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROWN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Percent Similarity: 41.94%
Best Local Similarity: 25.81%
Query Match: 13.64%
Conservative: 15
Mismatches: 40
Indels: 14
RESULT 705
ID AAL61329 standard; cDNA; 1668 BP.
DE Human polynucleotide SEQ ID NO 5318.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.35%
Best Local Similarity: 25.88%
Query Match: 13.64%
Conservative: 14
Mismatches: 29
Indels: 20
RESULT 706
ID ADJ67311 standard; DNA; 1851 BP.
DE Human ovarian specific gene SEQ ID NO:25.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.60%
Best Local Similarity: 29.82%
Query Match: 13.64%
Conservative: 5
Mismatches: 23
Indels: 12
RESULT 707
ID ADJ67492 standard; DNA; 1851 BP.
DE Human ovarian specific gene SEQ ID NO:206.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.60%
Best Local Similarity: 29.82%
Query Match: 13.64%
Conservative: 5
Mismatches: 23
Indels: 12
RESULT 708
ID ADB62669 standard; cDNA; 2317 BP.
DE Human cDNA encoding clone LIVER20013890.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 38.89%
Best Local Similarity: 25.00%
Query Match: 13.64%
Conservative: 10
Mismatches: 22
Indels: 8
RESULT 709
ID ADK65983 standard; DNA; 2832 BP.
DE Rice NADPH-oxidase coding sequence SEQ ID NO: 3.
PN WO2004009820-A1.
PD 29-JAN-2004.
PA (BADI-) BASF PLANT SCI GMBH.
Percent Similarity: 48.72%
Best Local Similarity: 29.49%
Query Match: 13.64%
Conservative: 15
Mismatches: 27
Indels: 13
RESULT 710
ID ABL65433 standard; DNA; 3153 BP.
DE Lung cancer related gene sequence SEQ ID NO:3770.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.35%
Best Local Similarity: 31.76%
Query Match: 13.64%
Conservative: 37
Mismatches: 12
Indels: 12
RESULT 711
ID ADK14130 standard; cDNA; 3153 BP.
DE Human autoimmune disorder gene #34.
PN US2003228617-A1.
PD 11-DEC-2003.
PA (UYVA-) UNIV VANDERBILT.
Percent Similarity: 42.35%
Best Local Similarity: 31.76%
Query Match: 13.64%
Conservative: 9
Mismatches: 37
Indels: 12
RESULT 712
ID AAT62360 standard; cDNA; 3214 BP.
DE Human origin of replication complex ORC1 gene.
PN WO9840977-A1.
PD 19-DEC-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (REGC-) UNIV CALIFORNIA.
Percent Similarity: 42.35%
Best Local Similarity: 31.76%
Query Match: 13.64%
Conservative: 9
Mismatches: 37
Indels: 12
RESULT 713
ID AAT73287 standard; cDNA; 3214 BP.
DE Human origin of replication complex protein 1 gene.
PN US5614618-A.
PD 25-MAR-1997.
PA (REGC-) UNIV CALIFORNIA.
PA (COLD-) COLD SPRING HARBOR LAB.
Percent Similarity: 42.35%
Best Local Similarity: 31.76%
Query Match: 13.64%
Conservative: 9
Mismatches: 37
Indels: 12
RESULT 714
ID ADB63192 standard; cDNA; 3231 BP.
DE Human cDNA encoding clone SPLEN20111450.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 38.89%
Best Local Similarity: 25.00%
Query Match: 13.64%
Conservative: 10
Mismatches: 22
Indels: 22
RESULT 715
ID AAH54495 standard; DNA; 3504 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3859.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX-) GLAXO GROUP LTD.
Percent Similarity: 44.16%
Best Local Similarity: 28.57%
Query Match: 13.64%
Conservative: 12
Mismatches: 35
Indels: 8
RESULT 716
ID ADM67075 standard; DNA; 4152 BP.
DE Murine adipocyte specific DNA SeqID 210.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Percent Similarity: 41.94%
Best Local Similarity: 24.73%
Query Match: 13.64%
Conservative: 16
Mismatches: 46
Indels: 8
RESULT 717
ID AAS30131 standard; DNA; 4861 BP.
DE Human lung antigen genomic DNA #201.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 41.94%
Best Local Similarity: 30.65%
Query Match: 13.64%
Conservative: 7
Mismatches: 24
Indels: 12
RESULT 718
ID ADB33468 standard; DNA; 4861 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 395.
PN US2003054368-A1.

PA (HECH/) HECHT R I.
PA (PELL/) PELLEYMOUNTER M A.
PA (TOOM/) TOOMBS C F. 47.83% Conservative: 12
Percent Similarity: 30.43% Mismatches: 27
Query Match: 13.53% Indels: 9
RESULT 734
ID ACH72436 standard; DNA; 584 BP.
DE Human genome derived single exon probe #5631.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K. 52.17% Conservative: 5
Percent Similarity: 41.30% Mismatches: 11
Best Local Similarity: 13.53% Indels: 11
Query Match:
RESULT 735
ID AAF08953 standard; cDNA; 633 BP.
DE Fusarium venenatum EST SEQ ID NO:1476.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 40.32% Conservative: 10
Best Local Similarity: 24.19% Mismatches: 12
Query Match: 13.53% Indels: 25
RESULT 736
ID ACD93676 standard; cDNA; 757 BP.
DE Human colon cancer cell expressed cDNA #2088.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Percent Similarity: 43.04% Conservative: 10
Best Local Similarity: 30.38% Mismatches: 36
Query Match: 13.53% Indels: 9
RESULT 737
ID ADB06389 standard; DNA; 855 BP.
DE Alloiooccus otitis antigenic protein encoding DNA SEQ ID NO:329.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02% Conservative: 14
Best Local Similarity: 26.74% Mismatches: 34
Query Match: 13.53% Indels: 15
RESULT 738
ID ADB06387 standard; DNA; 855 BP.
DE Alloiooccus otitis antigenic protein encoding DNA SEQ ID NO:327.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02% Conservative: 14
Best Local Similarity: 26.74% Mismatches: 34
Query Match: 13.53% Indels: 15
RESULT 739
ID ADB06395 standard; DNA; 855 BP.
DE Alloiooccus otitis antigenic protein encoding DNA SEQ ID NO:335.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02% Conservative: 14
Best Local Similarity: 26.74% Mismatches: 34
Query Match: 13.53% Indels: 15
RESULT 740
ID ADB06391 standard; DNA; 855 BP.
DE Alloiooccus otitis antigenic protein encoding DNA SEQ ID NO:331.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02% Conservative: 14
Best Local Similarity: 26.74% Mismatches: 34
Query Match: 13.53% Indels: 15

Query Match: 13.53% Indels: 15
RESULT 741
ID ADB06393 standard; DNA; 855 BP.
DE Alloiooccus otitis antigenic protein encoding DNA SEQ ID NO:333.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02% Conservative: 14
Best Local Similarity: 26.74% Mismatches: 34
Query Match: 13.53% Indels: 15
RESULT 742
ID ADB69278 standard; DNA; 984 BP.
DE C. neoformans coding sequence with introns SEQ ID NO:1044.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.50% Conservative: 10
Best Local Similarity: 25.00% Mismatches: 29
Query Match: 13.53% Indels: 21
RESULT 743
ID ABS63259 standard; cDNA; 1140 BP.
DE High level promoter polynucleotide #6.
PN WO200261098-A2.
PD 08-AUG-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Percent Similarity: 42.17% Conservative: 13
Best Local Similarity: 26.51% Mismatches: 41
Query Match: 13.53% Indels: 7
RESULT 744
ID ABZ40196 standard; DNA; 1191 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 4981.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 50.98% Conservative: 8
Best Local Similarity: 35.29% Mismatches: 24
Query Match: 13.53% Indels: 1
RESULT 745
ID ABZ40187 standard; DNA; 1215 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 4963.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 50.98% Conservative: 8
Best Local Similarity: 35.29% Mismatches: 24
Query Match: 13.53% Indels: 1
RESULT 746
ID ABL02893 standard; cDNA; 1379 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3161.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.79% Conservative: 9
Best Local Similarity: 28.36% Mismatches: 18
Query Match: 13.53% Indels: 21
RESULT 747
ID AAZ52575 standard; cDNA; 1458 BP.
DE Human secreted protein clone yk143_1 nucleotide sequence SEQ ID NO:201.
PN WO9958642-A2.
PD 18-NOV-1999.
PA (GENY) GENETICS INST INC.
Percent Similarity: 40.57% Conservative: 13
Best Local Similarity: 28.30% Mismatches: 30
Query Match: 13.53% Indels: 33
RESULT 748
ID ABL92621 standard; DNA; 1599 BP.
DE Chlamydia trachomatis DNA sequence SEQ ID NO:414.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 47.50% Conservative: 4
Best Local Similarity: 37.50% Mismatches: 10
Query Match: 13.53% Indels: 11

RESULT 749					
ID	ADAS2961 standard; cDNA; 2279 BP.				
DE	Human coding sequence, SEQ ID 529.				
PN	EP1293569-A2.				
PD	19-MAR-2003.				
PA	(HELI-) HELIX RES INST.				
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.				
Percent Similarity:	45.33%	Conservative:	9		
Best Local Similarity:	33.33%	Mismatches:	26		
Query Match:	13.53%	Indels:	15		
RESULT 750					
ID	ASR70444 standard; cDNA; 2409 BP.				
DE	Human bone remodelling gene #101.				
PN	US6426186-B1.				
PD	30-JUL-2002.				
PA	(INCY-) INCYTE GENOMICS INC.				
Percent Similarity:	38.16%	Conservative:	9		
Best Local Similarity:	26.32%	Mismatches:	36		
Query Match:	13.53%	Indels:	11		
RESULT 751					
ID	ADB62997 standard; cDNA; 2612 BP.				
DE	Human cDNA encoding clone PROST20082430.				
PN	EP1308459-A2.				
PD	07-MAY-2003.				
PA	(HELI-) HELIX RES INST.				
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.				
Percent Similarity:	38.82%	Conservative:	5		
Best Local Similarity:	32.94%	Mismatches:	30		
Query Match:	13.53%	Indels:	22		
RESULT 752					
ID	AAT12999 standard; cDNA to mRNA; 2982 BP.				
DE	Nitrate reductase coding sequence.				
PN	JF08023978-A.				
PD	30-JAN-1996.				
PA	(TOYW) TOYOTA CHUO KENKYUSHO KK.				
PA	(TOYT) TOYOTA JIDOSHA KK.				
Percent Similarity:	46.25%	Conservative:	14		
Best Local Similarity:	28.75%	Mismatches:	27		
Query Match:	13.53%	Indels:	16		
RESULT 753					
ID	ADB68917 standard; DNA; 2984 BP.				
DE	C. neoformans genomic DNA sequence SEQ ID NO:44.				
PN	WO2003052076-A2.				
PD	26-JUN-2003.				
PA	(ELIT-) ELITRA PHARM INC.				
Percent Similarity:	37.50%	Conservative:	10		
Best Local Similarity:	25.00%	Mismatches:	29		
Query Match:	13.53%	Indels:	21		
RESULT 754					
ID	ADB68954 standard; DNA; 3147 BP.				
DE	C. neoformans genomic DNA sequence SEQ ID NO:81.				
PN	WO2003052076-A2.				
PD	26-JUN-2003.				
PA	(ELIT-) ELITRA PHARM INC.				
Percent Similarity:	37.50%	Conservative:	10		
Best Local Similarity:	25.00%	Mismatches:	29		
Query Match:	13.53%	Indels:	21		
RESULT 755					
ID	ABL02892 standard; cDNA; 3563 BP.				
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 3158.				
PN	WO200171042-A2.				
PD	27-SEP-2001.				
PA	(PEKE) PE CORP NY.				
Percent Similarity:	41.79%	Conservative:	9		
Best Local Similarity:	23.36%	Mismatches:	18		
Query Match:	13.53%	Indels:	21		
RESULT 756					
ID	ABL25888 standard; DNA; 4282 BP.				
DE	Drosophila melanogaster genomic polynucleotide SEQ ID NO 29137.				
PN	WO200171042-A2.				
PD	27-SEP-2001.				
PA	(PEKE) PE CORP NY.				
Percent Similarity:	41.79%	Conservative:	9		

Best Local Similarity:	28.36%	Mismatches:	18
Query Match:	13.53%	Indels:	21
RESULT 757			
ID	ADN95876 standard; DNA; 5449 BP.		
DE	Human BEC/LEC-related gene sequence SeqID800.		
FN	WO2003080640-A1.		
PD	02-OCT-2003.		
PA	(LUDW-) LUDWIG INST CANCER RES.		
PA	(LICN) LICENTIA LTD.		
Percent Similarity:	40.62%	Conservative:	10
Best Local Similarity:	30.21%	Mismatches:	32
Query Match:	13.53%	Indels:	25
RESULT 758			
ID	AAU03406 standard; DNA; 7809 BP.		
DE	Human reproductive system related antigen DNA SEQ ID NO: 6094.		
FN	WO200155320-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	40.32%	Conservative:	6
Best Local Similarity:	30.65%	Mismatches:	24
Query Match:	13.53%	Indels:	13
RESULT 759			
ID	ABA15724 standard; DNA; 7809 BP.		
DE	Human nervous system related polynucleotide SEQ ID NO 8055.		
FN	WO200159063-A2.		
PD	16-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	40.32%	Conservative:	6
Best Local Similarity:	30.65%	Mismatches:	24
Query Match:	13.53%	Indels:	13
RESULT 760			
ID	AAW70608 standard; cDNA; 9202 BP.		
DE	VISNA sheep lentivirus genome.		
FN	FR2586427-A.		
PD	27-FEB-1987.		
PA	(INSP) INST PASTEUR.		
Percent Similarity:	50.00%	Conservative:	11
Best Local Similarity:	32.81%	Mismatches:	16
Query Match:	13.53%	Indels:	16
RESULT 761			
ID	AAU05933 standard; DNA; 15514 BP.		
DE	Human reproductive system related antigen DNA SEQ ID NO: 8621.		
FN	WO200155320-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	44.58%	Conservative:	12
Best Local Similarity:	30.12%	Mismatches:	27
Query Match:	13.53%	Indels:	19
RESULT 762			
ID	ABL98497 standard; DNA; 15514 BP.		
DE	Human testicular antigen encoding DNA fragment SEQ ID NO: 3149.		
FN	WO200155317-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	44.58%	Conservative:	12
Best Local Similarity:	30.12%	Mismatches:	27
Query Match:	13.53%	Indels:	19
RESULT 763			
ID	AAU05934 standard; DNA; 15517 BP.		
DE	Human reproductive system related antigen DNA SEQ ID NO: 8622.		
FN	WO200155320-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	44.58%	Conservative:	12
Best Local Similarity:	30.12%	Mismatches:	27
Query Match:	13.53%	Indels:	19
RESULT 764			
ID	ABL98498 standard; DNA; 15517 BP.		
DE	Human testicular antigen encoding DNA fragment SEQ ID NO: 3150.		
FN	WO200155317-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	44.58%	Conservative:	12
Best Local Similarity:	30.12%	Mismatches:	27
Query Match:	13.53%	Indels:	19
RESULT 765			
ID	ABL98499 standard; DNA; 15517 BP.		
DE	Human testicular antigen encoding DNA fragment SEQ ID NO: 3150.		
FN	WO200155317-A2.		
PD	02-AUG-2001.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity:	44.58%	Conservative:	12
Best Local Similarity:	30.12%	Mismatches:	27
Query Match:	13.53%	Indels:	19

Best Local Similarity: 30.12% Mismatches: 27
Query Match: 13.53% Indels: 19
RESULT 765
ID AAL05935 standard; DNA; 15518 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8623.
PN WO200153320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.58%
Best Local Similarity: 30.12%
Mismatches: 27
Query Match: 13.53% Indels: 19
RESULT 766
ID ABL98499 standard; DNA; 15518 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3151.
PN WO200153317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.58%
Best Local Similarity: 30.12%
Mismatches: 27
Query Match: 13.53% Indels: 19
RESULT 767
ID AAL35910 standard; DNA; 21833 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2275.
PN WO200153367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.44%
Best Local Similarity: 31.11%
Mismatches: 27
Query Match: 13.53% Indels: 23
RESULT 768
ID ABX5898 standard; cDNA; 21833 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1242.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BAPASH S C.
Percent Similarity: 44.44%
Best Local Similarity: 31.11%
Mismatches: 27
Query Match: 13.53% Indels: 23
RESULT 769
ID ADJ29648 standard; DNA; 21833 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2275.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.44%
Best Local Similarity: 31.11%
Mismatches: 27
Query Match: 13.53% Indels: 23
RESULT 770
ID ABA82622 standard; DNA; 33769 BP.
DE Human HBM gene region b527d12-h_contig308G.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 52.17%
Best Local Similarity: 41.30%
Mismatches: 11
Query Match: 13.53% Indels: 11
RESULT 771
ID ABK22781 standard; cDNA; 33769 BP.
DE Human high bone mass (HBM) polynucleotide clone #4.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Percent Similarity: 52.17%
Best Local Similarity: 41.30%
Mismatches: 11
Query Match: 13.53% Indels: 11
RESULT 772
ID ACC45363 standard; DNA; 33769 BP.
DE Human HBM gene fragment #4.
PN WO200292764-A2.
PD 21-NOV-2002.

PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Percent Similarity: 52.17%
Best Local Similarity: 41.30%
Mismatches: 11
Query Match: 13.53% Indels: 11
RESULT 773
ID ADB98063 standard; DNA; 33769 BP.
DE HBM-related clone contig b527d12-h contig308G.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Percent Similarity: 52.17%
Best Local Similarity: 41.30%
Mismatches: 11
Query Match: 13.53% Indels: 11
RESULT 774
ID ADE82432 standard; DNA; 33769 BP.
DE Human DNA sequence related to the invention #4.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Percent Similarity: 52.17%
Best Local Similarity: 41.30%
Mismatches: 11
Query Match: 13.53% Indels: 11
RESULT 775
ID ABX13172 standard; DNA; 65464 BP.
DE Human gene encoding a Noelin-1-like secreted protein.
PN US2002173459-A1.
PD 21-NOV-2002.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.02%
Best Local Similarity: 29.27%
Mismatches: 37
Query Match: 13.53% Indels: 13
RESULT 776
ID ADL15049 standard; DNA; 77781 BP.
DE Human melanoma associated MAGE-like DNA for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Percent Similarity: 48.05%
Best Local Similarity: 35.06%
Mismatches: 14
Query Match: 13.53% Indels: 14
RESULT 777
Percent Similarity: 40.00%
Best Local Similarity: 27.00%
Mismatches: 13
Query Match: 13.53% Indels: 30
RESULT 778
Percent Similarity: 40.00%
Best Local Similarity: 27.00%
Mismatches: 13
Query Match: 13.53% Indels: 30
RESULT 779
Percent Similarity: 40.00%
Best Local Similarity: 27.00%
Mismatches: 13
Query Match: 13.53% Indels: 30
RESULT 780
Percent Similarity: 40.00%
Best Local Similarity: 27.00%
Mismatches: 13
Query Match: 13.53% Indels: 30
RESULT 781
ID ADB12064 standard; DNA; 1754382 BP.
DE Alloiooccus otitis entire genome sequence SEQ ID NO: 6651.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 43.02%
Best Local Similarity: 26.74%
Mismatches: 15
Query Match: 13.53% Indels: 15
RESULT 782
Percent Similarity: 48.15%
Best Local Similarity: 35.19%
Mismatches: 7
Query Match: 13.53% Indels: 9
RESULT 783

Percent Similarity: 40.00% Conservative: 13
 Best Local Similarity: 27.00% Mismatches: 30
 Query Match: 13.53% Indels: 30
 RESULT 784
 ID ADL13813 standard; DNA; 179651 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #345.
 PN W02003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 40.26% Conservative: 10
 Best Local Similarity: 27.27% Mismatches: 37
 Query Match: 13.53% Indels: 9
 RESULT 785
 ID ABL71216 standard; cDNA; 280 BP.
 DE Corn tassal-derived polynucleotide (cdps) SEQ ID NO:590.
 PN US2001051335-A1.
 PD 13-DEC-2001.
 PA (LALG/) LALGUDI R V.
 PA (ITOL/) ITO L Y.
 PA (SHER/) SHERMAN B K.
 Percent Similarity: 53.70% Conservative: 10
 Best Local Similarity: 35.19% Mismatches: 21
 Query Match: 13.42% Indels: 4
 RESULT 786
 ID ADQ04607 standard; DNA; 294 BP.
 DE Maize homeobox transcription factor seqid 1453.
 PN US2004123339-A1.
 PD 24-JUN-2004.
 PA (CONN/) CONNER T W.
 PA (HECK/) HECK G R.
 PA (LIU/) LIU J.
 Percent Similarity: 43.48% Conservative: 12
 Best Local Similarity: 26.09% Mismatches: 23
 Query Match: 13.42% Indels: 16
 RESULT 787
 ID AAI83630 standard; cDNA; 425 BP.
 DE Human polynucleotide SEQ ID NO 3690.
 PN W0200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 43.75% Conservative: 3
 Best Local Similarity: 37.50% Mismatches: 13
 Query Match: 13.42% Indels: 14
 RESULT 788
 ID AAH10743 standard; cDNA; 595 BP.
 DE Human cDNA clone (3'-primer) SEQ ID NO:7578.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 44.78% Conservative: 6
 Best Local Similarity: 35.82% Mismatches: 19
 Query Match: 13.42% Indels: 18
 RESULT 789
 ID AAS26287 standard; cDNA; 889 BP.
 DE Human cDNA encoding a novel secreted protein, Seq ID 466.
 PN W0200155322-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 44.30% Conservative: 11
 Best Local Similarity: 30.38% Mismatches: 24
 Query Match: 13.42% Indels: 20
 RESULT 790
 ID ABX73628 standard; DNA; 889 BP.
 DE Human novel polynucleotide #456.
 PN US2002132753-A1.
 PD 19-SEP-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Percent Similarity: 44.30% Conservative: 11
 Best Local Similarity: 30.38% Mismatches: 24
 Query Match: 13.42% Indels: 20
 RESULT 791

ID AAK79093 standard; DNA; 988 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33905.
 PN W0200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 44.29% Conservative: 8
 Best Local Similarity: 32.86% Mismatches: 25
 Query Match: 13.42% Indels: 14
 RESULT 792
 ID ABQ14964 standard; DNA; 1082 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1555.
 PN W0200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 56.10% Conservative: 9
 Best Local Similarity: 34.15% Mismatches: 10
 Query Match: 13.42% Indels: 8
 RESULT 793
 ID ABQ14965 standard; DNA; 1082 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1556.
 PN W0200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 56.10% Conservative: 9
 Best Local Similarity: 34.15% Mismatches: 10
 Query Match: 13.42% Indels: 8
 RESULT 794
 ID AAD37784 standard; DNA; 1588 BP.
 DE Extended sequence for mouse IMX5_49.
 PN W0200231116-A2.
 PD 18-APR-2002.
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 Percent Similarity: 46.25% Conservative: 14
 Best Local Similarity: 28.75% Mismatches: 32
 Query Match: 13.42% Indels: 11
 RESULT 795
 ID ADE61223 standard; DNA; 1789 BP.
 DE Human gene U35246, SEQ ID NO 7141.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Percent Similarity: 38.37% Conservative: 9
 Best Local Similarity: 27.91% Mismatches: 41
 Query Match: 13.42% Indels: 12
 RESULT 796
 ID AAH15925 standard; cDNA; 1922 BP.
 DE Human cDNA sequence SEQ ID NO:14495.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 44.78% Conservative: 6
 Best Local Similarity: 35.82% Mismatches: 19
 Query Match: 13.42% Indels: 18
 RESULT 797
 ID ADD67219 standard; DNA; 2197 BP.
 DE Corn Ap1-like (ZM-MADS PRO1) promoter sequence.
 PN W02003078590-A2.
 PD 25-SEP-2003.
 PA (PION-) PIONEER HI-BRED INT INC.
 Percent Similarity: 41.05% Conservative: 13
 Best Local Similarity: 27.37% Mismatches: 38
 Query Match: 13.42% Indels: 19
 RESULT 798
 ID AAT08552 standard; cDNA; 2336 BP.
 DE Oncogene R-ras mutant cDNA (exon 1, intron A).
 PN W0953223-A1.
 PD 30-NOV-1995.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Percent Similarity: 39.33% Conservative: 9
 Best Local Similarity: 29.21% Mismatches: 38
 Query Match: 13.42% Indels: 17
 RESULT 799

ID ABR95766 standard; DNA; 2336 BP.
DE Gene #2264 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 39.33% Conservative: 9
Best Local Similarity: 29.21% Mismatches: 38
Query Match: 13.42% Indels: 17
RESULT 800
ID ABL25984 standard; DNA; 2376 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29425.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.27% Conservative: 8
Best Local Similarity: 28.40% Mismatches: 30
Query Match: 13.42% Indels: 20
RESULT 801
ID AAD08494 standard; cDNA; 2437 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HKABW11, SEQ ID NO:17.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 40.45% Conservative: 11
Best Local Similarity: 28.09% Mismatches: 29
Query Match: 13.42% Indels: 24
RESULT 802
ID AAD08514 standard; cDNA; 2755 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HKABW11, SEQ ID NO:37.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 40.45% Conservative: 11
Best Local Similarity: 28.09% Mismatches: 29
Query Match: 13.42% Indels: 24
RESULT 803
ID AAH17443 standard; cDNA; 2825 BP.
DE Human cDNA sequence SEQ ID NO:16894.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 42.88% Conservative: 13
Best Local Similarity: 27.38% Mismatches: 32
Query Match: 13.42% Indels: 16
RESULT 804
ID AAS81149 standard; cDNA; 2948 BP.
DE DNA encoding novel human diagnostic protein #16953.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.53% Conservative: 13
Best Local Similarity: 28.24% Mismatches: 26
Query Match: 13.42% Indels: 22
RESULT 805
ID AAZ94068 standard; DNA; 3054 BP.
DE Pneumocystis carinii major surface glycoprotein gene HMSG33.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 50.60% Conservative: 18
Best Local Similarity: 28.92% Mismatches: 25
Query Match: 13.42% Indels: 16
RESULT 806
ID AAZ94069 standard; DNA; 3072 BP.
DE Pneumocystis carinii major surface glycoprotein gene HMSG35.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 50.60% Conservative: 18
Best Local Similarity: 28.92% Mismatches: 25
Query Match: 13.42% Indels: 16
RESULT 807
ID AAZ94066 standard; DNA; 3084 BP.
DE Pneumocystis carinii major surface glycoprotein gene HMSG14.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 50.60% Conservative: 18
Best Local Similarity: 28.92% Mismatches: 25
Query Match: 13.42% Indels: 16
RESULT 808
ID ADM66974 standard; DNA; 3122 BP.
DE Murine adipocyte specific DNA SeqID 109.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Percent Similarity: 46.25% Conservative: 14
Best Local Similarity: 28.75% Mismatches: 32
Query Match: 13.42% Indels: 11
RESULT 809
ID ADO35561 standard; DNA; 3158 BP.
DE Novel mouse gene sequence #234.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 40.58% Conservative: 7
Best Local Similarity: 30.43% Mismatches: 23
Query Match: 13.42% Indels: 18
RESULT 810
ID ABT16642 standard; DNA; 3542 BP.
DE Human bcl-2 gene SEQ ID NO 4.
PN WO200299090-A1.
PD 12-DEC-2002.
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
Percent Similarity: 40.45% Conservative: 11
Best Local Similarity: 28.09% Mismatches: 29
Query Match: 13.42% Indels: 24
RESULT 811
ID ADP84427 standard; DNA; 3591 BP.
DE Human breast-specific protein coding sequence #26.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.37% Conservative: 9
Best Local Similarity: 28.28% Mismatches: 33
Query Match: 13.42% Indels: 29
RESULT 812
ID ACH04172 standard; cDNA; 3717 BP.
DE Human cDNA differentially expressed in lung cancer #377.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Percent Similarity: 44.19% Conservative: 12
Best Local Similarity: 30.23% Mismatches: 38
Query Match: 13.42% Indels: 10
RESULT 813
ID ABL06676 standard; cDNA; 4230 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14510.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.27% Conservative: 8
Best Local Similarity: 28.40% Mismatches: 30
Query Match: 13.42% Indels: 20
RESULT 814
ID ADP07683 standard; DNA; 4355 BP.
DE Human secreted protein encoding DNA, seq id 166.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.05% Conservative: 12
Best Local Similarity: 29.76% Mismatches: 25
Query Match: 13.42% Indels: 22
RESULT 815
ID ABL06694 standard; cDNA; 5069 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14564.

PA (HARD) HARVARD COLLEGE.
Percent Similarity: 40.91% Conservative: 11
Best Local Similarity: 28.41% Mismatches: 33
Query Match: 13.42% Indels: 19
RESULT 832
ID ADH69102 standard; DNA; 10372 BP.
DE HIV vaccine V3 DNA.
PN US2003220276-A1.
PD 27-NOV-2003.
PA (NARA/) NARAYAN O.
Percent Similarity: 40.91% Conservative: 11
Best Local Similarity: 28.41% Mismatches: 33
Query Match: 13.42% Indels: 19
RESULT 833
ID ADK14025 standard; DNA; 10535 BP.
DE SLV genomic DNA.
PN US6712612-B1.
PD 30-MAR-2004.
PA (GENE-) GENESECURE LLC.
Percent Similarity: 40.91% Conservative: 11
Best Local Similarity: 28.41% Mismatches: 33
Query Match: 13.42% Indels: 19
RESULT 834
ID ACB13393 standard; cDNA; 15382 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 64.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.04% Conservative: 8
Best Local Similarity: 32.91% Mismatches: 36
Query Match: 13.42% Indels: 10
RESULT 835
ID ABA16242 standard; DNA; 16818 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8573.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 60.00% Conservative: 6
Best Local Similarity: 42.86% Mismatches: 14
Query Match: 13.42% Indels: 0
RESULT 836
ID ABA15470 standard; DNA; 16818 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7801.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 60.00% Conservative: 6
Best Local Similarity: 42.86% Mismatches: 14
Query Match: 13.42% Indels: 0
RESULT 837
ID ABA18914 standard; DNA; 16818 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11245.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 60.00% Conservative: 6
Best Local Similarity: 42.86% Mismatches: 14
Query Match: 13.42% Indels: 0
RESULT 838
ID ADO79404 standard; DNA; 89900 BP.
DE DPF3 region, SEQ ID 3.
PN WO2004047514-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Percent Similarity: 38.38% Conservative: 16
Best Local Similarity: 22.22% Mismatches: 37
Query Match: 13.42% Indels: 24
RESULT 839
ID ADA03023 standard; DNA; 96597 BP.
DE Mouse Mbnl carcinoma associated gene, SEQ ID NO:1541.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 36.00% Conservative: 7
Best Local Similarity: 26.67% Mismatches: 14
Query Match: 13.42% Indels: 34
RESULT 840
ID ADB72761 standard; DNA; 96597 BP.
DE Mouse Mbnl gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 36.00% Conservative: 7
Best Local Similarity: 26.67% Mismatches: 14
Query Match: 13.42% Indels: 34
RESULT 841
ID ADC85503 standard; DNA; 96597 BP.
DE Mouse Mbnl genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 36.00% Conservative: 7
Best Local Similarity: 26.67% Mismatches: 14
Query Match: 13.42% Indels: 34
RESULT 842
ID ADM74618 standard; DNA; 96597 BP.
DE Murine carcinoma associated (CA) nucleic acid #145.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
Percent Similarity: 36.00% Conservative: 7
Best Local Similarity: 26.67% Mismatches: 14
Query Match: 13.42% Indels: 34
RESULT 843
ID AAA81464 standard; DNA; 102634 BP.
DE N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Percent Similarity: 34.94% Conservative: 9
Best Local Similarity: 24.10% Mismatches: 34
Query Match: 13.42% Indels: 20
RESULT 844
Percent Similarity: 41.67% Conservative: 9
Best Local Similarity: 29.17% Mismatches: 24
Query Match: 13.42% Indels: 18
RESULT 845
Percent Similarity: 34.94% Conservative: 9
Best Local Similarity: 24.10% Mismatches: 34
Query Match: 13.42% Indels: 20
RESULT 846
Percent Similarity: 45.56% Conservative: 20
Best Local Similarity: 23.33% Mismatches: 41
Query Match: 13.42% Indels: 8
RESULT 847
ID ABT10748 standard; cDNA; 121600 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 882.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.20% Conservative: 7
Best Local Similarity: 30.34% Mismatches: 22
Query Match: 13.42% Indels: 33
RESULT 848
ID ADQ18307 standard; DNA; 121600 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1125.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 38.20% Conservative: 7
Best Local Similarity: 30.34% Mismatches: 22
Query Match: 13.42% Indels: 33
RESULT 849
ID AAF21609 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.

PA (CURA-) CURAGEN CORP.
PD 09-NOV-2000.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 34.94%
Best Local Similarity: 24.10%
Query Match: 13.42%
Conservative: 9
Mismatch: 34
Indel: 20

RESULT 850
ID AAX40600 standard; cDNA; 354 BP.
DE Human secreted protein 5' EST SEQ ID NO: 200.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Percent Similarity: 48.57%
Best Local Similarity: 13.31%
Query Match: 13.31%
Conservative: 14
Mismatch: 27
Indel: 9

RESULT 851
ID ADD26879 standard; DNA; 429 BP.
DE Human adipocyte Selected Interacting Domain (SID) prey protein DNA #266.
PD 14-NOV-2002.
PA (LYNX-) LYNX THERAPEUTICS INC.
Percent Similarity: 44.64%
Best Local Similarity: 32.14%
Query Match: 13.31%
Conservative: 7
Mismatch: 28
Indel: 3

RESULT 852
ID ADO16890 standard; DNA; 429 BP.
DE Tobacco budworm voltage gated calcium channel subunit DNA seqID 3.
PD 27-MAY-2004.
PA (FMCC-) FMC CORP.
Percent Similarity: 51.06%
Best Local Similarity: 36.17%
Query Match: 13.31%
Conservative: 7
Mismatch: 22
Indel: 1

RESULT 853
ID ACH45879 standard; cDNA; 472 BP.
DE Human foetal brain cDNA #6604.
PD 17-APR-2003.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 40.20%
Best Local Similarity: 33.33%
Query Match: 13.31%
Conservative: 7
Mismatch: 33
Indel: 28

RESULT 854
ID ACH79523 standard; DNA; 570 BP.
DE Human genome derived single exon probe #12718.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 40.59%
Best Local Similarity: 28.71%
Query Match: 13.31%
Conservative: 12
Mismatch: 17
Indel: 43

RESULT 855
ID AAC74694 standard; cDNA; 662 BP.
DE Human ORFX ORF249 polynucleotide sequence SEQ ID NO:497.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 45.95%
Best Local Similarity: 32.43%
Query Match: 13.31%
Conservative: 10
Mismatch: 29
Indel: 11

RESULT 856
ID ABRN25258 standard; cDNA; 662 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:18993.
PD 06-DEC-2001.
PA (UYCH-) UNIV CHINESE HONG KONG.

PA (CURA-) CURAGEN CORP.
Percent Similarity: 45.95%
Best Local Similarity: 32.43%
Query Match: 13.31%
Conservative: 10
Mismatch: 29
Indel: 11

RESULT 857
ID AAH94539 standard; cDNA; 724 BP.
DE Human foetal cDNA, SEQ ID NO: 1226.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 29.41%
Query Match: 13.31%
Conservative: 8
Mismatch: 21
Indel: 43

RESULT 858
ID AAH94153 standard; cDNA; 742 BP.
DE Human foetal cDNA, SEQ ID NO: 682.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.25%
Best Local Similarity: 29.41%
Query Match: 13.31%
Conservative: 8
Mismatch: 21
Indel: 43

RESULT 859
ID AAC75059 standard; cDNA; 756 BP.
DE Human ORFX ORF614 polynucleotide sequence SEQ ID NO:1227.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.43%
Best Local Similarity: 24.24%
Query Match: 13.31%
Conservative: 19
Mismatch: 21
Indel: 35

RESULT 860
ID ABRN24288 standard; cDNA; 756 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:17053.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.43%
Best Local Similarity: 24.24%
Query Match: 13.31%
Conservative: 19
Mismatch: 21
Indel: 35

RESULT 861
ID AAX18432 standard; DNA; 875 BP.
DE P. ginseng ITS1-5.8S-ITS2 DNA sequence.
PD 02-MAR-1999.
PA (UYCH-) UNIV CHINESE HONG KONG.
Percent Similarity: 41.38%
Best Local Similarity: 29.89%
Query Match: 13.31%
Conservative: 10
Mismatch: 34
Indel: 17

RESULT 862
ID AAX18427 standard; DNA; 875 BP.
DE P. ginseng ITS1-5.8S-ITS2 DNA sequence.
PD 02-MAR-1999.
PA (UYCH-) UNIV CHINESE HONG KONG.
Percent Similarity: 41.38%
Best Local Similarity: 29.89%
Query Match: 13.31%
Conservative: 10
Mismatch: 34
Indel: 17

RESULT 863
ID AAD23814 standard; DNA; 875 BP.
DE Panax ginseng G1 rDNA.
PD 30-OCT-2001.
PA (UYCH-) UNIV CHINESE HONG KONG.
Percent Similarity: 41.38%
Best Local Similarity: 29.89%
Query Match: 13.31%
Conservative: 10
Mismatch: 34
Indel: 17

RESULT 864
ID AAD24231 standard; DNA; 875 BP.
DE Alternative version of Panax ginseng ITS1-5.8S-ITS2 rDNA.
PD 30-OCT-2001.
PA (UYCH-) UNIV CHINESE HONG KONG.

Percent Similarity: 41.38% Conservative: 10
Best Local Similarity: 29.8% Mismatches: 34
Query Match: 13.31% Indels: 17
RESULT 865
ID AAD23812 standard; DNA; 875 BP.
DE Panax quinquefolius ITS1-5.8S-ITS2 rDNA.
PN USG309840-B1.
PD 30-OCT-2001.
PA (UYCH-) UNIV CHINESE HONG KONG.
Percent Similarity: 41.38% Conservative: 10
Best Local Similarity: 29.8% Mismatches: 34
Query Match: 13.31% Indels: 17
RESULT 866
ID ADD17963 standard; cDNA; 1061 BP.
DE cDNA (SeqID 2031) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC-) DOW CHEM CO.
Percent Similarity: 46.27% Conservative: 10
Best Local Similarity: 31.34% Mismatches: 26
Query Match: 13.31% Indels: 10
RESULT 867
ID ABL66283 standard; DNA; 2061 BP.
DE Lung cancer related gene sequence SEQ ID NO:4620.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 40.59% Conservative: 12
Best Local Similarity: 28.71% Mismatches: 17
Query Match: 13.31% Indels: 43
RESULT 868
ID AEL67788 standard; DNA; 2061 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6125.
PN WO200094629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 40.59% Conservative: 12
Best Local Similarity: 28.71% Mismatches: 17
Query Match: 13.31% Indels: 43
RESULT 869
ID ADM01874 standard; cDNA; 2175 BP.
DE Human cDNA of the invention SEQ ID NO:559.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 42.17% Conservative: 10
Best Local Similarity: 30.12% Mismatches: 26
Query Match: 13.31% Indels: 22
RESULT 870
ID AAV16525 standard; DNA; 2367 BP.
DE DNA encoding a Bacillus thuringiensis toxin designated 185U2(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO-) MYCOGEN CORP.
Percent Similarity: 50.98% Conservative: 5
Best Local Similarity: 41.18% Mismatches: 10
Query Match: 13.31% Indels: 15
RESULT 871
ID AAX83886 standard; DNA; 2367 BP.
DE Bacillus thuringiensis toxin 185U2(a) encoding DNA.
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO-) MYCOGEN CORP.
Percent Similarity: 50.98% Conservative: 5
Best Local Similarity: 41.18% Mismatches: 10
Query Match: 13.31% Indels: 15
RESULT 872
ID AAV30289 standard; DNA; 2370 BP.
DE Bacillus thuringiensis insecticidal 81F toxin DNA.
PN WO9818932-A2.
PD 07-MAY-1998.
PA (MYCO-) MYCOGEN CORP.

Percent Similarity: 50.98% Conservative: 5
Best Local Similarity: 41.18% Mismatches: 10
Query Match: 13.31% Indels: 15
RESULT 873
ID ABS70375 standard; cDNA; 2497 BP.
DE Human bone remodelling gene #32.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 58.14% Conservative: 8
Best Local Similarity: 39.53% Mismatches: 17
Query Match: 13.31% Indels: 1
RESULT 874
ID ADBG2665 standard; cDNA; 2547 BP.
DE Human cDNA encoding clone LIVER20010510.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 42.17% Conservative: 10
Best Local Similarity: 30.12% Mismatches: 26
Query Match: 13.31% Indels: 22
RESULT 875
ID AAS78235 standard; cDNA; 2663 BP.
DE DNA encoding novel human diagnostic protein #14039.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 47.54% Conservative: 13
Best Local Similarity: 26.23% Mismatches: 31
Query Match: 13.31% Indels: 1
RESULT 876
ID ABZ24008 standard; cDNA; 2703 BP.
DE Human adipose abundant protein (AAP) 2.7 kb form cDNA sequence.
PN WO200296355-A2.
PD 05-DEC-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 45.95% Conservative: 10
Best Local Similarity: 32.43% Mismatches: 29
Query Match: 13.31% Indels: 11
RESULT 877
ID ABZ24026 standard; cDNA; 2703 BP.
DE Human adipose abundant protein (AAP) 2.7 kb form cDNA sequence.
PN WO200297036-A2.
PD 05-DEC-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 45.95% Conservative: 10
Best Local Similarity: 32.43% Mismatches: 29
Query Match: 13.31% Indels: 11
RESULT 878
ID ABL23365 standard; DNA; 2757 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21568.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 38.18% Conservative: 16
Best Local Similarity: 23.64% Mismatches: 41
Query Match: 13.31% Indels: 27
RESULT 879
ID AAZ50165 standard; DNA; 2774 BP.
DE Pichia pastoris Formaldehyde Dehydrogenase 1 (FLD1) gene.
PN WO200001829-A2.
PD 13-JAN-2000.
PA (RESE-) RESEARCH CORP TECHNOLOGIES INC.
Percent Similarity: 54.17% Conservative: 10
Best Local Similarity: 33.93% Mismatches: 13
Query Match: 13.31% Indels: 9
RESULT 880
ID ADQ24874 standard; DNA; 2999 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7694.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Percent Similarity: 45.95% Conservative: 10
Best Local Similarity: 32.43% Mismatches: 29
Query Match: 13.31% Indels: 11
RESULT 881
ID ABL03117 standard; cDNA; 3088 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3833.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.00% Conservative: 10
Best Local Similarity: 27.50% Mismatches: 37
Query Match: 13.31% Indels: 11
RESULT 882
ID ADB69070 standard; DNA; 3651 BP.
DE C. neoformans genomic DNA sequence SEQ ID NO:197.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 45.59% Conservative: 10
Best Local Similarity: 30.88% Mismatches: 30
Query Match: 13.31% Indels: 7
RESULT 883
ID ADO35919 standard; DNA; 3912 BP.
DE Novel mouse gene sequence #592.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 38.81% Conservative: 8
Best Local Similarity: 26.87% Mismatches: 26
Query Match: 13.31% Indels: 15
RESULT 884
ID ADO16892 standard; DNA; 5306 BP.
DE Tobacco budworm voltage gated calcium channel subunit DNA SeqID 5.
PN WO2004044553-A2.
PD 27-MAY-2004.
PA (FMCC) FMC CORP.
Percent Similarity: 51.06% Conservative: 7
Best Local Similarity: 36.17% Mismatches: 22
Query Match: 13.31% Indels: 1
RESULT 885
ID ABL07634 standard; cDNA; 5378 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17384.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.39% Conservative: 14
Best Local Similarity: 27.17% Mismatches: 36
Query Match: 13.31% Indels: 17
RESULT 886
ID ABL23364 standard; DNA; 6313 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21565.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.18% Conservative: 16
Best Local Similarity: 23.64% Mismatches: 41
Query Match: 13.31% Indels: 27
RESULT 887
ID AAK80005 standard; DNA; 6325 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34817.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.28% Conservative: 10
Best Local Similarity: 31.03% Mismatches: 20
Query Match: 13.31% Indels: 10
RESULT 888
ID ADD18777 standard; DNA; 8672 BP.
DE Human disease related protein DNA sequence SeqID208.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Percent Similarity: 48.94% Conservative: 2

Best Local Similarity: 44.68% Mismatches: 17
Query Match: 13.31% Indels: 7
RESULT 889
ID AAD26722 standard; DNA; 9057 BP.
DE Human G-protein coupled receptor 31 (GPR31) gene allelic variant.
PN WO200190124-A2.
PD 29-NOV-2001.
PA (GENA-) GENAISANCE PHARM INC.
Percent Similarity: 40.59% Conservative: 12
Best Local Similarity: 28.71% Mismatches: 17
Query Match: 13.31% Indels: 43
RESULT 890
ID AAD26665 standard; DNA; 9057 BP.
DE Human G-protein coupled receptor 31 (GPR31) gene.
PN WO200190124-A2.
PD 29-NOV-2001.
PA (GENA-) GENAISANCE PHARM INC.
Percent Similarity: 40.59% Conservative: 12
Best Local Similarity: 28.71% Mismatches: 17
Query Match: 13.31% Indels: 43
RESULT 891
ID AAV31271 standard; DNA; 9319 BP.
DE E. coli J96 pathogenicity island contig #85.
PN WO9822575-A2.
PD 28-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYWI-) UNIV WISCONSIN.
Percent Similarity: 39.56% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 30
Query Match: 13.31% Indels: 25
RESULT 892
ID AAL56717 standard; DNA; 17503 BP.
DE Mouse truncated Oct4 promoter gene DNA.
PN WO2003046129-A2.
PD 05-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 32.67% Conservative: 16
Best Local Similarity: 22.00% Mismatches: 32
Query Match: 13.31% Indels: 69
RESULT 893
ID AAD38802 standard; DNA; 17953 BP.
DE Rice RGA8 contig.30Nippon DNA.
PN WO200234927-A2.
PD 02-MAY-2002.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
PA (USDA) US DEPT OF AGRICULTURE.
Percent Similarity: 63.04% Conservative: 10
Best Local Similarity: 41.30% Mismatches: 13
Query Match: 13.31% Indels: 4
RESULT 894
ID AAD62371 standard; DNA; 21784 BP.
DE Human protease gene.
PN US2003129726-A1.
PD 10-JUL-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 42.17% Conservative: 10
Best Local Similarity: 30.12% Mismatches: 26
Query Match: 13.31% Indels: 22
RESULT 895
ID ABX16008 standard; DNA; 21784 BP.
DE Human novel protease gene.
PN US2002142440-A1.
PD 03-OCT-2002.
PA (GANW/) GAN W.
PA (YEJG/) YE J.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E. M.
Percent Similarity: 42.17% Conservative: 10
Best Local Similarity: 30.12% Mismatches: 26
Query Match: 13.31% Indels: 22
RESULT 896
ID AAK77432 standard; DNA; 28091 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32244.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.46% Conservative: 12
Best Local Similarity: 23.96% Mismatches: 48
Query Match: 13.31% Indels: 13
RESULT 897
ID ABA15375 standard; DNA; 28091 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7706.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.46% Conservative: 12
Best Local Similarity: 23.96% Mismatches: 48
Query Match: 13.31% Indels: 13
RESULT 898
ID AAK77434 standard; DNA; 28120 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32246.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.46% Conservative: 12
Best Local Similarity: 23.96% Mismatches: 48
Query Match: 13.31% Indels: 13
RESULT 899
ID ABA15379 standard; DNA; 28120 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7710.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.46% Conservative: 12
Best Local Similarity: 23.96% Mismatches: 48
Query Match: 13.31% Indels: 13
RESULT 900
ID AAS30619 standard; DNA; 31994 BP.
DE DNA encoding novel lung cancer antigen, Seq ID No 71.
PN WO200155300-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.53% Conservative: 12
Best Local Similarity: 28.74% Mismatches: 39
Query Match: 13.31% Indels: 11
RESULT 901
ID AAS28165 standard; DNA; 31994 BP.
DE Genomic sequence #5 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.53% Conservative: 12
Best Local Similarity: 28.74% Mismatches: 39
Query Match: 13.31% Indels: 11
RESULT 902
ID ACA03382 standard; DNA; 31994 BP.
DE DNA encoding human lung cancer antigen HCLCR09.
PN US2002173454-A1.
PD 21-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 42.53% Conservative: 12
Best Local Similarity: 28.74% Mismatches: 39
Query Match: 13.31% Indels: 11
RESULT 903
ID ADB96730 standard; DNA; 31994 BP.
DE Novel lung cancer antigen genomic DNA #1.
PN US2003049703-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.53% Conservative: 12
Best Local Similarity: 28.74% Mismatches: 39
Query Match: 13.31% Indels: 11
RESULT 904
ID ADG41361 standard; DNA; 31994 BP.

DE Human respiratory system associated genomic DNA seq id 599.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.53% Conservative: 12
Best Local Similarity: 28.74% Mismatches: 39
Query Match: 13.31% Indels: 11
RESULT 905
ID ADA02648 standard; DNA; 32874 BP.
DE Human TBX21 carcinoma associated gene, SEQ ID NO:1166.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.06% Conservative: 6
Best Local Similarity: 40.82% Mismatches: 18
Query Match: 13.31% Indels: 5
RESULT 906
ID ADB72386 standard; DNA; 32874 BP.
DE Human TBX21 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.06% Conservative: 6
Best Local Similarity: 40.82% Mismatches: 18
Query Match: 13.31% Indels: 5
RESULT 907
ID ADB95896 standard; DNA; 32874 BP.
DE Human TBX21 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.06% Conservative: 6
Best Local Similarity: 40.82% Mismatches: 18
Query Match: 13.31% Indels: 5
RESULT 908
ID AAA28150 standard; DNA; 41684 BP.
DE Human purH gene genomic DNA sequence.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 909
ID ABK22784 standard; cDNA; 57273 BP.
DE Human high bone mass (HBM) polynucleotide clone #7.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 910
ID ABA82625 standard; DNA; 66933 BP.
DE Human HBM gene region b200e21-h_contig4.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 911
ID ACC45366 standard; DNA; 66933 BP.
DE Human HBM gene fragment #7.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 912
ID ADB98066 standard; DNA; 66933 BP.
DE HBM-related clone contig b200e21-h contig4.
PN WO200292000-A2.


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PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 913
ID ADE82435 standard; DNA; 66933 BP.
DE Human DNA sequence related to the invention #7.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Percent Similarity: 44.00% Conservative: 11
Best Local Similarity: 29.33% Mismatches: 38
Query Match: 13.31% Indels: 4
RESULT 914
ID ADL27149 standard; DNA; 77932 BP.
DE Mouse genomic sequence for mCG9110.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENG/) ENGELHARD E K.
Percent Similarity: 48.94% Conservative: 4
Best Local Similarity: 40.43% Mismatches: 17
Query Match: 13.31% Indels: 7
RESULT 915
ID AAL57703 standard; DNA; 96599 BP.
DE Human prolactin receptor (PRLR) genomic DNA sequence.
PN US2003064383-A1.
PD 03-APR-2003.
PA (MORR/) MORRIS D W.
PA (ENG/) ENGELHARD E K.
Percent Similarity: 35.79% Conservative: 9
Best Local Similarity: 26.32% Mismatches: 28
Query Match: 13.31% Indels: 33
RESULT 916
ID ADA02672 standard; DNA; 96599 BP.
DE Human PRLR carcinoma associated gene, SEQ ID NO:1190.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 35.79% Conservative: 9
Best Local Similarity: 26.32% Mismatches: 28
Query Match: 13.31% Indels: 33
RESULT 917
ID ADB72410 standard; DNA; 96599 BP.
DE Human PRLR gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 35.79% Conservative: 9
Best Local Similarity: 26.32% Mismatches: 28
Query Match: 13.31% Indels: 33
RESULT 918
ID ADE95920 standard; DNA; 96599 BP.
DE Human PRLR gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 35.79% Conservative: 9
Best Local Similarity: 26.32% Mismatches: 28
Query Match: 13.31% Indels: 33
RESULT 919
ID ADQ18925 standard; DNA; 148497 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1744.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 44.26% Conservative: 5
Best Local Similarity: 36.07% Mismatches: 24
Query Match: 13.31% Indels: 10
RESULT 920
ID ABT10718 standard; cDNA; 185371 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 852.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.43% Conservative: 12
Best Local Similarity: 31.31% Mismatches: 39
Query Match: 13.31% Indels: 17
RESULT 921
ID ADP43517 standard; DNA; 347001 BP.
DE Human MAD1-like 1 DNA #7.
PN US2004115650-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 46.25% Conservative: 12
Best Local Similarity: 31.25% Mismatches: 32
Query Match: 13.31% Indels: 11
RESULT 922
ID ABQ81846 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST ) SOC PROD NESTLE SA.
Percent Similarity: 51.85% Conservative: 11
Best Local Similarity: 31.48% Mismatches: 23
Query Match: 13.31% Indels: 3
RESULT 923
ID AAT20689 standard; cDNA to mRNA; 134 BP.
DE Human gene signature HUMG01906.
PN WO9514772-A1.
PD 01-JUN-1995.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
Percent Similarity: 52.38% Conservative: 3
Best Local Similarity: 45.24% Mismatches: 14
Query Match: 13.20% Indels: 6
RESULT 924
ID AAV31227 standard; DNA; 314 BP.
DE E. coli J96 pathogenicity island contig #41.
PN WO9822575-A2.
PD 28-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYWI-) UNIV WISCONSIN.
Percent Similarity: 54.55% Conservative: 3
Best Local Similarity: 45.45% Mismatches: 15
Query Match: 13.20% Indels: 0
RESULT 925
ID ABN95539 standard; DNA; 363 BP.
DE Gene #2037 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 48.00% Conservative: 9
Best Local Similarity: 30.00% Mismatches: 12
Query Match: 13.20% Indels: 14
RESULT 926
ID AAC01286 standard; cDNA; 398 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 1284.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 34
Query Match: 13.20% Indels: 20
RESULT 927
ID ABZ54861 standard; cDNA; 496 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 3974.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORO ) NAT FOOD RES INST MIN AGRIC.
Percent Similarity: 37.50% Conservative: 9

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Best Local Similarity: 27.27% Mismatches: 29
Query Match: 13.20% Indels: 26
RESULT 928
ID AAK62620 standard; cDNA; 508 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:7680.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.62% Conservative: 11
Best Local Similarity: 27.69% Mismatches: 36
Query Match: 13.20% Indels: 0
RESULT 929
ID AAC75489 standard; cDNA; 731 BP.
DE Human ORF1044 polynucleotide sequence SEQ ID NO:2087.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 48.15% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 20
Query Match: 13.20% Indels: 8
RESULT 930
ID ABL19076 standard; cDNA; 731 BP.
DE Human ORF polynucleotide sequence SEQ ID NO:6629.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 48.15% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 20
Query Match: 13.20% Indels: 8
RESULT 931
ID ABZ33722 standard; cDNA; 732 BP.
DE Human colon tumour related cDNA sequence SEQ ID NO:1120.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 932
ID ABD06117 standard; DNA; 765 BP.
DE Pseudomonas aeruginosa polynucleotide #4721.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 46.58% Conservative: 13
Best Local Similarity: 28.77% Mismatches: 31
Query Match: 13.20% Indels: 8
RESULT 933
ID ABL64748 standard; DNA; 871 BP.
DE Lung cancer related gene sequence SEQ ID NO:3085.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 34
Query Match: 13.20% Indels: 20
RESULT 934
ID ABL65387 standard; DNA; 871 BP.
DE Lung cancer related gene sequence SEQ ID NO:3724.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 34
Query Match: 13.20% Indels: 20
RESULT 935
ID ABL69501 standard; DNA; 871 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7838.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 34

Query Match: 13.20% Indels: 20
RESULT 936
ID AD311782 standard; cDNA; 871 BP.
DE Human cDNA #1108.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 34
Query Match: 13.20% Indels: 20
RESULT 937
ID ABZ77954 standard; DNA; 939 BP.
DE Human G protein coupled receptor coding sequence SEQ ID 165.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS BHF.
Percent Similarity: 38.20% Conservative: 14
Best Local Similarity: 22.47% Mismatches: 23
Query Match: 13.20% Indels: 32
RESULT 938
ID AAQ27091 standard; DNA; 1028 BP.
DE XTY26 probe.
PN WO9212262-A1.
PD 23-JUL-1992.
PA (UNIW) UNIV WASHINGTON.
PA (ADEL-) ADELAIDE MEDICAL CENT WOMEN & CHILDREN.
Percent Similarity: 38.03% Conservative: 8
Best Local Similarity: 26.76% Mismatches: 40
Query Match: 13.20% Indels: 4
RESULT 939
ID AAA91542 standard; DNA; 1028 BP.
DE 1.0kb PstI fragment from Fragile X syndrome DNA library.
PN US6242576-B1.
PD 05-JUN-2001.
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 38.03% Conservative: 8
Best Local Similarity: 26.76% Mismatches: 40
Query Match: 13.20% Indels: 4
RESULT 940
ID AAS01347 standard; DNA; 1028 BP.
DE Human Fragile X Syndrome 1.0 kb PstI fragment DNA.
PN US6197500-B1.
PD 06-MAR-2001.
PA (ADEL-) ADELAIDE MEDICAL CENT WOMEN & CHILDREN.
Percent Similarity: 38.03% Conservative: 8
Best Local Similarity: 26.76% Mismatches: 40
Query Match: 13.20% Indels: 4
RESULT 941
ID ABZ33699 standard; cDNA; 1035 BP.
DE Human colon tumour cDNA for Ra12-C884P-PCR2 SEQ ID NO:1084.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 942
ID AAQ2438 standard; cDNA; 1104 BP.
DE CO-029 tumour associated antigen cDNA.
PN EP478146-A.
PD 01-APR-1992.
PA (WIST-) WISTAR INST.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 943
ID AA129498 standard; cDNA; 1104 BP.
DE C884P determined cDNA sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.55% Conservative: 15

Best Local Similarity: 26.60% Mismatches: 26 Indels: 28
Query Match: 13.20%
RESULT 944
ID ABL68522 standard; DNA; 1104 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6859.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 945
ID ABL68254 standard; DNA; 1104 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6591.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 946
ID ABL62378 standard; DNA; 1104 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:715.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 947
ID ABK64537 standard; DNA; 1104 BP.
DE Human benign prostatic hyperplasia gene #432.
PN WO200212440-A2.
PD 14-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 948
ID ABN95845 standard; DNA; 1104 BP.
DE Gene #2343 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 949
ID ABZ33684 standard; cDNA; 1104 BP.
DE Human colon tumour cDNA for clone C884P SEQ ID NO:1052.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 950
ID ADL24798 standard; DNA; 1104 BP.
DE Intestinal epithelium/peyer's patch M cell-associated DNA sequence #187.
PN WO200280852-A2.
PD 17-OCT-2002.
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 951
ID ADN39767 standard; cDNA; 1159 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C139.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 42.55% Conservative: 15

Best Local Similarity: 26.60% Mismatches: 26 Indels: 28
Query Match: 13.20%
RESULT 952
ID ADN04001 standard; cDNA; 1159 BP.
DE Antipsoriatic cDNA sequence #200.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 953
ID AAC35969 standard; DNA; 1205 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 12076.
PN EP1033485-A2.
PD 06-SEP-2000.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.86% Conservative: 14
Best Local Similarity: 27.47% Mismatches: 28
Query Match: 13.20% Indels: 24
RESULT 954
ID AAH33762 standard; cDNA; 1216 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:818.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 955
ID ACC61939 standard; DNA; 1218 BP.
DE Gene sequence #SEQ ID 2660.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Percent Similarity: 52.63% Conservative: 13
Best Local Similarity: 29.82% Mismatches: 22
Query Match: 13.20% Indels: 5
RESULT 956
ID ADK64831 standard; DNA; 1218 BP.
DE Disease treating protein complex-derived gene #1601.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Percent Similarity: 52.63% Conservative: 13
Best Local Similarity: 29.82% Mismatches: 22
Query Match: 13.20% Indels: 5
RESULT 957
ID ADI02511 standard; cDNA; 1248 BP.
DE Human cDNA differentially expressed in the vascular endothelium #52.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR-) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 958
ID ADL12486 standard; cDNA; 1248 BP.
DE Human steroid-induced C3A liver cell cDNA #215.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 959
ID AAC77799 standard; cDNA; 1317 BP.
DE Human cancer associated gene sequence SEQ ID NO:193.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.55% Conservative: 15

Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 960
ID ADA14516 standard; cDNA; 1317 BP.
DE Mouse spermatogenesis related cDNA sequence SEQ ID NO:75.
PN WC2003068969-A1.
PD 21-AUG-2003.
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 40.45% Conservative: 16
Best Local Similarity: 22.47% Mismatches: 37
Query Match: 13.20% Indels: 16
RESULT 961
ID ADP44547 standard; cDNA; 1317 BP.
DE Murine glyceraldehyde 3-phosphate dehydrogenase, spermatogenic cDNA.
PN WC2004050833-A2.
PD 17-JUN-2004.
PA (UYN-) UNIV NORTH CAROLINA.
PA (EDDY/) EDDY P D E M.
Percent Similarity: 40.45% Conservative: 16
Best Local Similarity: 22.47% Mismatches: 37
Query Match: 13.20% Indels: 16
RESULT 962
ID ABD06186 standard; cDNA; 1320 BP.
DE Pseudomonas aeruginosa polynucleotide #4790.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 46.58% Conservative: 13
Best Local Similarity: 28.77% Mismatches: 31
Query Match: 13.20% Indels: 8
RESULT 963
ID ABZ33721 standard; cDNA; 1341 BP.
DE Human colon tumour related cDNA sequence SEQ ID NO:1119.
PN WC200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.55% Conservative: 15
Best Local Similarity: 26.60% Mismatches: 26
Query Match: 13.20% Indels: 28
RESULT 964
ID AA169877 standard; cDNA; 1370 BP.
DE Human protein 17 coding sequence.
PN WC200170784-A1.
PD 27-SEP-2001.
PA (BTOW-) BLOWDOWN GENE DEV INC SHANGHAI.
Percent Similarity: 53.85% Conservative: 11
Best Local Similarity: 25.64% Mismatches: 18
Query Match: 13.20% Indels: 0
RESULT 965
ID ABD06100 standard; cDNA; 1557 BP.
DE Pseudomonas aeruginosa polynucleotide #4704.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 46.58% Conservative: 13
Best Local Similarity: 28.77% Mismatches: 31
Query Match: 13.20% Indels: 8
RESULT 966
ID AAD57511 standard; cDNA; 1718 BP.
DE Human enzyme (ENZM) cDNA #23.
PN WC2003052075-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.46% Conservative: 11
Best Local Similarity: 27.88% Mismatches: 44
Query Match: 13.20% Indels: 20
RESULT 967
ID AA668522 standard; cDNA; 1746 BP.
DE Nucleotide sequence of the human small secreted protein-1.
PN WC9846756-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS.
Percent Similarity: 33.87% Conservative: 10

Best Local Similarity: 25.81% Mismatches: 38
Query Match: 13.20% Indels: 44
RESULT 968
ID ADA71867 standard; cDNA; 2000 BP.
DE Rice gene, SEQ ID 5192.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 38.57% Conservative: 5
Best Local Similarity: 31.43% Mismatches: 29
Query Match: 13.20% Indels: 14
RESULT 969
ID ADC08459 standard; cDNA; 2000 BP.
DE Rice DNA sequence Seq ID764 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 40.00% Conservative: 13
Best Local Similarity: 26.32% Mismatches: 29
Query Match: 13.20% Indels: 28
RESULT 970
ID ABN79836 standard; cDNA; 2370 BP.
DE Fungal ZBC gene sequence #73.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Percent Similarity: 45.10% Conservative: 5
Best Local Similarity: 35.29% Mismatches: 24
Query Match: 13.20% Indels: 4
RESULT 971
ID ACA39934 standard; cDNA; 2397 BP.
DE Prokaryotic essential gene #21591.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 47.37% Conservative: 12
Best Local Similarity: 26.32% Mismatches: 30
Query Match: 13.20% Indels: 0
RESULT 972
ID ADJ40188 standard; cDNA; 2469 BP.
DE Plant cDNA #1188.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 50.00% Conservative: 5
Best Local Similarity: 39.13% Mismatches: 21
Query Match: 13.20% Indels: 2
RESULT 973
ID ADB10083 standard; cDNA; 2688 BP.
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:4979.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.54% Conservative: 10
Best Local Similarity: 31.15% Mismatches: 22
Query Match: 13.20% Indels: 10
RESULT 974
ID ADB10085 standard; cDNA; 2688 BP.
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:4977.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.54% Conservative: 10

Best Local Similarity: 31.15% Mismatches: 22
Query Match: 13.20% Indels: 10
RESULT 975
ID ABD06211 standard; DNA; 2922 BP.
DE Pseudomonas aeruginosa polynucleotide #4815.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 46.58%
Best Local Similarity: 28.77%
Query Match: 13.20%
Indels: 8
RESULT 976
ID ABS55002 standard; DNA; 2990 BP.
DE Mouse NKX-6.1 promoter sequence.
PN US6436667-B1.
PD 20-AUG-2002.
PA (REGC) UNIV CALIFORNIA.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 50.00%
Best Local Similarity: 36.96%
Query Match: 13.20%
Indels: 1
RESULT 977
ID AAD33238 standard; cDNA; 3107 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HPJUL22, SEQ ID NO:12.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.90%
Best Local Similarity: 28.05%
Query Match: 13.20%
Indels: 20
RESULT 978
ID ADA40081 standard; cDNA; 3107 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.90%
Best Local Similarity: 28.05%
Query Match: 13.20%
Indels: 20
RESULT 979
ID ADB91252 standard; cDNA; 3107 BP.
DE Human secreted protein cDNA #SEQ ID 198.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.90%
Best Local Similarity: 28.05%
Query Match: 13.20%
Indels: 20
RESULT 980
ID ADA56256 standard; DNA; 3107 BP.
DE Gene encoding human secreted protein #435.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.90%
Best Local Similarity: 28.05%
Query Match: 13.20%
Indels: 20
RESULT 981
ID ADE55895 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1727.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Percent Similarity: 50.00%
Best Local Similarity: 28.95%
Query Match: 13.20%
Indels: 0
RESULT 982
ID ADE55887 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1719.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Percent Similarity: 50.00%
Best Local Similarity: 28.95%
Query Match: 13.20%
Indels: 0
RESULT 983
ID ADE55891 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1723.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Percent Similarity: 50.00%
Best Local Similarity: 28.95%
Query Match: 13.20%
Indels: 0
RESULT 984
ID ADE55899 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1731.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Percent Similarity: 50.00%
Best Local Similarity: 28.95%
Query Match: 13.20%
Indels: 0
RESULT 985
ID ADP84424 standard; DNA; 3393 BP.
DE Human breast-specific protein coding sequence #23.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.50%
Best Local Similarity: 29.17%
Query Match: 13.20%
Indels: 29
RESULT 986
ID ADP84425 standard; DNA; 4034 BP.
DE Human breast-specific protein coding sequence #24.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.50%
Best Local Similarity: 29.17%
Query Match: 13.20%
Indels: 29
RESULT 987
ID ADP84426 standard; DNA; 4074 BP.
DE Human breast-specific protein coding sequence #25.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.50%
Best Local Similarity: 29.17%
Query Match: 13.20%
Indels: 29
RESULT 988
ID ADQ03081 standard; DNA; 4317 BP.
DE P. aeruginosa virulence gene, VIR15.
PN US200412212-A1.
PD 24-JUN-2004.
PA (COSS/) COSSON P.
PA (KOHL/) KOHLER T.
PA (BENG/) BENGHEZAL M.
PA (MARC/) MARCHETTI A.
PA (DELD/) DELDEN C V.
Percent Similarity: 46.58%
Best Local Similarity: 28.77%
Query Match: 13.20%
Indels: 8
RESULT 989
ID ADP84429 standard; DNA; 4658 BP.
DE Human breast-specific protein coding sequence #28.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.50%
Best Local Similarity: 29.17%
Query Match: 13.20%
Indels: 29
RESULT 990
ID ADE55887 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1727.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Percent Similarity: 50.00%
Best Local Similarity: 28.95%
Query Match: 13.20%
Indels: 0
RESULT 991
ID ADE55887 standard; DNA; 3376 BP.
DE Rat gene D14014, SEQ ID NO 1719.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.

RESULT 990
ID ADP84428 standard; DNA; 5050 BP.
DE Human breast-specific protein coding sequence #27.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 37.50%
Best Local Similarity: 29.17%
Query Match: 13.20%
Conservative: 8
Mismatch: 31
Indel: 29
RESULT 991
ID AD126350 standard; DNA; 5157 BP.
DE F. graminearum polyketide synthetase related polynucleotide SEQ ID NO:2.
PN WO2004005522-A2.
PD 15-JAN-2004.
PA (BADI-) BASF AG.
Percent Similarity: 41.67%
Best Local Similarity: 25.00%
Query Match: 13.20%
Conservative: 18
Mismatch: 26
Indel: 38
RESULT 992
ID AB274270 standard; DNA; 5158 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1417.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.35%
Best Local Similarity: 36.96%
Query Match: 13.20%
Conservative: 8
Mismatch: 17
Indel: 4
RESULT 993
ID ADA98799 standard; DNA; 5158 BP.
DE Human secreted protein-related DNA sequence #392.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.35%
Best Local Similarity: 36.96%
Query Match: 13.20%
Conservative: 8
Mismatch: 17
Indel: 4
RESULT 994
ID AB267836 standard; DNA; 5158 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1359.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 54.35%
Best Local Similarity: 36.96%
Query Match: 13.20%
Conservative: 8
Mismatch: 17
Indel: 4
RESULT 995
ID ABU32278 standard; DNA; 5198 BP.
DE Human immune system associated gene SEQ ID NO: 251.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 45.45%
Best Local Similarity: 27.27%
Query Match: 13.20%
Conservative: 10
Mismatch: 24
Indel: 6
RESULT 996
ID AD126349 standard; DNA; 5888 BP.
DE F. graminearum polyketide synthetase related polynucleotide SEQ ID NO:1.
PN WO2004005522-A2.
PD 15-JAN-2004.
PA (BADI-) BASF AG.
Percent Similarity: 41.67%
Best Local Similarity: 25.00%
Query Match: 13.20%
Conservative: 18
Mismatch: 26
Indel: 38
RESULT 997
ID AA54013 standard; DNA; 7131 BP.
DE 6-Methylsalicylic acid coding sequence.
PN WO20005340-A1.
PD 21-SEP-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 37.65%
Best Local Similarity: 27.06%
Query Match: 13.20%
Conservative: 9
Mismatch: 27
Indel: 26
RESULT 998

ID AAK90888 standard; DNA; 9184 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4464.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.00%
Best Local Similarity: 36.67%
Query Match: 13.20%
Conservative: 5
Mismatch: 25
Indel: 8
RESULT 999
ID AAA15186 standard; DNA; 11165 BP.
DE DNA encoding Escherichia coli virulence proteins.
PN WO200028038-A2.
PD 18-MAY-2000.
PA (MICR-) MICROSCIENCE LTD.
Percent Similarity: 54.55%
Best Local Similarity: 45.45%
Query Match: 13.20%
Conservative: 3
Mismatch: 15
Indel: 0
RESULT 1000
ID AAK82261 standard; DNA; 11297 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37073.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.00%
Best Local Similarity: 30.67%
Query Match: 13.20%
Conservative: 13
Mismatch: 28
Indel: 12
RESULT 1001
ID ADC67252 standard; DNA; 14562 BP.
DE Human GPCR gene SEQ ID NO:1705.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Percent Similarity: 54.35%
Best Local Similarity: 36.96%
Query Match: 13.20%
Conservative: 8
Mismatch: 17
Indel: 4
RESULT 1002
ID AB07998 standard; cDNA; 18445 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 18476.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 54.17%
Best Local Similarity: 37.50%
Query Match: 13.20%
Conservative: 8
Mismatch: 21
Indel: 1
RESULT 1003
ID ABU20384 standard; DNA; 18459 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12625.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 54.17%
Best Local Similarity: 37.50%
Query Match: 13.20%
Conservative: 8
Mismatch: 21
Indel: 1
RESULT 1004
ID AAG27804 standard; DNA; 31168 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1464.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Query Match: 13.20%
Conservative: 2
Mismatch: 15
Indel: 10
RESULT 1005
ID ABA07295 standard; DNA; 31168 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 614.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Query Match: 13.20%
Conservative: 2
Mismatch: 15
Indel: 10
RESULT 1006

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ID AAS42115 standard; DNA; 31168 BP.
DE Genomic sequence #431 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Indels: 10
Query Match:
RESULT 1007
Conservative: 2
Mismatch: 15
Indels: 10
ID AAK89940 standard; DNA; 31168 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3516.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Indels: 10
Query Match:
RESULT 1008
Conservative: 2
Mismatch: 15
Indels: 10
ID AAK64760 standard; DNA; 31168 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19572.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Indels: 10
Query Match:
RESULT 1009
Conservative: 2
Mismatch: 15
Indels: 10
ID ADB94607 standard; DNA; 31168 BP.
DE Novel human protein DNA #216.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 45.65%
Best Local Similarity: 41.30%
Indels: 10
Query Match:
RESULT 1010
Conservative: 2
Mismatch: 15
Indels: 10
ID ADA02894 standard; DNA; 32404 BP.
DE Human BLR1 carcinoma associated gene, SEQ ID NO:1412.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.85%
Best Local Similarity: 25.64%
Indels: 0
Query Match:
RESULT 1011
Conservative: 11
Mismatch: 18
Indels: 0
ID ADB72632 standard; DNA; 32404 BP.
DE Human BLR1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.85%
Best Local Similarity: 25.64%
Indels: 0
Query Match:
RESULT 1012
Conservative: 11
Mismatch: 18
Indels: 0
ID ADC85373 standard; DNA; 32404 BP.
DE Mouse Brl1 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 53.85%
Best Local Similarity: 25.64%
Indels: 0
Query Match:
RESULT 1013
Conservative: 11
Mismatch: 18
Indels: 0
ID ADM74489 standard; DNA; 32404 BP.
DE Human carcinoma associated (CA) nucleic acid #79.
PN US20004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 53.85%
Best Local Similarity: 25.64%
Indels: 0
Query Match:
RESULT 1014
Conservative: 7
Mismatch: 44
Indels: 4
ID AAK69758 standard; DNA; 32986 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24570.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.46%
Best Local Similarity: 29.49%
Indels: 4
Query Match:
RESULT 1015
Conservative: 7
Mismatch: 44
Indels: 4
ID AAK84629 standard; DNA; 32986 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39441.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.46%
Best Local Similarity: 29.49%
Indels: 4
Query Match:
RESULT 1016
Conservative: 7
Mismatch: 44
Indels: 4
ID AAD64732 standard; DNA; 34637 BP.
DE Mouse carcinoma-associated (CA) gene TBX21.
PN US200309963-A1.
PD 29-MAY-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 40.00%
Best Local Similarity: 30.00%
Indels: 24
Query Match:
RESULT 1017
Conservative: 7
Mismatch: 18
Indels: 24
ID ADA03086 standard; DNA; 94529 BP.
DE Human hCG23764 carcinoma associated gene, SEQ ID NO:1604.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1018
Conservative: 8
Mismatch: 34
Indels: 4
ID ADB72824 standard; DNA; 94529 BP.
DE Human hCG23764 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1019
Conservative: 8
Mismatch: 34
Indels: 4
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1020
Conservative: 12
Mismatch: 17
Indels: 21
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1021
Conservative: 12
Mismatch: 17
Indels: 21
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1022
Conservative: 10
Mismatch: 22
Indels: 10
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1023
Conservative: 11
Mismatch: 21
Indels: 4
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.28%
Best Local Similarity: 31.34%
Indels: 4
Query Match:
RESULT 1024
Conservative: 11
Mismatch: 21
Indels: 4
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ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.05%
Best Local Similarity: 29.55%
Query Match: 13.20%
Indels: 20
RESULT 1025
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 42.05%
Best Local Similarity: 29.55%
Query Match: 13.20%
Indels: 20
RESULT 1026
ID AQQ59207 standard; DNA; 262090 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:44.
PN K32004008012-A.
PD 28-JAN-2004.
PA (KIMH-) KIM H G.
PA (KIMN-) KIM N G.
PA (LEEJ-) LEE J S.
PA (RHEE-) RHEE H S.
Percent Similarity: 52.94%
Best Local Similarity: 38.24%
Query Match: 13.20%
Indels: 0
RESULT 1027
ID AAS37021 standard; cDNA; 339 BP.
DE Novel human diagnostic and therapeutic gene #79.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 11
RESULT 1028
ID AAC74745 standard; cDNA; 340 BP.
DE Human ORFX ORF300 polynucleotide sequence SEQ ID NO:599.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1029
ID ABN24479 standard; cDNA; 340 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:17435.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1030
ID AAI90280 standard; cDNA; 347 BP.
DE Human polynucleotide SEQ ID NO 10340.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1031
ID AAC00157 standard; cDNA; 363 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 155.
PN RP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Percent Similarity: 47.27%
Indels: 8
Conservative: 8
Mismatch: 8
Indel: 5

ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 42.05%
Best Local Similarity: 29.55%
Query Match: 13.20%
Indels: 20
RESULT 1025
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 42.05%
Best Local Similarity: 29.55%
Query Match: 13.20%
Indels: 20
RESULT 1026
ID AQQ59207 standard; DNA; 262090 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:44.
PN K32004008012-A.
PD 28-JAN-2004.
PA (KIMH-) KIM H G.
PA (KIMN-) KIM N G.
PA (LEEJ-) LEE J S.
PA (RHEE-) RHEE H S.
Percent Similarity: 52.94%
Best Local Similarity: 38.24%
Query Match: 13.20%
Indels: 0
RESULT 1027
ID AAS37021 standard; cDNA; 339 BP.
DE Novel human diagnostic and therapeutic gene #79.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 11
RESULT 1028
ID AAC74745 standard; cDNA; 340 BP.
DE Human ORFX ORF300 polynucleotide sequence SEQ ID NO:599.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1029
ID ABN24479 standard; cDNA; 340 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:17435.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1030
ID AAI90280 standard; cDNA; 347 BP.
DE Human polynucleotide SEQ ID NO 10340.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.73%
Best Local Similarity: 30.14%
Query Match: 13.10%
Indels: 7
RESULT 1031
ID AAC00157 standard; cDNA; 363 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 155.
PN RP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Percent Similarity: 47.27%
Indels: 8
Conservative: 8
Mismatch: 8
Indel: 5

Best Local Similarity: 32.73%
Query Match: 13.10%
Indels: 9
Mismatch: 9
Indel: 20
RESULT 1032
ID ACH20615 standard; cDNA; 383 BP.
DE Human adult liver cDNA #227.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatch: 34
Indel: 34
RESULT 1033
ID ADJ44348 standard; cDNA; 399 BP.
DE Plant cDNA #5348.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER E.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 53.57%
Best Local Similarity: 37.50%
Query Match: 13.10%
Indels: 4
Conservative: 9
Mismatch: 22
Indel: 4
RESULT 1034
ID ACH20641 standard; cDNA; 411 BP.
DE Human adult liver cDNA #253.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatch: 34
Indel: 34
RESULT 1035
ID AAS60605 standard; cDNA; 431 BP.
DE Human cancer agent-resistance marker #360.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatch: 34
Indel: 34
RESULT 1036
ID ACH20395 standard; cDNA; 437 BP.
DE Human adult liver cDNA #7.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatch: 34
Indel: 34
RESULT 1037
ID AAC00156 standard; cDNA; 460 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 154.
PN BP1033401-A2.

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PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
RESULT 1038
ID ACH28025 standard; cDNA; 475 BP.
DE Human adult ovary cDNA #6405.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Indels: 12
RESULT 1039
ID ADE82099 standard; cDNA; 483 BP.
DE Arabidopsis thaliana expressed polynucleotide seq id 870.
PN US2003115639-A1.
PD 19-JUN-2003.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYU/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Percent Similarity: 62.16%
Best Local Similarity: 40.54%
Query Match: 13.10%
Indels: 1
RESULT 1040
ID ACH78569 standard; DNA; 500 BP.
DE Human genome derived single exon probe #11764.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 50.79%
Best Local Similarity: 31.75%
Query Match: 13.10%
Indels: 13
RESULT 1041
ID ACH76127 standard; DNA; 506 BP.
DE Human genome derived single exon probe #9322.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 47.62%
Best Local Similarity: 33.33%
Query Match: 13.10%
Indels: 23
RESULT 1042
ID ABX56971 standard; DNA; 567 BP.
DE Arabidopsis thaliana polynucleotide #323.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.

PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYU/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Percent Similarity: 49.06%
Best Local Similarity: 32.08%
Query Match: 13.10%
Indels: 10
RESULT 1043
ID ADK53744 standard; DNA; 574 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #1127.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC/) DOW CHEM CO.
PA (DOWC/) DOW AGROSCIENCES LLC.
Percent Similarity: 44.44%
Best Local Similarity: 33.33%
Query Match: 13.10%
Indels: 13
RESULT 1044
ID ACH67680 standard; DNA; 595 BP.
DE Human genome derived single exon probe #875.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 40.30%
Best Local Similarity: 31.34%
Query Match: 13.10%
Indels: 27
RESULT 1045
ID ADK55700 standard; DNA; 657 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3083.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC/) DOW CHEM CO.
PA (DOWC/) DOW AGROSCIENCES LLC.
Percent Similarity: 44.94%
Best Local Similarity: 26.97%
Query Match: 13.10%
Indels: 21
RESULT 1046
ID ADK57820 standard; DNA; 657 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5203.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC/) DOW CHEM CO.
PA (DOWC/) DOW AGROSCIENCES LLC.
Percent Similarity: 44.94%
Best Local Similarity: 26.97%
Query Match: 13.10%
Indels: 21
RESULT 1047
ID AAK79094 standard; DNA; 659 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33906.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.86%
Best Local Similarity: 32.39%
Query Match: 13.10%
Indels: 15
RESULT 1048
ID ACF66493 standard; DNA; 693 BP.

DE Photorhabdus luminescens nucleotide sequence #4960.
PN WO200294867-A2.
PD 23-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 35.58%
Best Local Similarity: 26.92%
Query Match: 13.10%
Conservative: 9
Mismatch: 32
Indels: 35
RESULT 1049
ID AAH92909 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1375a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHE) WHITEHEAD INST BIOMEDICAL RES.
PA (ELI-) ELIPSIS BIOTHERAPEUTICS CORP.
Percent Similarity: 50.00%
Best Local Similarity: 36.36%
Query Match: 13.10%
Conservative: 6
Mismatch: 21
Indels: 1
RESULT 1050
ID AAX13949 standard; DNA; 766 BP.
DE H. pylori GHPO 1578 gene.
PN WO9843478-A1.
PD 03-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.05%
Best Local Similarity: 27.27%
Query Match: 13.10%
Conservative: 16
Mismatch: 29
Indels: 11
RESULT 1051
ID AAS52223 standard; DNA; 789 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #640.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 41.03%
Best Local Similarity: 23.93%
Query Match: 13.10%
Conservative: 20
Mismatch: 26
Indels: 43
RESULT 1052
ID AAS55158 standard; DNA; 789 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1470.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 41.03%
Best Local Similarity: 23.93%
Query Match: 13.10%
Conservative: 20
Mismatch: 26
Indels: 43
RESULT 1053
ID AAH07926 standard; cDNA; 825 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4761.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 43.18%
Best Local Similarity: 21.59%
Query Match: 13.10%
Conservative: 19
Mismatch: 25
Indels: 25
RESULT 1054
ID ABN98574 standard; DNA; 949 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 342.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL) GORLACH J.
PA (ANYI) AN Y.
PA (HAMI) HAMILTON C M.
PA (PRIC) PRICE J L.
PA (RAIN) RAINES T M.
PA (VUYI) YU Y.
PA (RAME) RAMEAKA J G.
PA (PAGE) PAGE A.
PA (MATH) MATHAW A V.
PA (LEDF) LEDFORD B L.
PA (WOES) WOESSNER J P.
PA (HAAS) HAAS W D.
PA (GARC) GARCIA C A.
Conservative: 4
Mismatch: 20
Indels: 3

PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURE/) HURBAN P.
Percent Similarity: 47.27%
Best Local Similarity: 30.91%
Query Match: 13.10%
Conservative: 24
Mismatch: 24
Indels: 5
RESULT 1055
ID ADC92950 standard; DNA; 996 BP.
DE E. faecium DNA sequence SEQ ID 2577.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 45.78%
Best Local Similarity: 30.12%
Query Match: 13.10%
Conservative: 13
Mismatch: 34
Indels: 11
RESULT 1056
ID AAC41895 standard; DNA; 1024 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33532.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 46.67%
Best Local Similarity: 26.67%
Query Match: 13.10%
Conservative: 12
Mismatch: 25
Indels: 7
RESULT 1059
ID AAF07696 standard; cDNA; 1124 BP.
DE Fusarium venenatum EST SEQ ID NO:219.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 41.03%
Best Local Similarity: 26.92%
Query Match: 13.10%
Conservative: 11
Mismatch: 41
Indels: 5
RESULT 1060
ID ADJ39371 standard; cDNA; 1158 BP.
DE Plant cDNA #371.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW) BUDWORTH P.
PA (MOUG) MOUGHAMER T.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZEBROOK J.
PA (GOLF) GOLF S A.
PA (KATA) KATAGIRI F.
PA (KREF) KREFS J.
PA (PROV) PROVANT N.
PA (RICK) RICK D.
PA (ZHUT) ZHU T.
Percent Similarity: 48.89%
Best Local Similarity: 40.00%
Query Match: 13.10%
Conservative: 4
Mismatch: 20
Indels: 3
RESULT 1061

ID AAS81043 standard; cDNA; 1188 BP.
DE DNA encoding novel human diagnostic protein #16847.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. Conservative: 7
Percent Similarity: 33.04% Mismatches: 22
Best Local Similarity: 26.96% Indels: 55
Query Match: 13.10%
RESULT 1062

ID ABQ45448 standard; DNA; 1283 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 32039.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG. Conservative: 9
Percent Similarity: 61.54% Mismatches: 10
Best Local Similarity: 38.46% Indels: 5
Query Match: 13.10%
RESULT 1063

ID ABQ45449 standard; DNA; 1283 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 32040.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG. Conservative: 9
Percent Similarity: 61.54% Mismatches: 10
Best Local Similarity: 38.46% Indels: 5
Query Match: 13.10%
RESULT 1064

ID ACA47846 standard; DNA; 1394 BP.
DE Prokaryotic essential gene #29503.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. Conservative: 21
Percent Similarity: 49.28% Mismatches: 32
Best Local Similarity: 18.84% Indels: 3
Query Match: 13.10%
RESULT 1065

ID ADC13534 standard; cDNA; 1411 BP.
DE Human NOVX protein encoding cDNA sequence, SEQ ID NO 13.
PN WO2003004617-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP. Conservative: 8
Percent Similarity: 37.35% Mismatches: 13
Best Local Similarity: 27.71% Indels: 39
Query Match: 13.10%
RESULT 1066

ID ABU12977 standard; cDNA; 1521 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33413.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. Conservative: 15
Percent Similarity: 41.46% Mismatches: 39
Best Local Similarity: 23.17% Indels: 9
Query Match: 13.10%
RESULT 1067

ID ADE76867 standard; cDNA; 1629 BP.
DE Human cDNA differentially expressed in a liver disorder #22.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1068

ID ADE58172 standard; DNA; 1674 BP.
DE Rat gene M91466, SEQ ID NO 4043.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP. Conservative: 5
Percent Similarity: 43.64% Mismatches: 26
Best Local Similarity: 34.55% Indels: 5
Query Match: 13.10%
RESULT 1069

ID ACF39414 standard; DNA; 1737 BP.
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:206.
PN WO200303530-A2.
PD 24-APR-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY. Conservative: 4
Percent Similarity: 47.92% Mismatches: 23
Best Local Similarity: 39.58% Indels: 2
Query Match: 13.10%
RESULT 1070

ID AAK51626 standard; cDNA; 1862 BP.
DE Human polynucleotide SEQ ID NO 171.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1071

ID ADP65676 standard; DNA; 1883 BP.
DE Human fibrinogen beta-chain mRNA, partial cds DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1072

ID ADP65552 standard; DNA; 1883 BP.
DE Human fibrinogen beta-chain mRNA, partial cds DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1073

ID ADP65102 standard; DNA; 1918 BP.
DE Human fibrinogen, B beta polypeptide (FGB) DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1074

ID ADP65031 standard; DNA; 1918 BP.
DE Human fibrinogen, B beta polypeptide (FGB) DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1075

ID ABN79808 standard; DNA; 1962 BP.
DE Fungal ZBC gene sequence #45.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC. Conservative: 14
Percent Similarity: 47.31% Mismatches: 34
Best Local Similarity: 32.26% Indels: 15
Query Match: 13.10%
RESULT 1076

ID AAK51625 standard; cDNA; 1976 BP.
DE Human polynucleotide SEQ ID NO 170.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC. Conservative: 15
Percent Similarity: 44.44% Mismatches: 34
Best Local Similarity: 27.78% Indels: 16
Query Match: 13.10%
RESULT 1077

ID AAD57334 standard; cDNA; 2024 BP.

DE Human kinase and phosphatase (KPP-7) cDNA.

PN WO200305084-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 42.31% Conservative: 2
Best Local Similarity: 38.46% Mismatches: 11
Query Match: 13.10% Indels: 19
RESULT 1078

ID ADA53914 standard; cDNA; 2033 BP.

DE Human coding sequence; SEQ ID 1482.

PN EP1293569-A2.

PD 19-MAR-2003.

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Percent Similarity: 39.08% Conservative: 9
Best Local Similarity: 28.74% Mismatches: 22
Query Match: 13.10% Indels: 31
RESULT 1079

ID AAC43014 standard; DNA; 2070 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37710.

PN EP1033405-A2.

PD 06-SEP-2000.

PA (GENE-) GENE LOGIC INC.

Percent Similarity: 49.06% Conservative: 9
Best Local Similarity: 32.08% Mismatches: 17
Query Match: 13.10% Indels: 10
RESULT 1080

ID ABZ13390 standard; DNA; 2070 BP.

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1195.

PN WO200216655-A2.

PD 23-FEB-2002.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Percent Similarity: 49.06% Conservative: 9
Best Local Similarity: 32.08% Mismatches: 17
Query Match: 13.10% Indels: 10
RESULT 1081

ID ADB53220 standard; DNA; 2080 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3762.

PN WO2003065993-A2.

PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Percent Similarity: 43.48% Conservative: 9
Best Local Similarity: 30.43% Mismatches: 11
Query Match: 13.10% Indels: 29
RESULT 1082

ID AAT10252 standard; cDNA; 2085 BP.

DE Human calpastatin coding sequence.

PN WO9533060-A1.

PD 07-DEC-1995.

PA (RHON) RHONE POULENC RORER SA.

Percent Similarity: 46.67% Conservative: 12
Best Local Similarity: 26.67% Mismatches: 25
Query Match: 13.10% Indels: 7
RESULT 1083

ID AAN92751 standard; DNA; 2148 BP.

DE DNA encoding human carbastatin-like polypeptide.

PN JP01283300-A.

PD 14-NOV-1989.

PA (TAKI) TAKARA SHUZO CO LTD.

Percent Similarity: 46.67% Conservative: 12
Best Local Similarity: 26.67% Mismatches: 25
Query Match: 13.10% Indels: 7
RESULT 1084

ID ADC14298 standard; DNA; 2160 BP.

DE Human enzyme ENZM-51 gene.

PN WO2003042357-A2.

PD 22-MAY-2003.

PA (INCY-) INCYTE GENOMICS INC.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1085

ID AAC93369 standard; cDNA; 2186 BP.

DE Human secreted protein gene 6 SEQ ID NO:16.

PN WO200061620-A1.

PD 19-OCT-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1086

ID ADA98091 standard; cDNA; 2186 BP.

DE Human secreted protein cDNA sequence #185.

PN WO2003004623-A2.

PD 16-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1087

ID ADA43966 standard; cDNA; 2186 BP.

DE Human secreted protein cDNA SEQ ID 154.

PN WO2003000865-A2.

PD 03-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1088

ID ADC20249 standard; DNA; 2186 BP.

DE Human secreted protein coding sequence #188.

PN WO200292787-A2.

PD 21-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1089

ID ADF10645 standard; DNA; 2186 BP.

DE Human secreted protein encoding sequence #98.

PN WO200299085-A2.

PD 12-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 46.15% Conservative: 8
Best Local Similarity: 35.90% Mismatches: 29
Query Match: 13.10% Indels: 13
RESULT 1090

ID AAC43116 standard; DNA; 2244 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38085.

PN EP1033405-A2.

PD 06-SEP-2000.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

Percent Similarity: 49.06% Conservative: 9
Best Local Similarity: 32.08% Mismatches: 17
Query Match: 13.10% Indels: 10
RESULT 1091

ID ADL61097 standard; DNA; 2290 BP.

DE Human protein tyrosine kinase biomarker calpastatin DNA.

PN WO2004020583-A2.

PD 11-MAR-2004.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

Percent Similarity: 46.67% Conservative: 12
Best Local Similarity: 26.67% Mismatches: 25
Query Match: 13.10% Indels: 7
RESULT 1092

ID AAS03910 standard; cDNA; 2450 BP.

DE Human secreted protein gene #29.

PN WO200123598-A1.

PD 05-APR-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 40.91% Conservative: 14
Best Local Similarity: 25.00% Mismatches: 39
Query Match: 13.10% Indels: 13
RESULT 1093

ID ABZ73460 standard; cDNA; 2450 BP.

DE Secreted protein-encoding gene 180 cDNA clone HLOAS12, SEQ ID NO:190.

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PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 40.91%
Best Local Similarity: 25.00%
Query Match: 13.10%
Indels: 13
Conservative: 14
Mismatches: 39
RESULT 1094
ID ADC20175 standard; DNA; 2450 BP.
DE Human secreted protein coding sequence #114.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 40.91%
Best Local Similarity: 25.00%
Query Match: 13.10%
Indels: 13
Conservative: 14
Mismatches: 39
RESULT 1095
ID AB267070 standard; cDNA; 2450 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 190.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 40.91%
Best Local Similarity: 25.00%
Query Match: 13.10%
Indels: 13
Conservative: 14
Mismatches: 39
RESULT 1096
ID AAS90426 standard; cDNA; 2495 BP.
DE DNA encoding novel human diagnostic protein #26230.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 46.67%
Best Local Similarity: 26.67%
Query Match: 13.10%
Indels: 7
Conservative: 12
Mismatches: 25
RESULT 1097
ID AAA47607 standard; cDNA; 2505 BP.
DE Human CARK (Cardiac related Ankyrin-Repeat Protein Kinase) cDNA.
PN WO200034330-A1.
PD 15-JUN-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 42.31%
Best Local Similarity: 38.46%
Query Match: 13.10%
Indels: 19
Conservative: 2
Mismatches: 11
RESULT 1098
ID AAF44702 standard; cDNA; 2508 BP.
DE Novel protein kinase cDNA, SEQ ID NO: 83.
PN WO200073469-A2.
PD 07-DEC-2000.
PA (SUGE-) SUGEN INC.
Percent Similarity: 42.31%
Best Local Similarity: 38.46%
Query Match: 13.10%
Indels: 19
Conservative: 2
Mismatches: 11
RESULT 1099
ID AD129400 standard; cDNA; 2508 BP.
DE Human MARK3-associated cDNA #60.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 42.31%
Best Local Similarity: 38.46%
Query Match: 13.10%
Indels: 19
Conservative: 2
Mismatches: 11
RESULT 1100
ID AB076480 standard; cDNA; 2531 BP.
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 385.
PN WO200284766-A2.
PD 22-AUG-2002.
PA (JANC ) JANSEN PHARM NV.
Percent Similarity: 46.55%
Best Local Similarity: 29.31%
Query Match: 13.10%
Indels: 17
Conservative: 10
Mismatches: 14
RESULT 1101
ID AAK52608 standard; cDNA; 2553 BP.
DE Human polynucleotide SEQ ID NO 2137.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatches: 34
RESULT 1102
ID AAK52609 standard; cDNA; 2553 BP.
DE Human polynucleotide SEQ ID NO 2138.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatches: 34
RESULT 1103
ID AAK52610 standard; cDNA; 2553 BP.
DE Human polynucleotide SEQ ID NO 2139.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.44%
Best Local Similarity: 27.78%
Query Match: 13.10%
Indels: 16
Conservative: 15
Mismatches: 34
RESULT 1104
ID ACA52311 standard; DNA; 2574 BP.
DE Prokaryotic essential gene #33968.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 46.75%
Best Local Similarity: 33.77%
Query Match: 13.10%
Indels: 31
Conservative: 10
Mismatches: 10
RESULT 1105
ID AAH18100 standard; cDNA; 2626 BP.
DE Human cDNA sequence SEQ ID NO:17956.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 43.18%
Best Local Similarity: 21.59%
Query Match: 13.10%
Indels: 25
Conservative: 19
Mismatches: 25
RESULT 1106
ID AAS80720 standard; cDNA; 2788 BP.
DE DNA encoding novel human diagnostic protein #16524.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.31%
Best Local Similarity: 38.46%
Query Match: 13.10%
Indels: 19
Conservative: 2
Mismatches: 11
RESULT 1107
ID AAS83784 standard; cDNA; 2805 BP.
DE DNA encoding novel human diagnostic protein #19588.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.22%
Best Local Similarity: 30.43%
Query Match: 13.10%
Indels: 17
Conservative: 9
Mismatches: 17
RESULT 1108
ID ABU29672 standard; DNA; 2930 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40489.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Percent Similarity: 36.00%
Best Local Similarity: 24.00%
Query Match: 13.10%
Indels: 21
Conservative: 12
Mismatches: 43
RESULT 1109
ID AD057041 standard; cDNA; 3001 BP.
DE Human cardiac ankyrin repeat kinase, CARK, cDNA.
PN WO200404164-A2.
PD 27-MAY-2004.
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PA (SEQU-) SEQUONUM INC.
 Percent Similarity: 42.31% Conservative: 2
 Best Local Similarity: 38.46% Mismatches: 11
 Query Match: 13.10% Indels: 19
 RESULT 1110
 ID ADP21369 standard; DNA; 3001 BP.
 DE Gene LOC51086 for screening for cardiac therapeutic preparation.
 PN WO2004050894-A2.
 PD 17-JUN-2004.
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.
 Percent Similarity: 42.31% Conservative: 2
 Best Local Similarity: 38.46% Mismatches: 11
 Query Match: 13.10% Indels: 19
 RESULT 1111
 ID AAA47606 standard; cDNA; 3025 BP.
 DE Human CARK (Cardiac related Ankyrin-Repeat Protein Kinase) cDNA.
 PN WO200034330-A1.
 PD 15-JUN-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 42.31% Conservative: 2
 Best Local Similarity: 38.46% Mismatches: 11
 Query Match: 13.10% Indels: 19
 RESULT 1112
 ID ACC48580 standard; cDNA; 3025 BP.
 DE Human cardiac-related ankyrin-repeat protein kinase (CARK) cDNA.
 PN WO2003020912-A2.
 PD 13-MAR-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 42.31% Conservative: 2
 Best Local Similarity: 38.46% Mismatches: 11
 Query Match: 13.10% Indels: 19
 RESULT 1113
 ID AAC46278 standard; DNA; 3108 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49559.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 47.27% Conservative: 9
 Best Local Similarity: 30.91% Mismatches: 24
 Query Match: 13.10% Indels: 5
 RESULT 1114
 ID ABL29698 standard; DNA; 3131 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40567.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 36.00% Conservative: 12
 Best Local Similarity: 24.00% Mismatches: 43
 Query Match: 13.10% Indels: 21
 RESULT 1115
 ID AAS90422 standard; cDNA; 3165 BP.
 DE DNA encoding novel human diagnostic protein #26226.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 46.67% Conservative: 12
 Best Local Similarity: 26.67% Mismatches: 25
 Query Match: 13.10% Indels: 7
 RESULT 1116
 ID AAC47620 standard; DNA; 3187 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54497.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 47.27% Conservative: 9
 Best Local Similarity: 30.91% Mismatches: 24
 Query Match: 13.10% Indels: 5
 RESULT 1117
 ID ADD93580 standard; DNA; 3228 BP.
 DE Arabidopsis pathogen-inducible promoter p30.
 PN WO2003083042-A2.
 PD 09-OCT-2003.
 PA (DNAP-) DNA PLANT TECHNOLOGY CORP.
 Percent Similarity: 49.06% Conservative: 9
 Best Local Similarity: 32.08% Mismatches: 17

Query Match: 13.10% Indels: 10
 RESULT 1118
 ID ABL11137 standard; cDNA; 3305 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27893.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 42.50% Conservative: 11
 Best Local Similarity: 28.75% Mismatches: 35
 Query Match: 13.10% Indels: 11
 RESULT 1119
 ID AAK79164 standard; DNA; 3371 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33976.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 41.41% Conservative: 10
 Best Local Similarity: 31.31% Mismatches: 38
 Query Match: 13.10% Indels: 20
 RESULT 1120
 ID AAK79165 standard; DNA; 3372 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33977.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 41.41% Conservative: 10
 Best Local Similarity: 31.31% Mismatches: 38
 Query Match: 13.10% Indels: 20
 RESULT 1121
 ID ACC72050 standard; DNA; 3541 BP.
 DE BCU0715C gene #SEQ ID 77.
 PN WO2003029421-A2.
 PD 10-APR-2003.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Percent Similarity: 46.67% Conservative: 12
 Best Local Similarity: 26.67% Mismatches: 25
 Query Match: 13.10% Indels: 7
 RESULT 1122
 ID AAS79155 standard; cDNA; 3549 BP.
 DE DNA encoding novel human diagnostic protein #14959.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 48.44% Conservative: 13
 Best Local Similarity: 28.12% Mismatches: 31
 Query Match: 13.10% Indels: 2
 RESULT 1123
 ID ACC72049 standard; DNA; 3598 BP.
 DE BCU0715B gene #SEQ ID 75.
 PN WO2003029421-A2.
 PD 10-APR-2003.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Percent Similarity: 46.67% Conservative: 12
 Best Local Similarity: 26.67% Mismatches: 25
 Query Match: 13.10% Indels: 7
 RESULT 1124
 ID ACC72048 standard; DNA; 3664 BP.
 DE BCU0715A gene #SEQ ID 73.
 PN WO2003029421-A2.
 PD 10-APR-2003.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 Percent Similarity: 46.67% Conservative: 12
 Best Local Similarity: 26.67% Mismatches: 25
 Query Match: 13.10% Indels: 7
 RESULT 1125
 ID ADF81505 standard; DNA; 3755 BP.
 DE Leukaemia-related DNA sequence #2061.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKE-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAPE-) HAFERLACH T.
 PA (SCHO/) SCHOCH C.

PA (KERN/) KERN W.
Percent Similarity: 50.94%
Best Local Similarity: 39.62%
Query Match: 13.10%
Conservative: 6
Mismatches: 18
Indels: 8
RESULT 1126
ID ABL23829 standard; DNA; 3795 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 22960.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 48.48%
Best Local Similarity: 27.27%
Query Match: 13.10%
Conservative: 14
Mismatches: 17
Indels: 17
RESULT 1127
ID AAL05882 standard; DNA; 3898 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8570.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1128
ID ABL98446 standard; DNA; 3898 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3098.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1129
ID AAL6959 standard; DNA; 3898 BP.
DE Human protein-encoding gene 5, SEQ IN NO:29.
PN WO200272763-A2.
PD 19-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1130
ID AAL05883 standard; DNA; 3899 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8571.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1131
ID AAL05884 standard; DNA; 3899 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8572.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1132
ID ABL98448 standard; DNA; 3899 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3100.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1133
ID ABL98447 standard; DNA; 3899 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3099.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1134
ID AAD46960 standard; DNA; 3899 BP.
DE Human protein-encoding gene 5, SEQ IN NO:30.
PN WO200272763-A2.
PD 19-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.43%
Best Local Similarity: 25.71%
Query Match: 13.10%
Conservative: 18
Mismatches: 29
Indels: 5
RESULT 1135
ID AAA37110 standard; cDNA; 3933 BP.
DE Human PRO1431 (UNQ737) cDNA sequence SEQ ID NO:314.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1136
ID AAF54425 standard; DNA; 3934 BP.
DE Primer #92 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1137
ID AAS46099 standard; cDNA; 3934 BP.
DE Human DNA encoding PRO polypeptide sequence #175.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1138
ID ACA89549 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1139
ID ACA73559 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1140
ID ACA05874 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1141
ID ACA66708 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO protein #175.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1142
ID ACA66708 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO protein #175.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12

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Query Match: 13.10% Indels: 12
RESULT 1142
ID ACF20283 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040063-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1143
ID ACF19669 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040064-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1144
ID ACD21957 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003027267-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1145
ID ACF13122 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036160-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1146
ID ACD23225 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003044925-A1.
PD 06-MAR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1147
ID ACF00274 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1148
ID ACA72331 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1149
ID ACD04855 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1150
ID ACD18316 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036124-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1151
ID ACD08323 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040054-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1152
ID ACA88757 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1153
ID ACA70199 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036134-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1154
ID ACD12421 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1155
ID ACC74336 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027275-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1156
ID ACD15964 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003027324-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1157
ID ACD25532 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1158
ID ACD18009 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036123-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1159
ID ACC88296 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036148-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
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Query Match: 13.10% Indels: 12
RESULT 1160
ID ACD21650 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040060-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1161
ID ACD18717 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003044916-A1.
PD 06-MAR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1162
ID ABX98327 standard; cDNA; 3934 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 349.
PN US2003036156-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1163
ID ACD14078 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032117-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1164
ID ACD09858 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036128-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1165
ID ACC88603 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027266-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1166
ID ACD21343 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1167
ID ABX75715 standard; cDNA; 3934 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1431.
PN US2003022298-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1168
ID ABX97918 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032102-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39

Query Match: 13.10% Indels: 12
RESULT 1169
ID ACA97394 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1170
ID ACAS7857 standard; cDNA; 3934 BP.
DE Human PRO1431 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1171
ID ACD14385 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032130-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1172
ID ACC91168 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1173
ID ACC89910 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036132-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1174
ID ACD07107 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1175
ID ACA67558 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003017542-A1.
PD 23-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1176
ID ACC81613 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032137-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1177
ID ACC69217 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027269-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1178
ID ACC86573 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027269-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1179
ID ACC89831 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027274-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1180
ID ACC93010 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1181
ID ACA72638 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003022295-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1182
ID ACA89156 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003022297-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1183
ID ACA69892 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032105-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1184
ID ACA97035 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1185
ID ACA91031 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1186
ID ACA70813 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032111-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1187
ID ACA95323 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1188
ID ACC86266 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027263-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1189
ID ACC90138 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1190
ID ACD12746 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036125-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1191
ID ACF19976 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1192
ID ABX76920 standard; cDNA; 3934 BP.
DE Human P30 polynucleotide #175.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1193
ID ACA73252 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1194
ID ACA68795 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1195
ID ACA74639 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1196
ID ACA70506 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1197
ID ACD14632 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003040066-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1198
ID ACA68364 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1199
ID ABX98829 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1200
ID ACC81306 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032120-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1201
ID ACA95630 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1202
ID ACD04548 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1203
ID ACC87989 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027281-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1204
ID ACFL2651 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040058-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1205
ID ACA96366 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003017540-A1.
PD 23-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1206
ID ACA65140 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032106-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1207
ID ACA73866 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032129-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1208
ID ACA74278 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1209
ID ACA96673 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032103-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1210
ID ACD10779 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003032107-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1211
ID ACC91475 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032139-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1212
ID ACD02810 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003022301-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1213
ID ACC87375 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036165-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Query Match: 13.10% Indels: 12
PA (GETH) GENENTECH INC.

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1214
ID ACC95959 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027262-A1.
PD 06-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1215
ID ACA65447 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032110-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1216
ID ACA94264 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036142-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1217
ID ACA98008 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003036145-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1218
ID ACA91510 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1219
ID ACA90724 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1220
ID ACD16271 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003044931-A1.
PD 06-MAR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1221
ID ACD17432 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036150-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1222
ID ACC92089 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040069-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39

Query Match: 13.10% Indels: 12
RESULT 1223
ID ACA74946 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003022293-A1.
PD 30-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1224
ID ACA91817 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003032128-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1225
ID ACA71461 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032116-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1226
ID ACC90861 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032122-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1227
ID ACA65871 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO protein #175.
PN US2003036139-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1228
ID ACA95016 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003017541-A1.
PD 23-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1229
ID ACD16578 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003017543-A1.
PD 23-JAN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1230
ID ACD15657 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036152-A1.
PD 20-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1231
ID ABX16760 standard; cDNA; 3934 BP.
DE Human cDNA encoding secreted/transmembrane protein #175.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39

Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1249
ID ACD84408 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003068701-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1250
ID ACD99182 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003068755-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1251
ID ADA78101 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003073180-AL.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1252
ID ACF48924 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104539-AL.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1253
ID ACD09244 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036131-AL.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1254
ID ACF12037 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040075-AL.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1255
ID ACF41271 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054459-AL.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1256
ID ACF15885 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044930-AL.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1257
ID ACF16192 standard; cDNA; 3934 BP.

DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040071-AL.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1258
ID ACD32019 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054471-AL.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1259
ID ACF18827 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064452-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1260
ID ACF09274 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068705-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1261
ID ACF78395 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054473-AL.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1262
ID ACF51994 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064440-AL.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1263
ID ACF26481 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068704-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1264
ID ACF24274 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068722-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1265
ID ACF63585 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073183-AL.

PD 17-APR-2003
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1266
ID ACF50459 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US200304549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1267
ID ACH07930 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1268
ID ACF13736 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1269
ID ACD41662 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1270
ID ACF32075 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1271
ID ACF23353 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1272
ID ACF40043 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1273
ID ACD45565 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064451-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1274
ID ACF53222 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1275
ID ACF27402 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1276
ID ACF45240 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1277
ID ACF29858 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1278
ID ACD89934 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1279
ID ACD84715 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1280
ID ACD98875 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1281
ID ACF77167 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003082717-A1.
PD 01-MAY-2003.
Percent Similarity: 43.96%
Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1282
ID ACF76860 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1283
ID ACF49845 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1284
ID ACF50152 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1285
ID ACD09551 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1286
ID ACD08630 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1287
ID ACF12344 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1288
ID ACC94852 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1289
ID ACD22571 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1290
ID ACF15271 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044917-A1.

PD 06-MAR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1291
ID ACC97366 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1292
ID ACC92396 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1293
ID ACF14043 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1294
ID ACF14350 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1295
ID ACF09581 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1296
ID ACD68464 standard; cDNA; 3934 BP.
DE Novel human secreted and transmembrane protein PRO1431 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1297
ID ACD45872 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1298
ID ACD48021 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17

ID ACF38873 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068692-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1316
ID ACF26788 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068709-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1317
ID ACF24888 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068716-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1318
ID ACF46468 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068740-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1319
ID ACF28016 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068751-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1320
ID ACD89320 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068684-AL.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1321
ID ACF63892 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073179-AL.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1322
ID ACF60532 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003087374-AL.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1323
ID ACH12656 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.

PN US2003049773-AL.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1324
ID ACH10079 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049777-AL.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1325
ID ACD03934 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040055-AL.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1326
ID ACD10472 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003036164-AL.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1327
ID ACD12114 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040074-AL.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1328
ID ACF42499 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054480-AL.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1329
ID ACF18520 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003059885-AL.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1330
ID ACF02310 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049740-AL.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1331
ID ACF21818 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049770-AL.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1332
ID ACF10502 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073169-A1.
PD 17-APR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1333
ID ACF33954 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1334
ID ACF4916 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1335
ID ACD90548 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1336
ID ACD91161 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1337
ID ACF30472 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1338
ID ACD87171 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1339
ID ACF60225 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12

RESULT 1340
ID ACF46775 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003087373-A1.
PD 08-MAY-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1341
ID ACF75632 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003096353-A1.
PD 22-MAY-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1342
ID ADA79893 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003073173-A1.
PD 17-APR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1343
ID ACF17292 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054458-A1.
PD 20-MAR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1344
ID ACF23046 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1345
ID ACF08046 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1346
ID ACF09353 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1347
ID ACF40657 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1348
ID ACF53836 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064456-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1349
ID ACD47100 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1350
ID ACF48003 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1351
ID ACF47389 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1352
ID ACF46161 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1353
ID ACD86250 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1354
ID ACF52608 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1355
ID ACF52915 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1356
ID ACF64908 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12

Query Match: 13.10%
Indels: 12
RESULT 1357
ID ACF76553 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1358
ID ACF61453 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1359
ID ACF61760 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1360
ID ACD30791 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1361
ID ACD31712 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1362
ID ACD32633 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1363
ID ACF17599 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1364
ID ACF07432 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1365
ID ACF20590 standard; cDNA; 3934 BP.

DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1366
ID ACF20897 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1367
ID ACF21204 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1368
ID ACD47714 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1369
ID ACF47696 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1370
ID ACF53529 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1371
ID ACD86864 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1372
ID ACH05112 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1373
ID ACF44609 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104557-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1374
ID ADA81620 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003092121-A1.
PD 13-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1375
ID ACD22264 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003072726-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1376
ID ACD24611 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1377
ID ACD39814 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003072726-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1378
ID ACD40121 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1379
ID ACF13429 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1380
ID ACF03231 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1381
ID ACF78702 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Conservative: 17
Mismatch: 39
Indels: 12
Query Match:
RESULT 1382
ID ACF44609 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104557-A1.
PD 05-JUN-2003.

RESULT 1382
ID ACF11423 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073171-A1.
PD 17-APR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1383
ID ACF50766 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US20030312121-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1384
ID ACF34261 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064458-A1.
PD 03-APR-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1385
ID ACD46486 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1386
ID ACD48328 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1387
ID ACF27709 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1388
ID ACP24581 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1389
ID ACD85636 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1390
ID ACD90241 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.

PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1391
ID ACD83794 standard; cDNA; 3934 BP.
DE Human PRO polynucleotide #175.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1392
ID ACF49231 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104540-A1.
PD 05-JUN-2003.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1393
ID ACH07316 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1394
ID ACH07623 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1395
ID ACH08237 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1396
ID ACH11428 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1397
ID ACH11735 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1398
ID ACH10386 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049779-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1399
ID ACF01389 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040059-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1400
ID ACF40964 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040078-A1.
PD 27-FEB-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1401
ID ACD24304 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003044918-A1.
PD 06-MAR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1402
ID ACD31405 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032132-A1.
PD 13-FEB-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1403
ID ACF17906 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054462-A1.
PD 20-MAR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1404
ID ACF32689 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064445-A1.
PD 03-APR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1405
ID ACF40350 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064449-A1.
PD 03-APR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1406
ID ACF48310 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064441-A1.
PD 03-APR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1407
ID ACH06340 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003049762-A1.

ID ACF38259 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1408
ID ACF25195 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1409
ID ACF27095 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003088730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1410
ID ACF29551 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073174-A1.
PD 17-APR-2003.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1411
ID ACD87785 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1412
ID ACF76246 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1413
ID ACF49538 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1414
ID ACF43995 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1415
ID ACH06340 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1416
ID ACH06647 standard; cDNA; 3934 BP.
DE CDNA encoding human PRO polypeptide #175.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1417
ID ADA83418 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1418
ID ACC92703 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1419
ID ACC93317 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1420
ID ACF19362 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1421
ID ACD13053 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1422
ID ACF06511 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1423
ID ACC94545 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1424

ID ACC97973 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1425
ID ACC94238 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1426
ID ACF42192 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1427
ID ACD31098 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1428
ID ACD43127 standard; cDNA; 3934 BP.
DE CDNA encoding human PRO polypeptide #175.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1429
ID ACD43434 standard; cDNA; 3934 BP.
DE CDNA encoding human PRO polypeptide #175.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1430
ID ACF14964 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1431
ID ACF01696 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
RESULT 1432
ID ACF31768 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1433
ID ACD67445 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1434
ID ACD48635 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1435
ID ACD48942 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1436
ID ACF51380 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1437
ID ACF54143 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1438
ID ACF25867 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1439
ID ACF39180 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1440
ID ACF28937 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17

Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1441
ID ACD30854 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1442
ID ACD86557 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1443
ID ACH05419 standard; cDNA; 3934 BP.
DE cDNA encoding human PRO polypeptide #175.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1444
ID ACF65215 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1445
ID ADB20461 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1446
ID ACF43688 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1447
ID ACH09158 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12
RESULT 1448
ID ACH09465 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96% Conservative: 17
Best Local Similarity: 25.27% Mismatches: 39
Query Match: 13.10% Indels: 12

RESULT 1449
ID ADA78713 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1450
ID ACF09888 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1451
ID ACF51073 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1452
ID ACF23967 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1453
ID ACD88399 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1454
ID ACH09772 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1455
ID ACH10693 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1456
ID ACD11500 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US200306126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1457
ID ACC96550 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1458
ID ACH04566 standard; cDNA; 3934 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1431.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1459
ID ACC98580 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1460
ID ACF41885 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1461
ID ACF16806 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1462
ID ACD32326 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1463
ID ACD30484 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1464
ID ACD41355 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #175.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12
RESULT 1465
ID ACF07739 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatches: 39
Indels: 12

Query Match: 13.10% Indels: 12
RESULT 1466
ID ACF31154 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003064455-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1467
ID ACF77474 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003054465-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1468
ID ACF11116 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073170-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1469
ID ACF32996 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003073176-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1470
ID ACF26174 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068717-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1471
ID ACD83487 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068728-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1472
ID ACF23660 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003068764-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1473
ID ACF43074 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104550-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1474
ID ACF43074 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104550-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12

ID ACF43381 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003104551-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1475
ID ACH06033 standard; cDNA; 3934 BP.
DE CDNA encoding human PRO polypeptide #175.
PN US2003049761-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1476
ID ACH08851 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #175.
PN US2003049757-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1477
ID ACC90445 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003027273-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1478
ID ACF10809 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036119-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1479
ID ACC91624 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036120-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1480
ID ACC96243 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003036161-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1481
ID ACD24918 standard; cDNA; 3934 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #175.
PN US2003044921-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.96%
Best Local Similarity: 25.27%
Query Match: 13.10%
Conservative: 17
Mismatch: 39
Indels: 12
RESULT 1482
ID ACF02003 standard; cDNA; 3934 BP.
DE Human secreted polypeptide PRO1431-encoding cDNA, SEQ ID NO:349.
PN US2003049739-A1.
PA (GETH) GENENTECH INC.

PN US2003054456-A1.
 PD 20-MAR-2003.
 Percent Similarity: 43.96%
 Best Local Similarity: 25.27%
 Query Match: 13.10%
 RESULT 1500
 ID ACD41048 standard; cDNA; 3934 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #175.
 PN US2003054482-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.96%
 Best Local Similarity: 25.27%
 Query Match: 13.10%
 Conservative: 17
 Mismatches: 39
 Indels: 12

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2004, 00:57:56 ; Search time 75 Seconds

(without alignments)

852.947 Million cell updates/sec

Perfect score: 462

Sequence: 1 MTFPLSLLLLYCEAIRSN.....DSRGLILGAEAGRGVKKNT 90

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO_spool/US09989293/runat_01122004_102023_13480/app_query.fasta_1.263
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi
-LIST=1500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=0
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQ=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
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5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	713	4	US-10-140-002-473
2	143.5	31.1	2298	3	US-08-772-440-1
3	139.5	30.2	528	3	US-08-772-440-7
4	122	26.4	85	4	US-09-513-999C-28212
5	70.5	15.3	1799	2	US-08-560-398-3
6	69.5	15.0	2271	4	US-09-205-258-243
7	69.5	15.0	2276	4	US-09-205-258-183
8	67.5	14.6	849	4	US-09-107-532A-1899
9	67	14.5	804	3	US-09-242-690A-35
10	67	14.5	804	4	US-09-908-855-35
11	67	14.5	2330	2	US-08-557-128-3
12	67	14.5	2330	3	US-09-242-690A-34
13	67	14.5	2330	4	US-09-908-855-34

14	66.5	14.4	1065	4	US-09-252-991A-16320	Sequence 16320, A
15	66.5	14.4	1332	4	US-09-252-991A-15961	Sequence 15961, A
16	65.5	14.2	369	4	US-09-248-796A-9562	Sequence 9562, Ap
17	65.5	14.2	548	4	US-09-621-976-3007	Sequence 3007, Ap
18	65.5	14.2	744	4	US-09-134-000C-2940	Sequence 2940, Ap
19	65.5	14.2	1341	4	US-09-252-991A-16544	Sequence 16544, A
20	65	14.1	1362	4	US-09-710-279-803	Sequence 803, App
21	65	14.1	1386	3	US-09-134-001C-767	Sequence 767, App
22	65	14.1	2003	4	US-09-148-545-109	Sequence 109, App
23	65	14.1	2070	4	US-09-148-545-51	Sequence 51, Appl
24	65	14.1	3553	4	US-09-710-279-4250	Sequence 4250, Ap
25	65	14.1	3935	4	US-09-060-482-1	Sequence 1, Appll
26	65	14.1	4095	4	US-09-710-279-4079	Sequence 4079, Ap
27	65	14.1	5833	4	US-09-976-594-183	Sequence 183, App
28	65	14.1	41708	3	US-09-470-512A-3	Sequence 3, Appli
29	65	14.1	41708	4	US-09-676-519-18	Sequence 18, Appl
30	64.5	14.0	243	4	US-09-270-767-26611	Sequence 26611, A
31	64.5	14.0	243	4	US-09-270-767-30802	Sequence 30802, A
32	64.5	14.0	801	4	US-09-248-796A-4231	Sequence 4231, App
33	64.5	14.0	1068	4	US-09-328-352-434	Sequence 434, App
34	64.5	14.0	1849	4	US-09-270-767-11089	Sequence 11089, A
35	64.5	14.0	2019	4	US-09-270-767-14598	Sequence 14598, A
36	64	13.9	3501	3	US-08-814-095-7	Sequence 7, Appli
37	64	13.9	3501	1	US-08-448-170-5	Sequence 4, Appli
38	64	13.9	3501	3	US-08-961-803-4	Sequence 21, Appl
39	64	13.9	3507	4	US-09-661-322A-21	Sequence 1, Appli
40	64	13.9	1230025	4	US-09-198-452A-1	Sequence 774, App
41	63.5	13.7	350	4	US-09-513-999C-774	Sequence 31460, A
42	63.5	13.7	397	4	US-09-270-767-31460	Sequence 37, Appl
43	63.5	13.7	739	4	US-08-948-113D-37	Sequence 29, Appl
44	63.5	13.7	1215	4	US-09-594-506-29	Sequence 15144, A
45	63.5	13.7	1476	4	US-09-270-767-15144	Sequence 4832, Ap
46	63.5	13.7	2646	4	US-09-489-039A-4832	Sequence 2329, App
47	63	13.6	561	4	US-09-710-279-2529	Sequence 994, App
48	63	13.6	729	3	US-08-998-416-994	Sequence 1418, Ap
49	63	13.6	948	3	US-09-134-001C-1418	Sequence 3, Appli
50	63	13.6	1499	3	US-09-300-672-3	Sequence 1, Appli
51	63	13.6	1500	3	US-09-300-672-1	Sequence 17, Appl
52	63	13.6	3214	1	US-08-484-105-17	Sequence 11, Appl
53	63	13.6	3214	1	US-08-484-106-17	Sequence 1, Appl
54	63	13.6	3504	4	US-09-710-279-3859	Sequence 3859, Ap
55	62.5	13.5	1031	4	US-09-270-767-10105	Sequence 10105, A
56	62.5	13.5	1458	4	US-09-311-021-201	Sequence 201, App
57	62.5	13.5	2409	4	US-09-484-970B-101	Sequence 101, App
58	62.5	13.5	33769	4	US-09-544-398B-8	Sequence 8, Appli
59	62.5	13.5	33769	4	US-09-543-771-8	Sequence 8, Appli
60	62	13.4	990	4	US-09-248-796A-2160	Sequence 2160, Ap
61	62	13.4	2336	1	US-08-247-946A-1	Sequence 1, Appli
62	62	13.4	2336	5	PCT-US95-06420-1	Sequence 1, Appli
63	62	13.4	3054	4	US-09-762-724-11	Sequence 11, Appl
64	62	13.4	3072	4	US-09-762-724-13	Sequence 13, Appl
65	62	13.4	3084	4	US-09-762-724-7	Sequence 7, Appli
66	62	13.4	10535	4	US-10-020-669-5	Sequence 5, Appli
67	62	13.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
68	62	13.4	1664976	4	US-09-692-570-1	Sequence 1, Appli
69	61.5	13.3	321	4	US-09-248-796A-9627	Sequence 9627, Ap
70	61.5	13.3	875	2	US-08-778-912A-2	Sequence 2, Appli
71	61.5	13.3	875	2	US-08-778-912A-3	Sequence 3, Appli
72	61.5	13.3	875	3	US-09-541-941B-1	Sequence 3, Appli
73	61.5	13.3	875	3	US-09-541-941B-3	Sequence 3, Appli
74	61.5	13.3	2367	3	US-09-002-285-91	Sequence 91, Appl
75	61.5	13.3	2367	4	US-09-589-477-91	Sequence 91, Appl
76	61.5	13.3	2367	4	US-10-039-285A-91	Sequence 5, Appli
77	61.5	13.3	2370	3	US-08-960-780-5	Sequence 5, Appli
78	61.5	13.3	2370	3	US-09-073-898-5	Sequence 5, Appli
79	61.5	13.3	2370	4	US-09-850-351A-5	Sequence 5, Appli
80	61.5	13.3	2497	4	US-09-484-970B-32	Sequence 32, Appl
81	61.5	13.3	2774	4	US-09-345-828-1	Sequence 1, Appli
82	61.5	13.3	2883	4	US-09-614-221A-371	Sequence 371, App
83	61.5	13.3	9319	3	US-08-976-259-85	Sequence 85, Appl
84	61.5	13.3	9319	4	US-09-956-004-85	Sequence 85, Appl
85	61.5	13.3	21784	4	US-09-820-002-3	Sequence 3, Appli
86	61.5	13.3	41684	4	US-09-536-059-1	Sequence 1, Appli

87	61.5	13.3	66933	4	US-09-544-398B-11	Sequence 11, Appl	c 160	59.5	12.9	1491	4	US-09-252-991A-10097	Sequence 10097, A
88	61.5	13.3	66933	4	US-09-543-771-11	Sequence 11, Appl	161	59.5	12.9	1655	4	US-09-794-422-1	Sequence 1, Appl
89	61	13.2	284	4	US-09-621-976-11262	Sequence 11262, A	162	59.5	12.9	2035	3	US-08-960-780-10	Sequence 10, Appl
90	61	13.2	282	4	US-09-621-976-117565	Sequence 117565, A	163	59.5	12.9	2035	3	US-09-073-898-10	Sequence 10, Appl
91	61	13.2	314	3	US-08-976-259-41	Sequence 41, Appl	164	59.5	12.9	2035	3	US-09-850-351A-10	Sequence 10, Appl
92	61	13.2	314	4	US-09-956-004-41	Sequence 41, Appl	165	59.5	12.9	2035	4	US-09-543-681A-1562	Sequence 1562, Ap
93	61	13.2	398	4	US-09-513-999C-1284	Sequence 1284, Ap	165	59.5	12.9	2035	4	US-09-614-221A-158	Sequence 158, App
94	61	13.2	471	4	US-09-621-976-11355	Sequence 11355, A	c 166	59.5	12.9	2970	4	US-09-620-312D-174	Sequence 174, App
95	61	13.2	492	4	US-09-248-796A-6093	Sequence 6093, Ap	c 167	59.5	12.9	4069	4	US-09-292-034-1	Sequence 1, Appl
96	61	13.2	534	4	US-09-248-796A-6093	Sequence 6093, Ap	c 168	59.5	12.9	34094	4	US-09-491-356C-1	Sequence 1, Appl
97	61	13.2	765	4	US-09-252-991A-4721	Sequence 4721, Ap	169	59.5	12.9	55298	4	US-09-103-840A-2	Sequence 2, Appl
98	61	13.2	871	4	US-09-023-655-1108	Sequence 1108, Ap	170	59.5	12.9	4403765	3	US-09-103-840A-1	Sequence 1, Appl
99	61	13.2	969	4	US-09-248-796A-1329	Sequence 1329, Ap	171	59.5	12.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl
100	61	13.2	1028	3	US-08-118-200-1	Sequence 1, Appl	c 172	59	12.8	285	4	US-09-621-976-18372	Sequence 18372, A
101	61	13.2	1028	4	US-08-458-748-1	Sequence 1, Appl	c 173	59	12.8	459	4	US-09-621-976-2234	Sequence 2234, Ap
102	61	13.2	1240	4	US-09-009-816-21	Sequence 21, Appl	c 174	59	12.8	492	4	US-09-513-999C-1570	Sequence 1570, Ap
103	61	13.2	1248	4	US-09-976-594-215	Sequence 215, Ap	c 175	59	12.8	514	4	US-09-270-767-6026	Sequence 6026, Ap
104	61	13.2	1320	4	US-09-252-991A-4790	Sequence 4790, Ap	c 176	59	12.8	514	4	US-09-270-767-21308	Sequence 21308, A
105	61	13.2	1557	4	US-09-252-991A-4704	Sequence 4704, Ap	c 177	59	12.8	1248	4	US-09-252-991A-15321	Sequence 15321, A
106	61	13.2	2922	4	US-09-252-991A-4815	Sequence 4815, Ap	c 178	59	12.8	1281	4	US-09-252-991A-10951	Sequence 10951, A
107	61	13.2	2990	4	US-09-009-816-19	Sequence 19, Appl	c 179	59	12.8	1382	2	US-08-596-387B-123	Sequence 123, App
108	60.5	13.1	363	4	US-09-513-999C-155	Sequence 155, Ap	c 180	59	12.8	1382	3	US-09-067-615-123	Sequence 123, App
109	60.5	13.1	460	4	US-09-513-999C-154	Sequence 154, Ap	c 181	59	12.8	1382	5	PCT-US95-09816A-123	Sequence 123, App
110	60.5	13.1	996	4	US-09-107-532A-2577	Sequence 2577, Ap	c 182	59	12.8	1385	2	US-08-596-387B-121	Sequence 121, App
111	60.5	13.1	1629	4	US-09-919-039-32	Sequence 32, Appl	c 183	59	12.8	1385	3	US-09-067-615-121	Sequence 121, App
112	60.5	13.1	2505	3	US-09-291-839-3	Sequence 3, Appl	c 184	59	12.8	1385	5	PCT-US95-09816A-121	Sequence 121, App
113	60.5	13.1	2505	4	US-09-458-457-3	Sequence 3, Appl	c 185	59	12.8	1469	3	US-09-074-912-1	Sequence 1, Appl
114	60.5	13.1	2505	4	US-09-947-199A-3	Sequence 3, Appl	c 186	59	12.8	1469	3	US-09-290-136-1	Sequence 1, Appl
115	60.5	13.1	3025	3	US-09-291-839-1	Sequence 1, Appl	c 187	59	12.8	1508	2	US-08-596-387B-122	Sequence 122, App
116	60.5	13.1	3025	4	US-09-458-457-1	Sequence 1, Appl	c 188	59	12.8	1508	3	US-08-960-190A-24	Sequence 24, Appl
117	60.5	13.1	3025	4	US-09-947-199A-1	Sequence 1, Appl	c 189	59	12.8	1508	5	PCT-US95-09816A-122	Sequence 122, App
118	60.5	13.1	229354	4	US-09-765-400-64	Sequence 64, Appl	c 190	59	12.8	1590	4	US-09-252-991A-15269	Sequence 15269, A
119	60.5	13.1	229354	4	US-09-705-400-64	Sequence 64, Appl	c 191	59	12.8	1887	4	US-09-107-532A-2783	Sequence 2783, Ap
120	60.5	13.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl	c 192	59	12.8	1897	1	US-08-453-477-1	Sequence 1, Appl
121	60.5	13.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl	193	59	12.8	1897	1	US-08-453-461-1	Sequence 1, Appl
122	60	13.0	654	4	US-09-107-532A-2746	Sequence 2746, Ap	194	59	12.8	1897	4	US-09-248-796A-1404	Sequence 1404, Ap
123	60	13.0	861	4	US-09-976-594-289	Sequence 289, Ap	195	59	12.8	2360	3	US-08-836-567-9	Sequence 9, Appl
124	60	13.0	1761	4	US-09-248-796A-882	Sequence 882, Ap	196	59	12.8	2360	4	US-09-608-304-9	Sequence 9, Appl
125	60	13.0	2260	4	US-09-270-767-15216	Sequence 15216, A	197	59	12.8	2957	4	US-09-710-279-4135	Sequence 4135, Ap
126	60	13.0	2366	4	US-09-620-312D-324	Sequence 324, A	198	59	12.8	3132	4	US-09-710-279-3455	Sequence 3455, Ap
127	60	13.0	2616	4	US-09-792-024-19	Sequence 19, Appl	199	59	12.8	3274	4	US-09-620-312D-4	Sequence 4, Appl
128	60	13.0	3090	4	US-09-762-724-5	Sequence 5, Appl	c 200	59	12.8	3293	2	US-08-442-809A-75	Sequence 75, Appl
129	60	13.0	3529	4	US-09-799-451-721	Sequence 721, Ap	201	59	12.8	3465	4	US-09-710-279-1779	Sequence 1779, Ap
130	60	13.0	3628	3	US-08-461-607-10	Sequence 10, Appl	202	59	12.8	3937	4	US-09-620-312D-280	Sequence 280, App
131	60	13.0	3628	3	US-08-461-607-12	Sequence 12, Appl	203	59	12.8	4483	4	US-09-799-451-390	Sequence 390, App
132	60	13.0	3628	3	US-08-461-607-14	Sequence 14, Appl	204	59	12.8	4627	4	US-09-710-279-3945	Sequence 3945, Ap
133	60	13.0	3628	3	US-09-363-600-10	Sequence 10, Appl	205	59	12.8	4713	3	US-09-194-285-7	Sequence 7, Appl
134	60	13.0	3628	3	US-09-363-600-12	Sequence 12, Appl	c 206	59	12.8	5406	4	US-09-386-962C-1	Sequence 1, Appl
135	60	13.0	3628	3	US-09-363-600-14	Sequence 14, Appl	207	59	12.8	5406	4	US-09-386-959-1	Sequence 1, Appl
136	60	13.0	4203	4	US-09-667-422-1	Sequence 1, Appl	208	59	12.8	5406	4	US-09-386-959-1	Sequence 1, Appl
137	60	13.0	4358	3	US-08-461-607-3	Sequence 3, Appl	209	59	12.8	36138	4	US-08-311-731A-136	Sequence 136, App
138	60	13.0	4358	3	US-09-363-600-3	Sequence 3, Appl	210	59	12.7	378	4	US-08-621-976-2339	Sequence 2339, Ap
139	60	13.0	4512	4	US-09-792-616-2	Sequence 2, Appl	211	58.5	12.7	660	1	US-08-325-553-28	Sequence 28, Appl
140	60	13.0	5363	3	US-08-461-607-4	Sequence 4, Appl	212	58.5	12.7	660	2	US-08-394-152A-28	Sequence 28, Appl
141	60	13.0	5363	3	US-08-461-607-6	Sequence 6, Appl	213	58.5	12.7	660	4	US-08-705-477E-28	Sequence 28, Appl
142	60	13.0	5363	3	US-08-461-607-8	Sequence 8, Appl	214	58.5	12.7	773	4	US-09-270-767-27982	Sequence 27982, A
143	60	13.0	5363	3	US-09-363-600-4	Sequence 4, Appl	215	58.5	12.7	822	4	US-09-543-681A-2818	Sequence 2818, Ap
144	60	13.0	5363	3	US-09-363-600-6	Sequence 6, Appl	216	58.5	12.7	1116	4	US-09-778-171-2	Sequence 2, Appl
145	60	13.0	5363	3	US-09-363-600-8	Sequence 8, Appl	217	58.5	12.7	1158	4	US-09-489-039A-2988	Sequence 2988, Ap
146	60	13.0	5993	3	US-09-383-630-1	Sequence 1, Appl	218	58.5	12.7	1231	4	US-09-270-767-12243	Sequence 12243, A
147	60	13.0	5993	3	US-09-383-630-2	Sequence 2, Appl	219	58.5	12.7	1254	3	US-09-030-267-4	Sequence 4, Appl
148	60	13.0	8083	3	US-09-383-630-4	Sequence 4, Appl	220	58.5	12.7	1642	1	US-08-310-693-1	Sequence 1, Appl
149	60	13.0	8083	3	US-09-383-630-5	Sequence 5, Appl	221	58.5	12.7	1642	5	PCT-US95-11280-1	Sequence 1, Appl
150	60	13.0	29604	3	US-08-781-891-207	Sequence 207, App	c 222	58.5	12.7	1747	1	US-08-486-037B-1	Sequence 1, Appl
151	60	13.0	29604	4	US-09-618-166-207	Sequence 207, App	c 223	58.5	12.7	1747	3	US-09-026-845-6	Sequence 6, Appl
152	60	13.0	786431	4	US-09-751-389-3	Sequence 3, Appl	c 224	58.5	12.7	1748	1	US-09-861-819-6	Sequence 6, Appl
153	59.5	12.9	286	4	US-09-313-294A-6591	Sequence 6591, Ap	225	58.5	12.7	1748	1	US-08-202-056-8	Sequence 8, Appl
154	59.5	12.9	612	4	US-09-248-796A-803	Sequence 803, Ap	226	58.5	12.7	1750	4	US-09-023-655-1135	Sequence 1135, Ap
155	59.5	12.9	714	4	US-09-252-991A-10006	Sequence 10006, A	227	58.5	12.7	2197	4	US-09-778-171-1	Sequence 1, Appl
156	59.5	12.9	836	3	US-08-998-416-313	Sequence 313, App	228	58.5	12.7	2794	1	US-07-960-932-1	Sequence 1, Appl
157	59.5	12.9	855	4	US-09-252-991A-9913	Sequence 9913, Ap	229	58.5	12.7	2794	1	US-07-908-253-1	Sequence 1, Appl
158	59.5	12.9	882	4	US-09-252-991A-10163	Sequence 10163, A	230	58.5	12.7	2794	1	US-08-455-970A-1	Sequence 1, Appl
159	59.5	12.9	1434	4	US-09-216-393B-93	Sequence 93, Appl	231	58.5	12.7	2794	1	US-08-387-156-5	Sequence 5, Appl
							232	58.5	12.7	2794	2	US-08-694-865-5	Sequence 5, Appl

233	58.5	12.7	2794	2	US-08-878-748-5	Sequence 5, Appli	306	57.5	12.4	304	4	US-09-313-294A-6868	Sequence 6868, Ap
234	58.5	12.7	2794	3	US-08-535-837-1	Sequence 1, Appli	307	57.5	12.4	304	4	US-09-513-999C-8275	Sequence 8275, Ap
235	58.5	12.7	2794	4	US-09-124-491-5	Sequence 5, Appli	308	57.5	12.4	411	3	US-08-803-085-4	Sequence 4, Appli
236	58.5	12.7	2794	4	US-09-383-912-5	Sequence 5, Appli	309	57.5	12.4	491	4	US-09-621-976-3009	Sequence 3009, Ap
237	58.5	12.7	2794	4	US-08-976-566-1	Sequence 1, Appli	c 310	57.5	12.4	602	4	US-09-513-999C-14868	Sequence 14868, A
238	58.5	12.7	2794	6	5476657-2	Patent No. 5476657	311	57.5	12.4	741	4	US-09-583-110-2052	Sequence 2052, Ap
239	58.5	12.7	2817	1	US-07-960-932-9	Sequence 9, Appli	c 312	57.5	12.4	960	3	US-09-130-749-1	Sequence 1, Appli
240	58.5	12.7	2817	1	US-08-455-970A-11	Sequence 11, Appli	c 313	57.5	12.4	960	3	US-09-130-749-1	Sequence 1, Appli
241	58.5	12.7	2817	4	US-08-976-566-11	Sequence 11, Appli	c 314	57.5	12.4	960	4	US-09-170-496B-59	Sequence 59, Appli
242	58.5	12.7	2838	1	US-07-960-932-8	Sequence 8, Appli	c 315	57.5	12.4	966	4	US-09-170-496B-195	Sequence 195, App
243	58.5	12.7	2838	1	US-08-455-970A-9	Sequence 9, Appli	c 316	57.5	12.4	966	2	US-08-766-738-2	Sequence 2, Appli
244	58.5	12.7	2838	4	US-08-976-566-9	Sequence 9, Appli	c 317	57.5	12.4	966	4	US-09-262-610-2	Sequence 2, Appli
245	58.5	12.7	2861	1	US-07-960-932-10	Sequence 10, Appli	c 318	57.5	12.4	1026	4	US-09-252-991A-6481	Sequence 6481, Ap
246	58.5	12.7	2861	1	US-08-455-970A-13	Sequence 13, Appli	c 319	57.5	12.4	1026	4	US-09-252-991A-6481	Sequence 6481, Ap
247	58.5	12.7	2861	4	US-08-976-566-13	Sequence 13, Appli	c 320	57.5	12.4	1230	4	US-09-252-991A-5993	Sequence 5993, Ap
248	58.5	12.7	2934	1	US-08-387-156-7	Sequence 7, Appli	321	57.5	12.4	1323	3	US-08-858-207A-50	Sequence 50, Appli
249	58.5	12.7	2934	2	US-08-694-865-7	Sequence 7, Appli	322	57.5	12.4	1888	3	US-09-002-285-105	Sequence 105, App
250	58.5	12.7	2934	2	US-08-878-748-7	Sequence 7, Appli	323	57.5	12.4	1888	4	US-09-589-477-105	Sequence 105, App
251	58.5	12.7	2934	3	US-09-124-491-7	Sequence 7, Appli	324	57.5	12.4	1888	4	US-10-099-285A-105	Sequence 105, App
252	58.5	12.7	2934	4	US-09-383-912-7	Sequence 7, Appli	325	57.5	12.4	2366	3	US-09-002-285-99	Sequence 99, Appli
253	58.5	12.7	3229	1	US-07-777-715-8	Sequence 8, Appli	326	57.5	12.4	2366	4	US-09-589-477-99	Sequence 99, Appli
254	58.5	12.7	3229	1	US-08-170-126-3	Sequence 3, Appli	327	57.5	12.4	2366	4	US-10-099-285A-99	Sequence 99, Appli
255	58.5	12.7	3229	3	US-08-954-418-3	Sequence 3, Appli	328	57.5	12.4	2369	3	US-09-002-285-93	Sequence 93, Appli
256	58.5	12.7	3311	1	US-07-777-715-6	Sequence 6, Appli	329	57.5	12.4	2369	4	US-09-589-477-93	Sequence 93, Appli
257	58.5	12.7	3311	1	US-08-170-126-1	Sequence 1, Appli	330	57.5	12.4	2369	4	US-10-099-285A-93	Sequence 93, Appli
258	58.5	12.7	3311	3	US-08-954-418-1	Sequence 1, Appli	331	57.5	12.4	2375	3	US-09-002-285-83	Sequence 83, Appli
259	58.5	12.7	3646	3	US-08-619-812-7	Sequence 7, Appli	332	57.5	12.4	2375	3	US-09-002-285-85	Sequence 85, Appli
260	58.5	12.7	5181	1	US-08-257-073-10	Sequence 10, Appli	333	57.5	12.4	2375	3	US-09-002-285-103	Sequence 103, App
261	58.5	12.7	34185	4	US-09-545-481-3	Sequence 3, Appli	334	57.5	12.4	2375	4	US-09-589-477-83	Sequence 83, Appli
c 262	58	12.6	192	4	US-09-134-000C-619	Sequence 619, App	335	57.5	12.4	2375	4	US-09-589-477-85	Sequence 85, Appli
c 263	58	12.6	277	4	US-09-313-294A-1186	Sequence 1186, Ap	336	57.5	12.4	2375	4	US-09-589-477-103	Sequence 103, App
c 264	58	12.6	420	4	US-09-107-532A-1825	Sequence 1825, Ap	337	57.5	12.4	2375	4	US-10-099-285A-83	Sequence 83, Appli
c 265	58	12.6	446	3	US-09-188-930-43	Sequence 43, Appli	338	57.5	12.4	2375	4	US-10-099-285A-85	Sequence 85, Appli
c 266	58	12.6	446	3	US-09-188-930-212	Sequence 43, Appli	339	57.5	12.4	2375	4	US-10-099-285A-103	Sequence 103, App
c 267	58	12.6	446	4	US-09-312-830C-42	Sequence 42, App	340	57.5	12.4	2376	3	US-09-002-285-87	Sequence 87, Appli
c 268	58	12.6	446	4	US-09-312-830C-212	Sequence 42, App	341	57.5	12.4	2376	4	US-09-589-477-87	Sequence 87, Appli
c 269	58	12.6	483	4	US-09-270-767-9516	Sequence 9516, Ap	342	57.5	12.4	2376	4	US-10-099-285A-87	Sequence 87, Appli
c 270	58	12.6	483	4	US-09-270-767-24798	Sequence 24798, A	343	57.5	12.4	2582	4	US-09-270-767-12851	Sequence 12851, A
c 271	58	12.6	610	4	US-09-702-705-933	Sequence 933, App	344	57.5	12.4	2694	4	US-09-252-991A-12457	Sequence 12457, A
c 272	58	12.6	610	4	US-09-736-457-933	Sequence 933, App	c 345	57.5	12.4	3199	4	US-09-023-655-947	Sequence 947, App
c 273	58	12.6	610	4	US-09-614-124B-933	Sequence 933, App	346	57.5	12.4	4250	4	US-09-533-220A-1	Sequence 1, Appli
c 274	58	12.6	610	4	US-09-671-325-933	Sequence 933, App	c 347	57.5	12.4	4250	4	US-09-706-594-6	Sequence 6, Appli
c 275	58	12.6	610	4	US-09-658-824-933	Sequence 933, App	348	57.5	12.4	9164	4	US-09-814-915A-80	Sequence 80, Appli
c 276	58	12.6	639	4	US-09-134-000C-618	Sequence 618, App	349	57.5	12.4	17000	4	US-09-691-220-3	Sequence 3, Appli
c 277	58	12.6	649	4	US-09-177-650-118	Sequence 118, App	c 350	57.5	12.4	20986	4	US-08-961-527-54	Sequence 54, Appli
c 278	58	12.6	840	4	US-09-252-991A-14967	Sequence 14967, A	351	57	12.3	413	4	US-09-621-976-9364	Sequence 9364, Ap
c 279	58	12.6	998	1	US-08-553-516-1	Sequence 1, Appli	c 352	57	12.3	420	4	US-09-252-991A-9208	Sequence 9208, Ap
c 280	58	12.6	998	1	US-08-238-130-1	Sequence 1, Appli	353	57	12.3	423	4	US-09-489-039A-4704	Sequence 4704, Ap
c 281	58	12.6	998	2	US-08-421-426-3	Sequence 3, Appli	354	57	12.3	474	4	US-09-252-991A-8848	Sequence 8848, Ap
c 282	58	12.6	998	3	US-08-816-915-3	Sequence 3, Appli	355	57	12.3	477	4	US-09-583-110-611	Sequence 611, App
c 283	58	12.6	998	5	PCT-US95-07743-3	Sequence 3, Appli	356	57	12.3	624	4	US-09-248-796A-4173	Sequence 4173, Ap
c 284	58	12.6	1149	4	US-09-252-991A-14783	Sequence 14783, A	357	57	12.3	627	4	US-09-248-796A-12309	Sequence 12309, A
c 285	58	12.6	1461	4	US-09-252-991A-14833	Sequence 14833, A	358	57	12.3	937	6	5248606-42	Patent No. 5248606
c 286	58	12.6	1669	2	US-08-916-902A-2	Sequence 2, Appli	359	57	12.3	987	6	US-09-107-532A-271	Sequence 271, App
c 287	58	12.6	1669	2	US-09-213-389-2	Sequence 2, Appli	c 360	57	12.3	1277	4	US-09-370-767-14339	Sequence 14339, A
c 288	58	12.6	1980	4	US-09-328-352-1895	Sequence 1895, Ap	361	57	12.3	1308	3	US-09-724-864-15	Sequence 15, Appli
c 289	58	12.6	2230	3	US-09-189-527-12	Sequence 12, Appli	c 362	57	12.3	1341	4	US-09-252-991A-1920	Sequence 1920, Ap
c 290	58	12.6	2436	4	US-09-489-039A-6668	Sequence 6668, Ap	c 363	57	12.3	1362	4	US-09-252-991A-1839	Sequence 1839, Ap
c 291	58	12.6	2520	4	US-09-311-021-83	Sequence 83, Appli	c 364	57	12.3	1386	4	US-09-252-991A-9044	Sequence 9044, Ap
c 292	58	12.6	3048	2	US-08-313-200-2	Sequence 2, Appli	365	57	12.3	1407	4	US-09-252-991A-2037	Sequence 2037, Ap
c 293	58	12.6	3048	2	US-09-251-039-1	Sequence 1, Appli	c 366	57	12.3	1409	4	US-09-573-906-3	Sequence 3, Appli
c 294	58	12.6	3048	5	PCT-US93-03837-2	Sequence 2, Appli	c 367	57	12.3	1465	4	US-09-573-906-1	Sequence 1, Appli
c 295	58	12.6	4635	4	US-09-221-017B-187	Sequence 187, App	368	57	12.3	1524	4	US-09-248-796A-4155	Sequence 4155, Ap
c 296	58	12.6	6156	4	US-09-614-121A-231	Sequence 231, App	369	57	12.3	1554	4	US-09-533-029-91	Sequence 91, Appli
c 297	58	12.6	7263	4	US-09-562-702A-31	Sequence 31, Appli	370	57	12.3	1557	4	US-09-248-796A-5190	Sequence 5190, Ap
c 298	58	12.6	7263	4	US-09-561-818A-27	Sequence 27, Appli	371	57	12.3	1608	4	US-09-252-991A-8961	Sequence 8961, Ap
c 299	58	12.6	7554	4	US-09-562-702A-29	Sequence 29, Appli	372	57	12.3	1749	4	US-09-252-991A-8742	Sequence 8742, Ap
c 300	58	12.6	7554	4	US-09-561-818A-25	Sequence 25, Appli	373	57	12.3	2019	4	US-09-248-796A-12892	Sequence 12892, A
c 301	58	12.6	11188	4	US-09-821-167-1	Sequence 1, Appli	375	57	12.3	2555	4	US-09-944-457-68	Sequence 68, Appli
c 302	58	12.6	22067	3	US-09-564-805-28	Sequence 3, Appli	376	57	12.3	2852	3	US-09-063-950-1	Sequence 1, Appli
c 303	58	12.6	26664	3	US-09-564-805-28	Sequence 28, Appli	377	57	12.3	3720	2	US-08-742-026-1	Sequence 1, Appli
c 304	58	12.6	64467	4	US-09-803-671B-3	Sequence 3, Appli	378	57	12.3	3720	2	US-08-742-026-22	Sequence 22, Appli
c 305	58	12.6	580073	4	US-08-545-528D-1	Sequence 1, Appli	c 379	57	12.3	6013	4	US-09-774-528-109	Sequence 109, App

c 380	57	12.3	13206	4	US-08-961-527-33	Sequence 33, Appl	454	56.5	12.2	2378	3	US-09-233-752A-1	Sequence 1, Appl
381	57	12.3	31328	3	US-09-215-694-19	Sequence 19, Appl	455	56.5	12.2	2378	3	US-09-402-036-1	Sequence 1, Appl
c 382	57	12.3	38519	4	US-09-952-060-29	Sequence 29, Appl	456	56.5	12.2	2378	4	US-09-904-236-1	Sequence 30, Appl
383	57	12.3	169998	4	US-09-676-610B-24	Sequence 24, Appl	457	56.5	12.2	2403	1	US-08-471-033-30	Sequence 30, Appl
c 384	57	12.3	193303	4	US-09-497-855A-37	Sequence 37, Appl	458	56.5	12.2	2403	2	US-08-471-044-30	Sequence 30, Appl
c 385	57	12.3	193303	4	US-09-497-855A-44	Sequence 44, Appl	459	56.5	12.2	2403	2	US-08-463-483A-30	Sequence 30, Appl
c 386	57	12.3	197496	4	US-09-877-177A-10	Sequence 10, Appl	460	56.5	12.2	2403	2	US-08-471-046A-30	Sequence 30, Appl
387	57	12.3	1830121	4	US-09-557-884-1	Sequence 1, Appl	461	56.5	12.2	2403	2	US-08-470-566B-30	Sequence 30, Appl
388	57	12.3	1830121	4	US-09-643-990A-1	Sequence 1, Appl	462	56.5	12.2	2403	2	US-08-838-219B-7	Sequence 7, Appl
389	57	12.3	1830121	4	US-10-329-960-1	Sequence 1, Appl	463	56.5	12.2	2403	2	US-08-469-334-30	Sequence 30, Appl
390	56.5	12.2	490	4	US-09-976-594-821	Sequence 821, App	464	56.5	12.2	2403	3	US-09-300-529-30	Sequence 30, Appl
391	56.5	12.2	765	4	US-09-614-221A-450	Sequence 45, App	465	56.5	12.2	2403	3	US-09-233-336A-7	Sequence 7, Appl
392	56.5	12.2	800	3	US-08-545-809A-39	Sequence 39, Appl	466	56.5	12.2	2403	3	US-09-233-752A-7	Sequence 7, Appl
393	56.5	12.2	879	4	US-09-602-787A-5	Sequence 5, Appl	467	56.5	12.2	2403	3	US-09-402-036-7	Sequence 7, Appl
394	56.5	12.2	891	4	US-09-252-991A-10773	Sequence 10773, A	468	56.5	12.2	2403	4	US-09-904-226-7	Sequence 7, Appl
c 395	56.5	12.2	913	3	US-08-986-769-4	Sequence 4, Appl	c 469	56.5	12.2	2515	1	US-08-061-465-3	Sequence 3, Appl
396	56.5	12.2	993	4	US-09-489-039A-4468	Sequence 4468, Ap	470	56.5	12.2	2612	1	US-08-471-033-31	Sequence 31, Appl
397	56.5	12.2	1153	4	US-09-023-655-832	Sequence 832, App	471	56.5	12.2	2612	2	US-08-471-044-31	Sequence 31, Appl
398	56.5	12.2	1245	4	US-09-270-767-9887	Sequence 9887, Ap	472	56.5	12.2	2612	2	US-08-463-483A-31	Sequence 31, Appl
399	56.5	12.2	1246	4	US-09-270-767-11500	Sequence 11500, A	473	56.5	12.2	2612	2	US-08-471-046A-31	Sequence 31, Appl
c 400	56.5	12.2	1284	4	US-09-252-991A-820	Sequence 820, App	474	56.5	12.2	2612	2	US-08-470-566B-31	Sequence 31, Appl
401	56.5	12.2	1380	4	US-09-328-352-397	Sequence 397, App	475	56.5	12.2	2612	2	US-08-838-219B-3	Sequence 3, Appl
403	56.5	12.2	1413	4	US-09-944-457-60	Sequence 60, Appl	476	56.5	12.2	2612	2	US-08-469-334-31	Sequence 31, Appl
404	56.5	12.2	1598	4	US-09-778-510-19	Sequence 19, Appl	477	56.5	12.2	2612	3	US-09-300-529-31	Sequence 31, Appl
c 405	56.5	12.2	1665	4	US-09-253-991A-10272	Sequence 10272, A	478	56.5	12.2	2612	3	US-09-233-336A-3	Sequence 3, Appl
406	56.5	12.2	1755	4	US-09-248-796A-3448	Sequence 3448, Ap	479	56.5	12.2	2612	3	US-09-233-752A-3	Sequence 3, Appl
407	56.5	12.2	1935	4	US-09-778-510-21	Sequence 21, Appl	480	56.5	12.2	2612	3	US-09-402-036-3	Sequence 3, Appl
408	56.5	12.2	2154	4	US-09-134-000C-2428	Sequence 2428, Ap	481	56.5	12.2	2612	4	US-09-904-226-3	Sequence 3, Appl
409	56.5	12.2	2169	4	US-09-105-058C-22	Sequence 22, Appl	482	56.5	12.2	2619	4	US-09-543-681A-596	Sequence 596, App
410	56.5	12.2	2241	4	US-08-838-219B-20	Sequence 20, Appl	483	56.5	12.2	2619	4	US-09-543-681A-1613	Sequence 1613, Ap
411	56.5	12.2	2241	3	US-09-233-336A-20	Sequence 20, Appl	c 484	56.5	12.2	2685	2	US-08-935-450-5	Sequence 5, Appl
412	56.5	12.2	2241	3	US-09-233-752A-20	Sequence 20, Appl	c 485	56.5	12.2	2685	4	US-09-338-123-5	Sequence 5, Appl
413	56.5	12.2	2241	3	US-09-402-036-20	Sequence 20, Appl	c 486	56.5	12.2	3090	5	PCT-US93-06251-7	Sequence 7, Appl
414	56.5	12.2	2241	3	US-09-904-226-20	Sequence 20, Appl	c 487	56.5	12.2	3119	3	US-09-199-637A-173	Sequence 173, App
415	56.5	12.2	2280	4	US-09-328-352-3524	Sequence 3524, Ap	c 488	56.5	12.2	3195	4	US-09-527-058-3	Sequence 3, Appl
416	56.5	12.2	2364	2	US-08-838-219B-5	Sequence 5, Appl	c 489	56.5	12.2	3883	4	US-09-620-312D-780	Sequence 780, App
417	56.5	12.2	2364	3	US-09-233-336A-5	Sequence 5, Appl	c 490	56.5	12.2	5006	4	US-09-620-312D-262	Sequence 262, App
418	56.5	12.2	2364	3	US-09-402-036A-5	Sequence 5, Appl	c 491	56.5	12.2	5676	2	US-08-663-998-3	Sequence 3, Appl
419	56.5	12.2	2364	3	US-09-402-036A-5	Sequence 5, Appl	c 492	56.5	12.2	6766	4	US-09-527-058-1	Sequence 1, Appl
420	56.5	12.2	2364	4	US-09-904-226-5	Sequence 5, Appl	c 493	56.5	12.2	6828	1	US-08-061-465-1	Sequence 1, Appl
421	56.5	12.2	2370	2	US-08-838-219B-19	Sequence 19, Appl	c 494	56.5	12.2	7188	4	US-10-101-957B-1	Sequence 1, Appl
422	56.5	12.2	2370	3	US-09-233-336A-19	Sequence 19, Appl	495	56.5	12.2	10399	4	US-08-961-527-160	Sequence 160, App
423	56.5	12.2	2370	3	US-09-233-752A-19	Sequence 19, Appl	496	56.5	12.2	16063	3	US-09-801-052-3	Sequence 3, Appl
424	56.5	12.2	2370	3	US-09-402-036-19	Sequence 19, Appl	497	56.5	12.2	16063	4	US-10-020-121-3	Sequence 3, Appl
425	56.5	12.2	2370	3	US-09-002-285-79	Sequence 79, Appl	c 498	56.5	12.2	19736	3	US-09-740-035-3	Sequence 3, Appl
426	56.5	12.2	2370	3	US-09-002-285-95	Sequence 95, Appl	c 499	56.5	12.2	19988	4	US-09-596-002-10	Sequence 10, Appl
427	56.5	12.2	2370	4	US-09-904-226-19	Sequence 19, Appl	500	56.5	12.2	20951	4	US-08-805-455-3	Sequence 3, Appl
428	56.5	12.2	2370	4	US-09-589-477-79	Sequence 79, Appl	501	56.5	12.2	36241	4	US-08-311-731A-134	Sequence 134, App
429	56.5	12.2	2370	4	US-09-589-477-95	Sequence 95, Appl	502	56.5	12.2	40000	4	US-08-780-049-18	Sequence 18, Appl
430	56.5	12.2	2370	4	US-10-099-285A-79	Sequence 79, Appl	503	56.5	12.2	41171	4	US-08-311-731A-122	Sequence 122, App
431	56.5	12.2	2370	4	US-10-099-285A-95	Sequence 95, Appl	c 504	56.5	12.2	47981	4	US-09-679-279-1	Sequence 1, Appl
432	56.5	12.2	2374	3	US-09-002-285-97	Sequence 97, Appl	c 505	56.5	12.2	162450	3	US-09-345-882-1	Sequence 1, Appl
433	56.5	12.2	2374	4	US-09-589-477-97	Sequence 97, Appl	c 506	56.5	12.2	168174	4	US-10-071-411A-63	Sequence 63, Appl
434	56.5	12.2	2374	4	US-10-099-285A-97	Sequence 97, Appl	c 507	56.5	12.2	168273	4	US-10-071-411A-63	Sequence 2, Appl
435	56.5	12.2	2375	3	US-08-960-780-3	Sequence 3, Appl	508	56	12.1	329	4	US-09-621-976-2313	Sequence 2313, Ap
436	56.5	12.2	2375	3	US-08-960-780-7	Sequence 7, Appl	509	56	12.1	330	4	US-09-513-999C-12052	Sequence 12052, A
437	56.5	12.2	2375	3	US-09-073-898-3	Sequence 3, Appl	c 510	56	12.1	462	3	US-09-280-116-164	Sequence 164, App
438	56.5	12.2	2375	3	US-09-073-898-7	Sequence 7, Appl	511	56	12.1	462	3	US-08-854-531-1	Sequence 1, Appl
439	56.5	12.2	2375	3	US-09-002-285-81	Sequence 81, Appl	512	56	12.1	462	5	PCT-US95-13552-14	Sequence 1, Appl
440	56.5	12.2	2375	4	US-09-589-477-81	Sequence 81, Appl	513	56	12.1	621	4	US-09-270-767-1348	Sequence 1348, Ap
441	56.5	12.2	2375	4	US-09-307-106-1	Sequence 1, Appl	514	56	12.1	621	4	US-09-270-767-16630	Sequence 16630, A
442	56.5	12.2	2375	4	US-09-850-351A-3	Sequence 3, Appl	c 515	56	12.1	648	4	US-09-252-991A-2486	Sequence 2486, Ap
443	56.5	12.2	2375	4	US-09-850-351A-7	Sequence 7, Appl	c 516	56	12.1	670	4	US-09-967-669-12	Sequence 12, Appl
444	56.5	12.2	2375	4	US-10-099-285A-81	Sequence 81, Appl	517	56	12.1	923	3	US-08-869-380-1	Sequence 1, Appl
445	56.5	12.2	2378	1	US-08-471-033-28	Sequence 28, Appl	518	56	12.1	923	5	PCT-US95-13552-14	Sequence 14, Appl
446	56.5	12.2	2378	2	US-08-471-044-28	Sequence 28, Appl	c 519	56	12.1	1026	4	US-09-248-796A-472	Sequence 472, App
447	56.5	12.2	2378	2	US-08-463-483A-28	Sequence 28, Appl	520	56	12.1	1155	4	US-09-328-352-3733	Sequence 3733, Ap
448	56.5	12.2	2378	2	US-08-471-046A-28	Sequence 28, Appl	521	56	12.1	1245	4	US-09-134-001C-2535	Sequence 2535, Ap
449	56.5	12.2	2378	2	US-08-470-566B-28	Sequence 28, Appl	522	56	12.1	1279	3	US-08-985-950-5	Sequence 5, Appl
450	56.5	12.2	2378	2	US-08-838-219B-1	Sequence 1, Appl	523	56	12.1	1279	4	US-09-546-049-5	Sequence 5, Appl
451	56.5	12.2	2378	3	US-08-469-334-28	Sequence 28, Appl	524	56	12.1	1728	3	US-08-985-950-7	Sequence 7, Appl
452	56.5	12.2	2378	3	US-09-300-529-28	Sequence 28, Appl	525	56	12.1	1728	4	US-09-546-049-7	Sequence 7, Appl
453	56.5	12.2	2378	3	US-09-233-336A-1	Sequence 1, Appl	c 526	56	12.1	1765	4	US-09-270-767-11023	Sequence 11023, A

527	56	12.1	1790	4	US-09-016-434-1359	Sequence 1359, Ap	600	55.5	12.0	1596	4	US-09-252-991A-5938	Sequence 5938, Ap
528	56	12.1	1790	4	US-09-023-655-1398	Sequence 1398, Ap	C 601	55.5	12.0	1674	4	US-09-252-991A-5894	Sequence 5894, Ap
529	56	12.1	1827	4	US-09-583-110-1663	Sequence 1663, Ap	C 602	55.5	12.0	1813	3	US-08-123-934A-1	Sequence 1, Appli
c 530	56	12.1	1863	4	US-09-482-273-28	Sequence 28, Appl	C 603	55.5	12.0	1813	3	US-08-123-934A-1	Sequence 1, Appli
c 531	56	12.1	1876	4	US-09-794-422-33	Sequence 33, Appl	C 604	55.5	12.0	1813	5	PCT-US94-10080-1	Sequence 1, Appli
c 532	56	12.1	1938	4	US-09-673-395A-140	Sequence 140, App	C 605	55.5	12.0	1876	4	US-09-324-258-1	Sequence 1, Appli
533	56	12.1	1969	4	US-09-794-422-45	Sequence 45, Appl	C 606	55.5	12.0	2018	4	US-09-270-767-1800	Sequence 1800, Ap
534	56	12.1	2013	4	US-10-132-920B-26	Sequence 26, Appl	C 607	55.5	12.0	2018	4	US-09-270-767-17082	Sequence 17082, A
c 535	56	12.1	2016	4	US-09-583-110-498	Sequence 498, App	C 608	55.5	12.0	2031	4	US-08-706-054A-2	Sequence 2, Appli
536	56	12.1	2019	4	US-09-794-422-5	Sequence 5, Appli	C 609	55.5	12.0	2031	4	US-09-313-293-2	Sequence 2, Appli
537	56	12.1	2070	4	US-09-252-991A-2189	Sequence 2189, Ap	C 610	55.5	12.0	2040	1	US-08-247-475-36	Sequence 36, Appl
538	56	12.1	2112	4	US-09-794-422-7	Sequence 7, Appli	C 611	55.5	12.0	2040	1	US-08-479-650-36	Sequence 36, Appl
539	56	12.1	2244	4	US-09-543-681A-1525	Sequence 1525, Ap	C 612	55.5	12.0	2040	1	US-08-191-866D-57	Sequence 57, Appl
c 540	56	12.1	2460	3	US-08-952-365-1	Sequence 1, Appli	C 613	55.5	12.0	2040	1	US-08-674-169-36	Sequence 36, Appl
c 541	56	12.1	2619	4	US-09-543-681A-1613	Sequence 1613, Ap	C 614	55.5	12.0	2040	2	US-08-185-949B-57	Sequence 57, Appl
c 542	56	12.1	2821	4	US-09-484-970B-44	Sequence 44, Appl	C 615	55.5	12.0	2130	4	US-09-425-335-1	Sequence 1, Appli
543	56	12.1	3001	4	US-09-539-333D-154	Sequence 154, App	C 616	55.5	12.0	2163	4	US-09-710-279-2057	Sequence 2057, Ap
544	56	12.1	3001	4	US-09-539-333D-155	Sequence 155, App	C 617	55.5	12.0	2187	3	US-09-134-001C-2131	Sequence 2131, Ap
c 545	56	12.1	3572	3	US-09-575-574-3	Sequence 3, Appli	C 618	55.5	12.0	2286	4	US-09-800-729-43	Sequence 43, Appl
546	56	12.1	3660	3	US-08-470-260-2	Sequence 2, Appli	C 619	55.5	12.0	2329	4	US-09-800-729-11	Sequence 11, Appl
547	56	12.1	3660	3	US-08-471-491-2	Sequence 2, Appli	C 620	55.5	12.0	2355	4	US-09-800-729-27	Sequence 27, Appl
548	56	12.1	3960	3	US-08-466-662-2	Sequence 2, Appli	C 621	55.5	12.0	2367	4	US-09-620-312D-1064	Sequence 1064, Ap
549	56	12.1	4319	3	US-08-296-791-1	Sequence 1, Appli	C 622	55.5	12.0	2393	3	US-09-393-529-1	Sequence 1, Appli
550	56	12.1	4319	4	US-09-839-996-1	Sequence 1, Appli	C 623	55.5	12.0	2495	3	US-09-668-113A-1	Sequence 1, Appli
551	56	12.1	4319	4	US-10-080-505-1	Sequence 1, Appli	C 624	55.5	12.0	2765	3	US-08-706-344C-1	Sequence 1, Appli
552	56	12.1	4319	5	PCT-US96-12545-5	Sequence 5, Appli	C 625	55.5	12.0	2765	3	US-08-706-344C-3	Sequence 3, Appli
c 553	56	12.1	5390	5	PCT-US96-12545-5	Sequence 5, Appli	C 626	55.5	12.0	2765	3	US-08-706-344C-27	Sequence 27, Appl
c 554	56	12.1	5609	3	US-09-313-677-14	Sequence 14, Appl	C 627	55.5	12.0	2765	3	US-08-706-344C-29	Sequence 29, Appl
c 555	56	12.1	5609	3	US-09-313-677-15	Sequence 15, Appl	C 628	55.5	12.0	2765	3	US-08-706-344C-31	Sequence 31, Appl
556	56	12.1	5703	3	US-09-280-590A-36	Sequence 36, Appl	C 629	55.5	12.0	3202	4	US-09-710-279-3774	Sequence 3774, Ap
557	56	12.1	5703	4	US-09-892-398-36	Sequence 36, Appl	C 630	55.5	12.0	3396	3	US-08-974-549A-642	Sequence 642, App
c 558	56	12.1	5793	4	US-09-869-855A-3	Sequence 3, Appli	C 631	55.5	12.0	3396	3	US-09-721-456-642	Sequence 642, App
c 559	56	12.1	5943	4	US-09-869-855A-2	Sequence 2, Appli	C 632	55.5	12.0	3756	3	US-09-085-848-1	Sequence 1, Appli
560	56	12.1	6169	2	US-08-875-154-2	Sequence 2, Appli	C 633	55.5	12.0	3756	1	US-09-562-616-1	Sequence 1, Appli
561	56	12.1	6405	4	US-09-869-855A-1	Sequence 1, Appli	C 634	55.5	12.0	3766	1	US-08-032-364-1	Sequence 1, Appli
c 562	56	12.1	7026	3	US-09-313-677-20	Sequence 20, Appl	C 635	55.5	12.0	3792	4	US-09-710-279-3396	Sequence 3396, Ap
c 563	56	12.1	7344	3	US-09-313-677-16	Sequence 16, Appl	C 636	55.5	12.0	3998	4	US-09-710-279-3962	Sequence 3962, Ap
564	56	12.1	9144	3	US-08-556-978B-79	Sequence 79, Appl	C 637	55.5	12.0	4047	3	US-09-534-407-4	Sequence 4, Appli
565	56	12.1	9465	4	US-09-206-551-1	Sequence 1, Appli	C 638	55.5	12.0	4047	4	US-09-399-201B-3	Sequence 3, Appli
566	56	12.1	9663	4	US-09-869-588-22	Sequence 22, Appl	C 639	55.5	12.0	4047	4	US-10-281-673A-3	Sequence 3, Appli
567	56	12.1	9726	4	US-09-869-588-22	Sequence 22, Appl	C 640	55.5	12.0	4285	3	US-09-040-774-1	Sequence 1, Appli
568	56	12.1	12665	4	US-08-561-527-134	Sequence 134, App	C 641	55.5	12.0	4406	1	US-08-233-788A-39	Sequence 39, Appl
569	56	12.1	43950	3	US-09-735-934A-3	Sequence 3, Appli	C 642	55.5	12.0	4500	2	US-08-743-637B-35	Sequence 35, Appl
570	56	12.1	43950	4	US-10-060-332-3	Sequence 3, Appli	C 643	55.5	12.0	4500	3	US-08-526-840B-35	Sequence 35, Appl
571	56	12.1	43950	4	US-10-339-657-3	Sequence 3, Appli	C 644	55.5	12.0	5331	4	US-09-453-956-1	Sequence 1, Appli
572	56	12.1	319608	4	US-09-539-333D-1	Sequence 1, Appli	C 645	55.5	12.0	9726	4	US-09-841-786-8	Sequence 8, Appli
573	56	12.1	319608	4	US-09-679-409-1	Sequence 1, Appli	C 646	55.5	12.0	11130	4	US-09-841-786-15	Sequence 15, Appl
574	56	12.1	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 647	55.5	12.0	13987	2	US-08-804-227C-13	Sequence 13, Appl
c 575	56	12.1	1830121	4	US-09-557-884-1	Sequence 1, Appli	C 648	55.5	12.0	41684	4	US-09-536-059-1	Sequence 1, Appli
c 576	56	12.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli	C 649	55.5	12.0	42571	2	US-09-810-347-3	Sequence 3, Appli
c 577	56	12.1	1830121	4	US-10-329-960-1	Sequence 1, Appli	C 650	55.5	12.0	44377	2	US-08-804-227C-7	Sequence 7, Appli
c 578	55.5	12.0	255	4	US-09-489-039A-1446	Sequence 1446, Ap	C 651	55.5	12.0	44377	2	US-08-804-198-1	Sequence 1, Appli
c 579	55.5	12.0	318	3	US-09-134-001C-2112	Sequence 2112, Ap	C 652	55.5	12.0	63563	4	US-09-596-002-33	Sequence 33, Appl
580	55.5	12.0	378	4	US-09-071-035-169	Sequence 169, App	C 653	55.5	12.0	193303	4	US-09-497-855A-37	Sequence 37, Appl
c 581	55.5	12.0	428	4	US-09-621-976-17842	Sequence 17842, A	C 654	55.5	12.0	193303	4	US-09-497-855A-44	Sequence 44, Appl
c 582	55.5	12.0	444	4	US-09-248-796A-10169	Sequence 10169, A	C 655	55.5	12.0	536165	4	US-09-214-808-1	Sequence 1, Appli
583	55.5	12.0	431	4	US-09-621-976-2979	Sequence 2979, Ap	C 656	55.5	12.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
584	55.5	12.0	503	4	US-09-621-976-2189	Sequence 2189, Ap	C 657	55.5	12.0	1664976	4	US-09-692-570-1	Sequence 1, Appli
585	55.5	12.0	510	4	US-09-252-991A-5973	Sequence 5973, Ap	C 658	55.5	12.0	183	4	US-09-248-796A-13572	Sequence 13572, A
586	55.5	12.0	651	4	US-09-248-796A-10912	Sequence 10912, A	C 659	55.5	11.9	279	4	US-09-313-294A-1307	Sequence 1307, Ap
587	55.5	12.0	702	4	US-09-248-796A-3522	Sequence 3522, Ap	C 660	55.5	11.9	357	4	US-09-513-999C-9803	Sequence 9803, Ap
588	55.5	12.0	793	3	US-08-971-158-2	Sequence 2, Appli	C 661	55.5	11.9	434	4	US-08-956-171B-1064	Sequence 1064, Ap
589	55.5	12.0	793	4	US-09-416-488-2	Sequence 2, Appli	C 662	55.5	11.9	434	4	US-08-781-986A-1064	Sequence 1064, Ap
c 590	55.5	12.0	844	4	US-10-000-489-19	Sequence 19, Appl	C 663	55.5	11.9	454	4	US-09-621-976-14103	Sequence 14103, A
c 591	55.5	12.0	1040	4	US-09-589-287B-22	Sequence 22, Appl	C 664	55.5	11.9	477	4	US-09-248-796A-9048	Sequence 9048, Ap
c 592	55.5	12.0	1040	4	US-09-588-947A-22	Sequence 22, Appl	C 665	55.5	11.9	547	3	US-09-011-151-14	Sequence 14, Appl
c 593	55.5	12.0	1040	4	US-09-589-286A-22	Sequence 22, Appl	C 666	55.5	11.9	570	3	US-08-425-315-7	Sequence 7, Appli
594	55.5	12.0	1077	3	US-09-134-001C-2796	Sequence 2796, Ap	C 667	55.5	11.9	570	3	US-08-716-190-3	Sequence 3, Appli
595	55.5	12.0	1130	4	US-09-841-786-9	Sequence 9, Appli	C 668	55.5	11.9	585	4	US-09-134-000C-3197	Sequence 3197, Ap
c 596	55.5	12.0	1176	4	US-09-016-434-1144	Sequence 1144, Ap	C 669	55.5	11.9	735	6	US-09-105-058C-7	Sequence 7, Appli
597	55.5	12.0	1246	3	US-09-336-643A-28	Sequence 28, Appl	C 670	55.5	11.9	785	6	5498694-1	Patent No. 5498694
c 598	55.5	12.0	1263	4	US-09-134-000C-3231	Sequence 3231, Ap	C 671	55.5	11.9	837	4	US-09-134-000C-319	Sequence 319, App
599	55.5	12.0	1521	4	US-09-107-532A-2340	Sequence 2340, Ap	C 672	55.5	11.9	872	2	US-08-933-750C-56	Sequence 56, Appl

c 673	55	11.9	872	3	US-09-234-613-56	Sequence 56, Appl	c 746	55	11.9	90050	3	US-09-245-041-5	Sequence 5, Appli
674	55	11.9	1038	4	US-09-248-796A-11086	Sequence 11086, A	c 747	55	11.9	90050	4	US-09-358-055B-5	Sequence 5, Appli
675	55	11.9	1044	4	US-09-710-279-461	Sequence 461, App	c 748	55	11.9	90050	4	US-09-893-238-5	Sequence 5, Appli
676	55	11.9	1044	4	US-09-710-279-1267	Sequence 1267, App	c 749	55	11.9	99629	4	US-09-596-002-37	Sequence 37, Appl
677	55	11.9	1056	3	US-09-134-001C-2655	Sequence 2655, A	750	55	11.9	536165	4	US-09-214-808-1	Sequence 1, Appli
678	55	11.9	1257	4	US-09-252-991A-16527	Sequence 16527, A	751	54.5	11.8	281	1	US-08-087-772A-5	Sequence 5, Appli
c 679	55	11.9	1377	1	US-07-803-457A-14	Sequence 14, Appl	c 752	54.5	11.8	283	4	US-09-513-999C-3229	Sequence 3229, Ap
c 680	55	11.9	1377	1	US-08-476-008-9	Sequence 9, Appli	c 753	54.5	11.8	285	4	US-08-956-171E-4458	Sequence 4458, Ap
c 681	55	11.9	1377	1	US-08-306-063-9	Sequence 9, Appli	754	54.5	11.8	351	4	US-08-781-986A-4458	Sequence 4458, Ap
c 682	55	11.9	1377	1	US-08-553-943-14	Sequence 14, Appl	c 755	54.5	11.8	358	4	US-09-513-999C-8705	Sequence 8705, Ap
c 683	55	11.9	1377	1	US-08-833-485-9	Sequence 9, Appli	c 756	54.5	11.8	354	4	US-09-621-976-3761	Sequence 3761, Ap
c 684	55	11.9	1377	1	US-09-137-440-9	Sequence 9, Appli	c 757	54.5	11.8	492	4	US-09-134-000C-613	Sequence 613, App
c 685	55	11.9	1377	5	PCT-US91-06148A-9	Sequence 9, Appli	c 758	54.5	11.8	515	5	PCT-US96-04648-2	Sequence 2, Appli
c 686	55	11.9	1377	5	PCT-US91-09437-14	Sequence 14, Appl	c 759	54.5	11.8	506	4	US-09-621-976-15297	Sequence 15297, A
c 687	55	11.9	1473	4	US-09-252-991A-1584	Sequence 1584, Ap	760	54.5	11.8	604	4	US-09-636-215-638	Sequence 638, App
c 688	55	11.9	1551	3	US-09-461-474-7	Sequence 7, Appli	761	54.5	11.8	606	4	US-03-685-166A-638	Sequence 638, App
c 689	55	11.9	1702	3	US-08-858-207A-79	Sequence 79, Appl	762	54.5	11.8	606	4	US-09-679-426-638	Sequence 638, App
c 690	55	11.9	1785	4	US-09-489-039A-6762	Sequence 6762, Ap	763	54.5	11.8	606	4	US-09-107-532A-554	Sequence 554, App
c 691	55	11.9	1859	4	US-09-807-258-7	Sequence 7, Appli	c 764	54.5	11.8	870	2	US-08-778-912A-4	Sequence 4, Appli
c 692	55	11.9	2290	4	US-09-149-476-177	Sequence 177, App	c 765	54.5	11.8	870	3	US-09-541-941B-4	Sequence 4, Appli
c 693	55	11.9	2295	4	US-09-270-767-1016	Sequence 1016, Ap	766	54.5	11.8	930	4	US-09-248-796A-6794	Sequence 6794, Ap
c 694	55	11.9	2295	4	US-09-270-767-16298	Sequence 16298, A	767	54.5	11.8	933	4	US-09-107-532A-1926	Sequence 1926, Ap
c 695	55	11.9	2334	4	US-09-434-039A-32	Sequence 32, Appl	768	54.5	11.8	987	4	US-09-964-850-5	Sequence 5, Appli
c 696	55	11.9	2352	4	US-09-434-039A-30	Sequence 30, Appl	769	54.5	11.8	1044	4	US-09-270-767-8440	Sequence 8440, Ap
c 697	55	11.9	2354	4	US-09-710-279-4410	Sequence 4410, Ap	770	54.5	11.8	1044	4	US-09-270-767-1351	Sequence 1351, A
c 698	55	11.9	2631	4	US-09-252-991A-16070	Sequence 16070, A	c 771	54.5	11.8	1068	4	US-09-543-681A-1757	Sequence 1757, Ap
c 699	55	11.9	2749	1	US-07-717-331F-4	Sequence 4, Appli	c 772	54.5	11.8	1105	2	US-08-799-173A-1	Sequence 1, Appli
700	55	11.9	2769	4	US-09-869-588-14	Sequence 14, Appl	c 773	54.5	11.8	1105	4	US-09-170-042A-1	Sequence 1, Appli
701	55	11.9	2769	4	US-09-869-588-20	Sequence 20, Appl	774	54.5	11.8	1184	4	US-09-270-767-10677	Sequence 10677, A
c 702	55	11.9	2864	4	US-09-799-451-2	Sequence 2, Appli	775	54.5	11.8	1218	4	US-09-248-796A-5004	Sequence 5004, Ap
703	55	11.9	2997	4	US-09-539-333D-190	Sequence 190, App	c 776	54.5	11.8	1218	4	US-09-270-767-1351	Sequence 1351, A
704	55	11.9	3001	4	US-09-539-333D-189	Sequence 189, App	c 777	54.5	11.8	1247	4	US-09-270-767-16633	Sequence 16633, A
705	55	11.9	3001	4	US-09-539-333D-191	Sequence 191, App	778	54.5	11.8	1265	4	US-09-964-850-3	Sequence 3, Appli
706	55	11.9	3111	4	US-09-543-681A-3564	Sequence 3564, Ap	779	54.5	11.8	1315	2	US-08-343-101A-8	Sequence 8, Appli
c 707	55	11.9	3153	4	US-09-710-279-3348	Sequence 3348, Ap	780	54.5	11.8	1315	3	US-09-183-688-8	Sequence 8, Appli
c 708	55	11.9	3159	3	US-09-437-054A-7	Sequence 7, Appli	781	54.5	11.8	1315	4	US-09-519-489-8	Sequence 8, Appli
709	55	11.9	3170	3	US-09-344-520-1	Sequence 1, Appli	782	54.5	11.8	1360	1	US-08-087-772A-4	Sequence 4, Appli
710	55	11.9	3170	4	US-09-023-655-1093	Sequence 1093, Ap	c 783	54.5	11.8	1386	2	US-08-408-095-22	Sequence 22, Appl
711	55	11.9	3170	4	US-09-054-272-7	Sequence 7, Appli	c 784	54.5	11.8	1605	2	US-08-356-786-9	Sequence 9, Appli
712	55	11.9	3250	3	US-08-617-860B-1	Sequence 1, Appli	785	54.5	11.8	1688	2	US-08-793-410-1	Sequence 1, Appli
713	55	11.9	3267	4	US-09-710-279-4042	Sequence 4042, Ap	c 786	54.5	11.8	1688	2	US-08-793-410-27	Sequence 27, Appl
714	55	11.9	3281	3	US-09-453-702B-85	Sequence 85, Appl	787	54.5	11.8	1785	4	US-09-117-415B-1	Sequence 1, Appli
715	55	11.9	3618	4	US-09-710-279-3564	Sequence 3564, Ap	c 788	54.5	11.8	1785	4	US-09-732-357B-1	Sequence 1, Appli
716	55	11.9	3873	4	US-09-869-588-31	Sequence 31, Appl	789	54.5	11.8	1839	4	US-09-461-325-23	Sequence 23, Appl
717	55	11.9	3997	3	US-09-409-648-1	Sequence 1, Appli	790	54.5	11.8	1839	4	US-10-012-542-23	Sequence 23, Appl
718	55	11.9	3997	3	US-09-409-648-2	Sequence 2, Appli	791	54.5	11.8	1839	4	US-10-115-123-23	Sequence 23, Appl
719	55	11.9	3997	4	US-09-054-272-43	Sequence 43, Appl	792	54.5	11.8	1842	4	US-09-117-415B-21	Sequence 21, Appl
c 720	55	11.9	4329	4	US-09-614-221A-357	Sequence 357, App	793	54.5	11.8	1896	4	US-09-117-415B-17	Sequence 17, Appl
c 721	55	11.9	6306	1	US-08-466-390-3	Sequence 3, Appli	794	54.5	11.8	1896	4	US-09-117-415B-19	Sequence 19, Appl
c 722	55	11.9	6306	1	US-08-470-950-3	Sequence 3, Appli	795	54.5	11.8	1920	1	US-08-087-772A-1	Sequence 1, Appli
c 723	55	11.9	6306	1	US-08-467-781-3	Sequence 3, Appli	796	54.5	11.8	1949	4	US-09-740-027-1	Sequence 1, Appli
c 724	55	11.9	6306	2	US-08-195-487-3	Sequence 3, Appli	797	54.5	11.8	1950	4	US-09-117-415B-15	Sequence 15, Appl
c 725	55	11.9	6306	2	US-08-483-924-3	Sequence 3, Appli	c 798	54.5	11.8	1954	3	US-09-370-807-3	Sequence 3, Appli
c 726	55	11.9	6306	5	PCT-US93-06160-3	Sequence 3, Appli	c 799	54.5	11.8	1954	3	US-09-921-259-3	Sequence 3, Appli
c 727	55	11.9	6534	3	US-09-194-613-4	Sequence 4, Appli	c 800	54.5	11.8	1961	3	US-09-509-902A-15	Sequence 15, Appl
c 728	55	11.9	6803	3	US-08-665-259-19	Sequence 19, Appl	801	54.5	11.8	2259	1	US-08-420-235B-20	Sequence 20, Appl
c 729	55	11.9	6803	3	US-08-762-500-19	Sequence 19, Appl	c 802	54.5	11.8	2259	2	US-08-845-998-3	Sequence 3, Appli
c 730	55	11.9	8012	3	US-09-182-117-1	Sequence 1, Appli	c 803	54.5	11.8	2259	3	US-09-206-537-3	Sequence 3, Appli
c 731	55	11.9	8012	4	US-09-434-039A-1	Sequence 1, Appli	804	54.5	11.8	2259	3	US-08-793-624-20	Sequence 20, Appl
c 732	55	11.9	8418	3	US-09-182-117-5	Sequence 5, Appli	c 805	54.5	11.8	2259	3	US-09-430-854-3	Sequence 3, Appli
c 733	55	11.9	8418	3	US-09-434-039A-5	Sequence 5, Appli	806	54.5	11.8	2259	5	PCT-US95-10194-20	Sequence 20, Appl
c 734	55	11.9	8798	3	US-09-182-117-4	Sequence 4, Appli	807	54.5	11.8	2290	1	US-08-584-226-1	Sequence 1, Appli
c 735	55	11.9	8798	4	US-09-434-039A-4	Sequence 4, Appli	808	54.5	11.8	2290	3	US-08-961-083-65	Sequence 65, Appl
c 736	55	11.9	10846	4	US-09-098-219B-5	Sequence 5, Appli	809	54.5	11.8	2290	4	US-09-536-784-65	Sequence 65, Appl
c 737	55	11.9	10846	4	US-10-164-204-5	Sequence 5, Appli	810	54.5	11.8	2313	4	US-09-107-532A-734	Sequence 734, App
c 738	55	11.9	10846	4	US-09-923-109-5	Sequence 5, Appli	811	54.5	11.8	2359	4	US-08-961-527-243	Sequence 243, App
c 739	55	11.9	10900	4	US-09-098-219B-6	Sequence 6, Appli	812	54.5	11.8	2417	3	US-09-439-313-334	Sequence 334, App
c 740	55	11.9	10900	4	US-10-164-204-6	Sequence 6, Appli	813	54.5	11.8	2417	3	US-09-352-616A-334	Sequence 334, App
c 741	55	11.9	10900	4	US-09-923-109-6	Sequence 6, Appli	814	54.5	11.8	2417	4	US-09-232-149A-334	Sequence 334, App
742	55	11.9	30350	4	US-10-118-328-3	Sequence 3, Appli	815	54.5	11.8	2417	4	US-09-636-215-334	Sequence 334, App
743	55	11.9	50000	3	US-09-146-053-4	Sequence 4, Appli	816	54.5	11.8	2417	4	US-09-685-166A-334	Sequence 334, App
c 744	55	11.9	54550	4	US-10-327-189-42	Sequence 42, Appli	817	54.5	11.8	2417	4	US-09-688-489-334	Sequence 334, App
745	55	11.9	70559	4	US-09-409-800B-1	Sequence 1, Appli	818	54.5	11.8	2417	4	US-09-679-426-334	Sequence 334, App

819	54.5	11.8	2517	4	US-09-583-110-2564	Sequence 2564, Ap	892	54	11.7	482	4	US-09-370-767-6610	Sequence 6610, Ap
820	54.5	11.8	2531	4	US-09-468-656A-11	Sequence 5, Appli	893	54	11.7	482	4	US-09-270-767-21892	Sequence 21892, A
821	54.5	11.8	2531	4	US-09-468-656A-11	Sequence 11, Appl	894	54	11.7	487	4	US-09-621-976-106	Sequence 106, App
C 822	54.5	11.8	2532	4	US-09-620-312B-888	Sequence 888, App	C 895	54	11.7	525	4	US-09-248-796A-11132	Sequence 11132, A
823	54.5	11.8	3141	4	US-09-614-221A-390	Sequence 390, App	C 896	54	11.7	531	4	US-09-248-796A-113850	Sequence 113850, A
824	54.5	11.8	3437	3	US-08-450-962-3	Sequence 3, Appli	C 897	54	11.7	559	4	US-09-597-771-31	Sequence 31, Appl
825	54.5	11.8	3437	3	US-08-450-962-3	Sequence 3, Appli	C 898	54	11.7	573	2	US-08-290-665A-115	Sequence 115, App
826	54.5	11.8	3451	3	US-08-974-549A-721	Sequence 721, App	899	54	11.7	573	5	PC9-US95-10398-115	Sequence 115, App
C 827	54.5	11.8	3451	4	US-09-721-456-721	Sequence 721, App	900	54	11.7	573	4	US-09-540-236-1408	Sequence 1408, App
828	54.5	11.8	3674	4	US-09-636-215-698	Sequence 698, App	901	54	11.7	897	4	US-09-248-796A-13634	Sequence 13634, A
829	54.5	11.8	3674	4	US-09-636-215-698	Sequence 698, App	902	54	11.7	912	4	US-09-248-796A-5359	Sequence 5359, App
830	54.5	11.8	3674	4	US-09-679-426-698	Sequence 698, App	903	54	11.7	955	4	US-09-270-767-11826	Sequence 11826, A
831	54.5	11.8	3758	4	US-09-976-594-491	Sequence 491, App	904	54	11.7	1017	4	US-09-543-681A-1951	Sequence 1951, Ap
832	54.5	11.8	3839	4	US-09-988-361-10	Sequence 10, Appl	905	54	11.7	1017	4	US-09-489-039A-5737	Sequence 5737, Ap
833	54.5	11.8	4010	2	US-08-785-310A-3	Sequence 3, Appli	906	54	11.7	1124	4	US-09-270-767-11733	Sequence 11733, A
834	54.5	11.8	4465	4	US-09-799-451-142	Sequence 142, App	907	54	11.7	1182	4	US-09-252-991A-16079	Sequence 16079, A
835	54.5	11.8	4898	4	US-09-919-497-35	Sequence 35, Appl	C 908	54	11.7	1455	4	US-09-107-532A-1176	Sequence 107, App
C 836	54.5	11.8	5276	4	US-09-233-857-2	Sequence 2, Appli	C 909	54	11.7	1465	3	US-09-280-116-207	Sequence 207, App
C 837	54.5	11.8	5476	4	US-10-204-708-81	Sequence 81, Appl	C 910	54	11.7	1512	4	US-08-377-031B-4	Sequence 4, Appli
C 838	54.5	11.8	5894	3	US-08-665-259-24	Sequence 24, Appl	C 911	54	11.7	1539	4	US-09-328-352-2066	Sequence 2066, Ap
C 839	54.5	11.8	5894	3	US-08-665-259-24	Sequence 24, Appl	C 912	54	11.7	1560	4	US-09-270-767-11208	Sequence 11208, A
C 840	54.5	11.8	6525	3	US-08-762-500-74	Sequence 74, Appl	913	54	11.7	1642	4	US-09-737-698B-24	Sequence 24, Appl
C 841	54.5	11.8	6775	4	US-09-620-312D-289	Sequence 289, App	914	54	11.7	1642	4	US-09-737-626A-24	Sequence 24, Appl
842	54.5	11.8	6972	4	US-09-595-684B-38	Sequence 38, Appl	C 915	54	11.7	1679	2	US-08-708-958-5	Sequence 5, Appli
843	54.5	11.8	8195	4	US-08-961-527-94	Sequence 94, Appl	916	54	11.7	1798	4	US-09-799-451-669	Sequence 669, App
C 844	54.5	11.8	8453	3	US-09-167-681-45	Sequence 45, Appl	C 917	54	11.7	1838	3	US-08-948-564-1	Sequence 1, Appli
C 845	54.5	11.8	8637	4	US-08-561-527-123	Sequence 123, App	C 918	54	11.7	1914	4	US-09-543-681A-2340	Sequence 2340, Ap
846	54.5	11.8	10182	4	US-08-956-171E-116	Sequence 116, App	C 919	54	11.7	2059	4	US-09-023-655-1062	Sequence 1062, Ap
847	54.5	11.8	10182	4	US-08-781-986A-116	Sequence 116, App	C 920	54	11.7	2073	4	US-09-565-264-1	Sequence 1, Appli
848	54.5	11.8	13863	4	US-09-814-915A-83	Sequence 83, Appl	C 921	54	11.7	2073	4	US-09-565-264-3	Sequence 3, Appli
849	54.5	11.8	14231	4	US-08-961-527-81	Sequence 81, Appl	922	54	11.7	2170	4	US-09-614-034-190	Sequence 190, App
850	54.5	11.8	14753	3	US-09-821-736-3	Sequence 3, Appli	923	54	11.7	2333	1	US-08-392-678-33	Sequence 33, Appl
C 851	54.5	11.8	20710	1	US-08-420-235B-1	Sequence 1, Appli	924	54	11.7	2333	1	US-08-457-304B-33	Sequence 33, Appl
C 852	54.5	11.8	20710	3	US-08-793-624-1	Sequence 1, Appli	925	54	11.7	2334	1	US-08-456-701A-33	Sequence 33, Appl
C 853	54.5	11.8	20710	5	PC9-US95-10194-1	Sequence 1, Appli	926	54	11.7	2334	1	US-08-684-932A-33	Sequence 33, Appl
854	54.5	11.8	31036	4	US-08-956-171E-59	Sequence 59, Appl	927	54	11.7	2334	4	US-09-023-655-996	Sequence 996, App
855	54.5	11.8	31036	4	US-08-781-986A-116	Sequence 59, Appl	928	54	11.7	2335	4	US-09-799-451-346	Sequence 346, App
856	54.5	11.8	35081	2	US-08-752-760A-1	Sequence 1, Appli	929	54	11.7	2449	4	US-09-149-476-241	Sequence 241, App
C 857	54.5	11.8	35100	2	US-08-770-379-18	Sequence 18, Appl	930	54	11.7	2589	4	US-09-328-352-1401	Sequence 1401, Ap
C 858	54.5	11.8	35100	3	US-08-757-669A-18	Sequence 18, Appl	931	54	11.7	2673	3	US-09-336-447A-12	Sequence 12, Appl
C 859	54.5	11.8	35100	3	US-09-230-371A-18	Sequence 18, Appl	932	54	11.7	2673	4	US-09-952-267B-12	Sequence 12, Appl
C 860	54.5	11.8	35408	3	US-08-973-334-3	Sequence 3, Appli	933	54	11.7	2689	2	US-08-876-546A-15	Sequence 15, Appl
C 861	54.5	11.8	35408	3	US-09-563-869A-3	Sequence 3, Appli	934	54	11.7	2689	3	US-09-412-252-15	Sequence 15, Appl
C 862	54.5	11.8	35408	3	US-08-549-489-3	Sequence 3, Appli	C 935	54	11.7	2748	4	US-09-799-451-598	Sequence 598, App
C 863	54.5	11.8	35935	2	US-08-735-609-1	Sequence 1, Appli	C 936	54	11.7	2759	4	US-09-144-367-1	Sequence 1, Appli
C 864	54.5	11.8	35935	3	US-08-735-609-1	Sequence 1, Appli	C 937	54	11.7	2769	4	US-09-252-991A-16403	Sequence 16403, A
C 865	54.5	11.8	35935	3	US-08-379-452-43	Sequence 43, Appl	938	54	11.7	2769	4	US-09-252-991A-16188	Sequence 16188, A
C 866	54.5	11.8	35935	3	US-09-315-372-1	Sequence 1, Appli	939	54	11.7	2934	4	US-09-248-796A-1476	Sequence 1476, Ap
C 867	54.5	11.8	35935	3	US-09-244-752-1	Sequence 1, Appli	C 940	54	11.7	3161	4	US-09-799-451-385	Sequence 385, App
C 868	54.5	11.8	35935	3	US-09-405-497-1	Sequence 1, Appli	941	54	11.7	3222	4	US-09-206-942-48	Sequence 48, Appl
C 869	54.5	11.8	35935	3	US-09-409-670-43	Sequence 43, Appl	942	54	11.7	3240	4	US-09-206-942-46	Sequence 46, Appl
C 870	54.5	11.8	35935	4	US-09-362-919-1	Sequence 1, Appli	C 943	54	11.7	3306	1	US-08-261-206A-71	Sequence 71, Appl
C 871	54.5	11.8	36620	4	US-09-952-060-30	Sequence 30, Appl	944	54	11.7	3417	4	US-09-489-039A-6403	Sequence 6403, Ap
C 872	54.5	11.8	37474	4	US-09-952-060-25	Sequence 25, Appl	945	54	11.7	3636	1	US-07-753-520B-1	Sequence 1, Appli
C 873	54.5	11.8	38519	4	US-09-952-060-28	Sequence 28, Appl	946	54	11.7	3840	3	US-09-245-248B-55	Sequence 55, Appl
C 874	54.5	11.8	87350	3	US-08-781-891-79	Sequence 79, Appl	C 947	54	11.7	4067	4	US-08-894-454-164	Sequence 164, App
C 875	54.5	11.8	87350	4	US-09-618-166-79	Sequence 79, Appl	948	54	11.7	4154	1	US-08-131-365B-37	Sequence 37, Appl
C 876	54.5	11.8	87543	4	US-09-791-211-3	Sequence 3, Appli	949	54	11.7	4154	2	US-08-668-123-37	Sequence 37, Appl
C 877	54.5	11.8	118067	4	US-09-497-855A-32	Sequence 32, Appl	C 950	54	11.7	4286	4	US-09-976-594-632	Sequence 632, App
C 878	54.5	11.8	580073	4	US-08-545-528D-1	Sequence 1, Appli	C 951	54	11.7	4700	2	US-08-928-692-16	Sequence 16, Appl
C 879	54	11.7	234	4	US-08-956-171E-3203	Sequence 3203, Ap	C 952	54	11.7	4700	3	US-09-339-972-16	Sequence 16, Appl
C 880	54	11.7	234	4	US-08-781-986A-3203	Sequence 3203, Ap	C 953	54	11.7	5789	3	US-09-242-948-3	Sequence 3, Appli
C 881	54	11.7	257	4	US-09-513-999C-989	Sequence 989, App	C 954	54	11.7	5904	1	US-07-745-206A-6	Sequence 6, Appli
882	54	11.7	303	4	US-09-843-472-10	Sequence 10, Appl	C 955	54	11.7	5904	1	US-08-455-543A-3	Sequence 3, Appli
883	54	11.7	317	4	US-09-270-767-1902	Sequence 900, App	C 956	54	11.7	5904	2	US-08-193-078B-3	Sequence 3, Appli
884	54	11.7	317	4	US-09-270-767-1492	Sequence 1492, App	C 957	54	11.7	5904	2	US-08-223-305C-3	Sequence 3, Appli
885	54	11.7	317	4	US-09-270-767-16182	Sequence 16182, A	C 958	54	11.7	5904	2	US-08-149-097D-3	Sequence 3, Appli
886	54	11.7	317	4	US-09-270-767-16774	Sequence 16774, A	C 959	54	11.7	5904	2	US-08-311-363-6	Sequence 6, Appli
887	54	11.7	364	4	US-09-513-999C-8646	Sequence 8646, App	C 960	54	11.7	6575	3	US-08-949-386-3	Sequence 3, Appli
888	54	11.7	367	4	US-09-270-767-27358	Sequence 27358, A	C 961	54	11.7	6575	3	US-08-450-562-3	Sequence 3, Appli
889	54	11.7	432	4	US-09-134-000C-889	Sequence 889, App	C 962	54	11.7	6575	3	US-08-984-709A-3	Sequence 3, Appli
890	54	11.7	465	4	US-09-252-991A-15982	Sequence 15982, A	C 963	54	11.7	6575	3	US-08-450-272-3	Sequence 3, Appli
C 891	54	11.7	471	4	US-09-248-796A-5664	Sequence 5664, Ap	C 964	54	11.7	6575	4	US-08-450-273-3	Sequence 3, Appli

c 965	54	11.7	6725	3	US-08-949-386-36	Sequence 36, Appl	c1038	53.5	11.6	2378	4	US-09-148-545-45	Sequence 45, Appl
c 966	54	11.7	6725	3	US-08-450-562-36	Sequence 36, Appl	1039	53.5	11.6	2415	3	US-09-134-001C-2381	Sequence 2381, Ap
c 967	54	11.7	6725	3	US-08-984-709A-36	Sequence 36, Appl	1040	53.5	11.6	2472	4	US-09-107-532A-2013	Sequence 407, Appl
c 968	54	11.7	6725	3	US-08-450-272-36	Sequence 36, Appl	c1041	53.5	11.6	2497	4	US-09-620-312D-47	Sequence 47, Appl
c 969	54	11.7	6725	4	US-08-450-273-36	Sequence 36, Appl	1042	53.5	11.6	2607	4	US-09-520-781-11	Sequence 11, Appl
c 970	54	11.7	9633	6	5223423-1	Patent No. 5223423	c1043	53.5	11.6	2820	1	US-08-286-305A-4	Sequence 4, Appl
c 971	54	11.7	18994	1	US-08-453-586-4	Sequence 4, Appl	c1044	53.5	11.6	2820	2	US-08-441-104A-4	Sequence 4, Appl
c 972	54	11.7	18994	2	US-08-282-696-4	Sequence 4, Appl	c1045	53.5	11.6	2820	2	US-08-440-816A-4	Sequence 4, Appl
c 973	54	11.7	26016	4	US-09-328-480A-1	Sequence 1, Appl	c1046	53.5	11.6	2820	3	US-09-417-361A-4	Sequence 6, Appl
c 974	54	11.7	44453	3	US-09-146-053-5	Sequence 5, Appl	c1047	53.5	11.6	3061	3	US-09-147-119-6	Sequence 6, Appl
c 975	54	11.7	46718	4	US-09-816-093-3	Sequence 3, Appl	c1048	53.5	11.6	3108	4	US-09-206-942-72	Sequence 72, Appl
c 976	54	11.7	72604	3	US-09-268-992-7	Sequence 7, Appl	c1049	53.5	11.6	3169	4	US-09-620-312D-713	Sequence 713, App
c 977	54	11.7	72604	3	US-09-657-474-7	Sequence 7, Appl	c1050	53.5	11.6	3172	4	US-09-976-594-400	Sequence 400, App
c 978	54	11.7	94750	4	US-09-596-002-38	Sequence 38, Appl	c1051	53.5	11.6	3328	4	US-09-710-279-3446	Sequence 3446, Ap
c 979	54	11.7	229354	4	US-09-765-400-64	Sequence 64, Appl	c1052	53.5	11.6	3701	4	US-09-710-279-3392	Sequence 3392, Ap
c 980	54	11.7	229354	4	US-09-705-400-64	Sequence 64, Appl	c1053	53.5	11.6	3760	2	US-08-724-354D-1	Sequence 1, Appl
c 981	54	11.7	269223	4	US-09-596-002-41	Sequence 41, Appl	c1054	53.5	11.6	3760	3	US-09-270-984A-1	Sequence 1, Appl
c 982	54	11.7	640681	4	US-09-790-988-1	Sequence 1, Appl	c1055	53.5	11.6	4680	1	US-08-254-358-1	Sequence 1, Appl
c 983	53.5	11.6	267	4	US-09-543-681A-1151	Sequence 1151, Ap	c1056	53.5	11.6	4680	1	US-08-475-391-1	Sequence 1, Appl
c 984	53.5	11.6	363	4	US-08-635-109-16	Sequence 16, Appl	c1057	53.5	11.6	4680	2	US-08-709-609-1	Sequence 1, Appl
c 985	53.5	11.6	363	4	US-08-844-215-25	Sequence 25, Appl	c1058	53.5	11.6	4680	5	PCT-US95-07178-1	Sequence 1, Appl
c 986	53.5	11.6	377	4	US-09-621-976-17228	Sequence 17228, A	c1059	53.5	11.6	4681	4	US-09-807-802A-18	Sequence 18, Appl
c 987	53.5	11.6	378	4	US-09-621-976-18563	Sequence 18563, A	c1060	53.5	11.6	4683	4	US-09-807-802A-19	Sequence 19, Appl
c 988	53.5	11.6	393	4	US-09-513-999C-1152	Sequence 1152, Ap	c1061	53.5	11.6	4937	1	US-08-038-682-3	Sequence 3, Appl
c 989	53.5	11.6	432	4	US-09-543-681A-3204	Sequence 3204, Ap	c1062	53.5	11.6	4937	1	US-08-302-832-3	Sequence 3, Appl
c 990	53.5	11.6	473	4	US-09-621-976-1652	Sequence 1652, Ap	c1063	53.5	11.6	4937	2	US-08-530-198-3	Sequence 3, Appl
c 991	53.5	11.6	489	4	US-09-543-681A-2007	Sequence 2007, Ap	c1064	53.5	11.6	4937	2	US-08-469-880-3	Sequence 3, Appl
c 992	53.5	11.6	489	4	US-09-621-976-3289	Sequence 3289, Ap	c1065	53.5	11.6	4937	2	US-08-728-470-3	Sequence 3, Appl
c 993	53.5	11.6	564	4	US-09-621-976-1172	Sequence 1172, Ap	c1066	53.5	11.6	4937	2	US-08-617-697-3	Sequence 3, Appl
c 994	53.5	11.6	564	4	US-09-621-976-3738	Sequence 3738, Ap	c1067	53.5	11.6	4937	3	US-08-719-641-3	Sequence 3, Appl
c 995	53.5	11.6	621	4	US-09-252-991A-13664	Sequence 13664, A	c1068	53.5	11.6	4937	4	US-09-206-942-70	Sequence 70, Appl
c 996	53.5	11.6	631	4	US-09-569-098A-93	Sequence 93, Appl	c1069	53.5	11.6	5263	4	US-09-060-299-31	Sequence 31, Appl
c 997	53.5	11.6	641	4	US-09-270-767-1313	Sequence 1313, Ap	c1070	53.5	11.6	5263	4	US-09-402-923A-31	Sequence 31, Appl
c 998	53.5	11.6	641	4	US-09-270-767-16595	Sequence 16595, A	c1071	53.5	11.6	5342	3	US-08-902-632-1	Sequence 1, Appl
c 999	53.5	11.6	678	3	US-08-998-416-985	Sequence 985, App	c1072	53.5	11.6	5455	1	US-08-342-930-1	Sequence 1, Appl
c1000	53.5	11.6	897	4	US-09-248-796A-4056	Sequence 4056, Ap	c1073	53.5	11.6	5512	4	US-09-866-153-5	Sequence 5, Appl
c1001	53.5	11.6	936	4	US-09-543-681A-1391	Sequence 1391, Ap	c1074	53.5	11.6	5512	4	US-09-693-467A-5	Sequence 5, Appl
c1002	53.5	11.6	987	4	US-09-142-584-1	Sequence 1, Appl	c1075	53.5	11.6	5512	4	US-09-270-976-5	Sequence 5, Appl
c1003	53.5	11.6	987	4	US-09-142-584-3	Sequence 3, Appl	c1076	53.5	11.6	5590	3	US-09-050-159-129	Sequence 129, App
c1004	53.5	11.6	987	4	US-09-142-584-5	Sequence 5, Appl	c1077	53.5	11.6	6142	3	US-09-514-302-1	Sequence 1, Appl
c1005	53.5	11.6	1029	4	US-10-010-577-1	Sequence 1, Appl	c1078	53.5	11.6	6142	4	US-10-014-436-1	Sequence 1, Appl
c1006	53.5	11.6	1093	4	US-09-489-039A-381	Sequence 381, App	c1079	53.5	11.6	6314	4	US-09-620-312D-98	Sequence 98, Appl
c1007	53.5	11.6	1047	3	US-09-137-885-3	Sequence 3, Appl	c1080	53.5	11.6	6426	4	US-09-976-594-136	Sequence 136, App
c1008	53.5	11.6	1128	4	US-09-107-532A-1134	Sequence 1134, Ap	c1081	53.5	11.6	8698	4	US-09-770-315-2	Sequence 2, Appl
c1009	53.5	11.6	1178	3	US-09-091-405-1	Sequence 1, Appl	c1082	53.5	11.6	9323	1	US-08-038-682-6	Sequence 6, Appl
c1010	53.5	11.6	1266	3	US-09-193-637A-115	Sequence 115, App	c1083	53.5	11.6	9323	1	US-08-302-832-6	Sequence 6, Appl
c1011	53.5	11.6	1299	3	US-09-199-637A-160	Sequence 160, App	c1084	53.5	11.6	9323	2	US-08-530-198-6	Sequence 6, Appl
c1012	53.5	11.6	1299	3	US-09-543-681A-1197	Sequence 1197, Ap	c1085	53.5	11.6	9323	2	US-08-469-880-6	Sequence 6, Appl
c1013	53.5	11.6	1353	3	US-09-518-657-3	Sequence 3, Appl	c1086	53.5	11.6	9323	2	US-08-728-470-6	Sequence 6, Appl
c1014	53.5	11.6	1365	3	US-09-134-001C-710	Sequence 710, App	c1087	53.5	11.6	9323	2	US-08-617-697-6	Sequence 6, Appl
c1015	53.5	11.6	1368	4	US-09-489-039A-6962	Sequence 6962, Ap	c1088	53.5	11.6	9323	2	US-08-719-641-6	Sequence 6, Appl
c1016	53.5	11.6	1405	4	US-09-016-434-1316	Sequence 1316, Ap	c1089	53.5	11.6	148567	4	US-09-801-876B-3	Sequence 3, Appl
c1017	53.5	11.6	1490	4	US-09-774-528-79	Sequence 79, Appl	c1090	53.5	11.6	148567	4	US-10-254-869-3	Sequence 3, Appl
c1018	53.5	11.6	1498	3	US-09-412-102-5	Sequence 5, Appl	c1091	53.5	11.6	161652	4	US-09-497-855A-40	Sequence 40, Appl
c1019	53.5	11.6	1498	3	US-09-412-102-9	Sequence 9, Appl	c1092	53.5	11.6	174493	4	US-09-804-471A-3	Sequence 3, Appl
c1020	53.5	11.6	1498	3	US-09-217-787-5	Sequence 5, Appl	c1093	53.5	11.6	174493	4	US-10-238-709-3	Sequence 3, Appl
c1021	53.5	11.6	1498	3	US-09-217-787-9	Sequence 9, Appl	c1094	53	11.5	146	4	US-09-513-999C-20330	Sequence 20330, A
c1022	53.5	11.6	1598	3	US-09-518-657-6	Sequence 6, Appl	c1095	53	11.5	228	4	US-09-621-976-11271	Sequence 11271, A
c1023	53.5	11.6	1685	6	5340934-1	Patent No. 5340934	c1096	53	11.5	247	4	US-09-016-434-771	Sequence 771, App
c1024	53.5	11.6	1752	3	US-09-360-779-1	Sequence 1, Appl	c1097	53	11.5	253	4	US-09-491-356C-13	Sequence 13, Appl
c1025	53.5	11.6	1752	3	US-09-435-335-1	Sequence 1, Appl	c1098	53	11.5	257	4	US-09-270-767-4642	Sequence 4642, Ap
c1026	53.5	11.6	1792	2	US-08-386-198A-18	Sequence 18, Appl	c1099	53	11.5	257	4	US-09-270-767-19924	Sequence 19924, A
c1027	53.5	11.6	1884	3	US-08-784-582-70	Sequence 70, Appl	c1100	53	11.5	282	4	US-09-313-294A-6585	Sequence 6585, Ap
c1028	53.5	11.6	1890	3	US-08-935-855-19	Sequence 19, Appl	c1101	53	11.5	303	4	US-09-543-681A-1734	Sequence 1734, Ap
c1029	53.5	11.6	2051	3	US-09-199-637A-114	Sequence 114, App	c1102	53	11.5	306	2	US-08-537-811-35	Sequence 35, Appl
c1030	53.5	11.6	2086	3	US-08-589-028-9	Sequence 9, Appl	c1103	53	11.5	312	3	US-08-793-450-1	Sequence 1, Appl
c1031	53.5	11.6	2086	3	US-08-784-582-9	Sequence 9, Appl	c1104	53	11.5	384	4	US-09-621-976-19060	Sequence 19060, A
c1032	53.5	11.6	2086	3	US-08-785-271-9	Sequence 9, Appl	c1105	53	11.5	455	4	US-09-270-767-28009	Sequence 28009, A
c1033	53.5	11.6	2136	4	US-09-023-655-1144	Sequence 1144, Ap	c1106	53	11.5	468	1	US-08-236-311-12	Sequence 12, Appl
c1034	53.5	11.6	2225	4	US-09-799-451-833	Sequence 833, App	c1107	53	11.5	468	3	US-08-457-918-12	Sequence 12, Appl
c1035	53.5	11.6	2259	4	US-09-710-279-347	Sequence 347, App	c1108	53	11.5	468	4	US-10-157-408-12	Sequence 12, Appl
c1036	53.5	11.6	2341	4	US-09-520-781-9	Sequence 9, Appl	c1109	53	11.5	485	4	US-09-686-583B-34	Sequence 34, Appl
c1037	53.5	11.6	2356	3	US-08-784-582-72	Sequence 72, Appl	c1110	53	11.5	533	3	US-09-097-767A-36	Sequence 36, Appl

1111	53	11.5	573	2	US-08-290-665A-119	Sequence 119, App	1184	53	11.5	1317	1	US-08-153-848-45	Sequence 45, Appl
1112	53	11.5	573	5	PCT-US96-10398-119	Sequence 119, App	1185	53	11.5	1317	3	US-09-299-843A-45	Sequence 45, Appl
1113	53	11.5	573	4	US-09-270-767-28647	Sequence 28647, A	1186	53	11.5	1317	3	US-09-088-337B-45	Sequence 45, Appl
1114	53	11.5	666	4	US-09-489-039A-3457	Sequence 3457, App	1187	53	11.5	1317	5	PCT-US93-11153-45	Sequence 45, Appl
1115	53	11.5	666	4	US-09-252-991A-11037	Sequence 11037, A	1188	53	11.5	1422	1	US-08-378-761A-16	Sequence 16, Appl
1116	53	11.5	716	3	US-08-793-445A-5	Sequence 5, Appl	1189	53	11.5	1422	1	US-08-485-286-16	Sequence 16, Appl
1117	53	11.5	716	3	US-08-323-445A-5	Sequence 5, Appl	1190	53	11.5	1470	3	US-09-212-609B-11	Sequence 11, Appl
1118	53	11.5	755	1	US-08-515-903A-5	Sequence 5, Appl	1191	53	11.5	1483	1	US-07-966-187-11	Sequence 11, Appl
1119	53	11.5	755	5	PCT-US95-12840-5	Sequence 5, Appl	1192	53	11.5	1483	1	US-07-966-187-13	Sequence 13, Appl
1120	53	11.5	785	4	US-09-252-991A-4869	Sequence 4869, App	1193	53	11.5	1488	4	US-09-579-182-4	Sequence 4, Appl
1121	53	11.5	765	4	US-09-252-991A-16546	Sequence 16546, A	1194	53	11.5	1509	4	US-09-799-451-644	Sequence 44, App
1122	53	11.5	776	3	US-08-462-351-4	Sequence 4, Appl	1195	53	11.5	1513	4	US-09-686-583B-39	Sequence 39, Appl
1123	53	11.5	776	4	US-09-602-807-4	Sequence 4, Appl	1196	53	11.5	1513	4	US-09-686-583B-41	Sequence 41, Appl
1124	53	11.5	776	6	5194425-5	Patent No. 5194425	1197	53	11.5	1515	4	US-09-614-221A-207	Sequence 207, App
1125	53	11.5	776	6	5468481-4	Patent No. 5468481	1198	53	11.5	1515	4	US-09-543-681A-338	Sequence 338, App
1126	53	11.5	783	4	US-09-270-767-2254	Sequence 2254, App	1199	53	11.5	1539	3	US-09-383-318A-1	Sequence 1, Appl
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1170	53	11.5	1161	4	US-09-686-583B-49	Sequence 49, App	1243	53	11.5	2200	4	US-09-168-595-102	Sequence 102, App
1171	53	11.5	1191	4	US-09-686-583B-45	Sequence 45, App	1244	53	11.5	2259	4	US-09-489-039A-6360	Sequence 6360, App
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1173	53	11.5	1192	4	US-09-774-528-90	Sequence 90, App	1246	53	11.5	2712	3	US-09-370-767-10233	Sequence 10233, A
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1175	53	11.5	1202	4	US-09-270-767-15418	Sequence 15418, A	1248	53	11.5	2979	4	US-09-206-942-58	Sequence 58, Appl
1176	53	11.5	1219	4	US-09-799-451-166	Sequence 166, App	1249	53	11.5	3430	4	US-09-484-970B-59	Sequence 59, Appl
1177	53	11.5	1227	4	US-09-248-796A-3484	Sequence 3484, App	1250	53	11.5	3521	4	US-09-585-173B-35	Sequence 35, Appl
1178	53	11.5	1244	3	US-09-097-767A-22	Sequence 22, App	1251	53	11.5	3521	3	US-09-081-345-1	Sequence 1, Appl
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1308	52.5	11.4	485	4	US-09-956-004-104	Sequence 104, App	1381	52.5	11.4	1785	4	US-09-355-214-4	Sequence 4, Appli
1309	52.5	11.4	486	4	US-09-270-767-9165	Sequence 9165, Ap	1382	52.5	11.4	1794	4	US-09-252-991A-15502	Sequence 15502, A
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1312	52.5	11.4	528	4	US-09-248-796A-12627	Sequence 12627, A	1385	52.5	11.4	1806	4	US-09-355-214-2	Sequence 2, Appli
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1316	52.5	11.4	603	4	US-09-107-532A-2314	Sequence 2314, Ap	c1389	52.5	11.4	1839	2	US-08-564-900A-1	Sequence 1, Appli
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1323	52.5	11.4	652	4	US-09-270-767-13153	Sequence 13153, A	1396	52.5	11.4	1894	3	US-09-137-440-66	Sequence 66, Appli
1324	52.5	11.4	654	1	US-08-187-756C-1	Sequence 1, Appli	1397	52.5	11.4	1914	2	US-08-670-479-24	Sequence 24, Appli
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2004, 04:05:35 ; Search time 2628 Seconds

(without alignments)
188.179 Million cell updates/sec

Perfect score: 462

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 3694831 seqs, 2747406616 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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84	462	100.0	713	14	US-10-140-002-473	Sequence 473, App
214	462	100.0	713	15	US-10-175-590-473	Sequence 473, Appli
518	247.5	53.6	1018	15	US-10-270-470-5	Sequence 5, Appli
519	247.5	53.6	1281	9	US-09-764-870-223	Sequence 223, App
520	247.5	53.6	1281	14	US-10-125-540-223	Sequence 223, App
521	79	17.1	168325	13	US-10-087-192-955	Sequence 955, App
c 522	76.5	16.6	1737	9	US-09-764-864-133	Sequence 133, App
523	75	16.2	595	9	US-09-864-761-9478	Sequence 9478, App
524	75	16.2	1537	16	US-10-424-599-16789	Sequence 16789, A
525	73	15.8	1941	16	US-10-424-599-73057	Sequence 73057, A
526	72.5	15.7	21064	17	US-10-322-281-741	Sequence 741, App
c 527	72	15.6	649	17	US-10-767-701-8829	Sequence 8829, Ap
528	72	15.6	671	18	US-10-425-115-137331	Sequence 137331,
c 529	72	15.6	863	18	US-10-425-115-37046	Sequence 37046, A
c 530	70.5	15.3	1799	9	US-09-349-385-13	Sequence 13, Appli
531	70	15.2	629	18	US-10-653-047-4053	Sequence 4053, Ap
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533	70	15.2	771	16	US-10-398-221-2515	Sequence 2515, Ap
534	70	15.2	1855	17	US-10-437-963-61089	Sequence 61089, A
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536	70	15.2	181259	16	US-10-456-930-2	Sequence 2, Appli
c 537	70	15.2	684707	16	US-10-398-221-9	Sequence 9, Appli
c 538	70	15.2	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
c 539	69.5	15.0	729	17	US-10-437-963-66878	Sequence 66878, A
540	69.5	15.0	771	13	US-10-044-090-474	Sequence 474, App
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544	69.5	15.0	2271	14	US-10-004-860-243	Sequence 243, App
545	69.5	15.0	2271	14	US-10-023-282-243	Sequence 243, App
546	69.5	15.0	2276	10	US-09-933-767-183	Sequence 183, App
547	69.5	15.0	2276	14	US-10-004-860-183	Sequence 183, App
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c 551	69	14.9	14637	15	US-10-074-024-574	Sequence 574, App
552	69	14.9	70215	13	US-10-087-192-217	Sequence 217, App
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557	68.5	14.8	535	15	US-10-027-632-87173	Sequence 87173, A
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c 560	68.5	14.8	1742	9	US-09-764-864-575	Sequence 575, App
561	68.5	14.8	2165	18	US-10-425-115-164694	Sequence 164694,
562	68.5	14.8	3413	14	US-10-165-603-27	Sequence 27, Appli
563	68.5	14.8	3413	16	US-10-152-319A-1480	Sequence 1480, Ap
c 564	68.5	14.8	126192	13	US-10-087-192-1459	Sequence 1459, Ap
565	68	14.7	843	16	US-10-282-122A-41234	Sequence 41234, A
c 566	68	14.7	1990	15	US-10-104-047-1103	Sequence 1103, Ap
c 567	68	14.7	2625	10	US-09-957-880A-4	Sequence 4, Appli
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569	68	14.7	4051	15	US-10-369-493-46393	Sequence 46393, A
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c 572	67.5	14.6	1539	15	US-10-084-817-232	Sequence 232, App
c 573	67.5	14.6	1699	13	US-10-002-600-62	Sequence 62, Appli
c 574	67.5	14.6	1700	13	US-10-098-841-329	Sequence 329, App
c 575	67.5	14.6	2922	10	US-09-374-046A-93	Sequence 93, Appli
c 576	67.5	14.6	2922	16	US-10-616-263-93	Sequence 93, Appli
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579	67	14.5	804	9	US-09-908-855-35	Sequence 35, Appli
c 580	67	14.5	1080	16	US-10-425-114-23160	Sequence 29160, A
c 581	67	14.5	1132	16	US-10-425-114-33690	Sequence 33690, A
c 582	67	14.5	1132	18	US-10-425-115-21180	Sequence 21180, A
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587	67	14.5	87311	13	US-10-087-192-1417	Sequence 1417, App	65	14.1	3935	17	US-10-775-920-195	Sequence 195, App
588	66.5	14.4	724	18	US-10-363-345A-39839	Sequence 39839, A	65	14.1	3969	17	US-10-437-963-10511	Sequence 10511, A
589	66.5	14.4	724	18	US-10-363-345A-39840	Sequence 39840, A	66	14.1	4125	17	US-10-775-920-198	Sequence 198, App
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593	66	14.3	971	17	US-10-417-973-128	Sequence 101931, A	65	14.1	9345	17	US-10-742-350-28	Sequence 28, Appl
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601	66	14.3	3659	10	US-09-764-864-1668	Sequence 1668, App	65	14.1	251364	14	US-10-175-523-58	Sequence 61, Appl
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631	65	14.1	1898	14	US-10-197-666A-29	Sequence 29, Appl	65	14.0	6251	15	US-10-299-642-19	Sequence 8995, App
632	65	14.1	1898	15	US-10-024-298A-84	Sequence 84, Appl	65	14.0	10812	10	US-09-764-891-8995	Sequence 2110, App
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639	65	14.1	2018	15	US-10-024-298A-86	Sequence 86, Appl	65	14.0	371	9	US-09-960-352-11197	Sequence 1205, App
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655	65	14.1	3922	14	US-10-116-802-133	Sequence 133, App	65	14.0	2670	15	US-10-369-493-32390	Sequence 32390, A
656	65	14.1	3935	14	US-10-238-876-1	Sequence 1, Appl	65	14.0	2670	15	US-10-369-493-32390	Sequence 21, Appl
657	65	14.1	3935	15	US-10-177-2935-1	Sequence 1, Appl	65	14.0	3507	17	US-10-428-961-21	Sequence 547, App
658	65	14.1	3935	16	US-10-159-563-288	Sequence 288, App	65	14.0	5817	17	US-10-755-889-547	Sequence 121, App

732	64	13.9	83698	17	US-10-416-898-9	Sequence 9, Appli	C 805	63.5	13.7	52479	11	US-09-997-722-61	Sequence 61, Appl
733	64	13.9	91697	18	US-10-417-375-36	Sequence 36, Appl	C 806	63.5	13.7	119501	15	US-10-174-319-15	Sequence 15, Appl
734	64	13.9	172570	17	US-10-450-826-114	Sequence 114, App	C 807	63.5	13.7	122186	10	US-09-563-728A-36	Sequence 36, Appl
735	64	13.9	219352	17	US-10-322-281-45	Sequence 45, Appl	C 808	63.5	13.7	326014	9	US-09-731-231A-3	Sequence 3, Appli
736	64	13.9	3011208	16	US-10-289-762-1	Sequence 1, Appli	C 809	63.5	13.7	326014	17	US-10-751-985-3	Sequence 3, Appli
737	64	13.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap	C 810	63.5	13.7	2731748	17	US-10-297-465A-1	Sequence 1, Appli
738	63.5	13.7	213	18	US-10-425-115-15406	Sequence 15406, A	C 811	63	13.6	357	16	US-10-424-599-75614	Sequence 75614, A
739	63.5	13.7	313	16	US-10-242-535A-11477	Sequence 11477, A	C 812	63	13.6	444	16	US-10-243-535A-27210	Sequence 27210, A
740	63.5	13.7	313	16	US-10-085-783A-11477	Sequence 11477, A	C 813	63	13.6	444	16	US-10-085-783A-27210	Sequence 27210, A
741	63.5	13.7	473	17	US-10-767-701-29827	Sequence 29827, A	C 814	63	13.6	445	9	US-09-867-550-1349	Sequence 1349, Ap
742	63.5	13.7	537	18	US-10-425-115-87598	Sequence 87598, A	C 815	63	13.6	528	17	US-10-767-701-25616	Sequence 25616, A
743	63.5	13.7	562	9	US-09-796-692-4924	Sequence 4924, Ap	C 816	63	13.6	555	18	US-10-425-115-95611	Sequence 95611, A
744	63.5	13.7	562	14	US-10-040-862-4924	Sequence 4924, Ap	C 817	63	13.6	586	9	US-09-917-800A-1093	Sequence 1093, Ap
745	63.5	13.7	562	16	US-10-057-475B-4924	Sequence 4924, Ap	C 818	63	13.6	602	17	US-10-021-323-14825	Sequence 14825, A
746	63.5	13.7	562	16	US-10-154-884B-4924	Sequence 4924, Ap	C 819	63	13.6	623	16	US-10-424-599-27918	Sequence 27918, A
747	63.5	13.7	562	17	US-10-764-324-4924	Sequence 4924, Ap	C 820	63	13.6	753	16	US-10-239-656-64	Sequence 64, Appl
748	63.5	13.7	568	9	US-09-796-692-4890	Sequence 4890, Ap	C 821	63	13.6	771	9	US-09-910-943-8	Sequence 8, Appli
749	63.5	13.7	568	14	US-10-040-862-4890	Sequence 4890, Ap	C 822	63	13.6	940	17	US-10-437-963-28126	Sequence 28126, A
750	63.5	13.7	568	16	US-10-057-475B-4890	Sequence 4890, Ap	C 823	63	13.6	963	15	US-10-387-629-245	Sequence 245, App
751	63.5	13.7	568	16	US-10-154-884B-4890	Sequence 4890, Ap	C 824	63	13.6	1173	17	US-10-437-963-86718	Sequence 86718, A
752	63.5	13.7	568	17	US-10-764-324-4890	Sequence 4890, Ap	C 825	63	13.6	1282	15	US-10-017-161-885	Sequence 815, App
753	63.5	13.7	588	10	US-09-764-891-2018	Sequence 2018, Ap	C 826	63	13.6	1363	15	US-10-292-798-699	Sequence 699, App
754	63.5	13.7	604	13	US-10-027-632-224616	Sequence 224616, A	C 827	63	13.6	1500	15	US-10-225-086A-541	Sequence 541, App
755	63.5	13.7	604	13	US-10-027-632-224616	Sequence 224616, A	C 828	63	13.6	1500	16	US-10-374-780A-2385	Sequence 2385, Ap
756	63.5	13.7	604	13	US-10-027-632-224616	Sequence 224616, A	C 829	63	13.6	1613	16	US-10-425-114-27030	Sequence 27030, A
757	63.5	13.7	604	13	US-10-027-632-224616	Sequence 224616, A	C 830	63	13.6	1628	18	US-10-425-115-157042	Sequence 157042, A
758	63.5	13.7	604	15	US-10-027-632-224616	Sequence 224616, A	C 831	63	13.6	2118	18	US-10-425-115-156673	Sequence 156673, A
759	63.5	13.7	604	15	US-10-027-632-224616	Sequence 224616, A	C 832	63	13.6	2317	15	US-10-104-047-823	Sequence 823, App
760	63.5	13.7	604	15	US-10-027-632-224616	Sequence 224616, A	C 833	63	13.6	2322	18	US-10-425-115-28507	Sequence 28507, A
761	63.5	13.7	604	15	US-10-027-632-224616	Sequence 224616, A	C 834	63	13.6	2403	18	US-10-425-115-28507	Sequence 2857, Ap
762	63.5	13.7	632	17	US-10-767-701-3096	Sequence 3096, Ap	C 835	63	13.6	2666	18	US-10-739-930-1684	Sequence 1684, Ap
763	63.5	13.7	650	17	US-10-767-701-6949	Sequence 6949, Ap	C 836	63	13.6	2685	15	US-10-156-761-1696	Sequence 1696, Ap
764	63.5	13.7	715	13	US-10-027-632-19262	Sequence 19262, A	C 837	63	13.6	3153	9	US-09-954-456-743	Sequence 743, App
765	63.5	13.7	715	15	US-10-027-632-19262	Sequence 19262, A	C 838	63	13.6	3153	15	US-10-439-388-34	Sequence 34, Appl
766	63.5	13.7	733	13	US-10-027-632-174269	Sequence 174269, A	C 839	63	13.6	3231	15	US-10-104-047-1346	Sequence 1346, Ap
767	63.5	13.7	733	13	US-10-027-632-174270	Sequence 174270, A	C 840	63	13.6	3988	17	US-10-437-963-96143	Sequence 96143, A
768	63.5	13.7	733	15	US-10-027-632-174269	Sequence 174269, A	C 841	63	13.6	4207	18	US-10-425-115-13783	Sequence 13783, A
769	63.5	13.7	733	15	US-10-027-632-174270	Sequence 174270, A	C 842	63	13.6	4861	9	US-09-764-878-395	Sequence 395, App
770	63.5	13.7	760	13	US-10-027-632-172304	Sequence 172304, A	C 843	63	13.6	4861	14	US-10-079-854-395	Sequence 395, App
771	63.5	13.7	760	13	US-10-027-632-172305	Sequence 172305, A	C 844	63	13.6	6068	18	US-10-425-115-112850	Sequence 112850, A
772	63.5	13.7	760	15	US-10-027-632-172305	Sequence 172305, A	C 845	63	13.6	24942	13	US-10-087-192-850	Sequence 850, App
773	63.5	13.7	760	15	US-10-027-632-172305	Sequence 172305, A	C 846	63	13.6	49356	17	US-10-367-094-66	Sequence 66, Appl
774	63.5	13.7	824	16	US-10-425-114-11436	Sequence 11436, A	C 847	63	13.6	83888	13	US-10-087-192-541	Sequence 541, App
775	63.5	13.7	839	13	US-10-027-632-153580	Sequence 153580, A	C 848	63	13.6	146793	17	US-10-388-838-65	Sequence 65, Appl
776	63.5	13.7	839	13	US-10-027-632-153581	Sequence 153581, A	C 849	63	13.6	713059	13	US-10-027-632-174581	Sequence 174581, A
777	63.5	13.7	839	15	US-10-027-632-153580	Sequence 153580, A	C 850	63	13.6	713059	15	US-10-027-632-174581	Sequence 174581, A
778	63.5	13.7	839	15	US-10-027-632-153581	Sequence 153581, A	C 851	62.5	13.5	329	9	US-09-960-352-105	Sequence 105, App
779	63.5	13.7	847	14	US-10-198-846-9879	Sequence 9879, Ap	C 852	62.5	13.5	496	10	US-09-971-392-239	Sequence 239, App
780	63.5	13.7	1090	16	US-10-424-599-4663	Sequence 4663, Ap	C 853	62.5	13.5	499	17	US-10-679-998-1	Sequence 1, Appli
781	63.5	13.7	1097	16	US-10-424-599-26783	Sequence 26783, A	C 854	62.5	13.5	549	18	US-10-425-115-78669	Sequence 78669, A
782	63.5	13.7	1728	9	US-09-864-761-17660	Sequence 17660, A	C 855	62.5	13.5	584	15	US-10-029-386-5831	Sequence 5831, Ap
783	63.5	13.7	1800	15	US-10-190-115-101	Sequence 101, App	C 856	62.5	13.5	609	13	US-10-027-632-33270	Sequence 33270, A
784	63.5	13.7	1800	15	US-10-190-115-103	Sequence 103, App	C 857	62.5	13.5	609	13	US-10-027-632-33270	Sequence 33270, A
785	63.5	13.7	1807	17	US-10-437-963-73509	Sequence 73509, A	C 858	62.5	13.5	609	15	US-10-027-632-33270	Sequence 33270, A
786	63.5	13.7	1927	16	US-10-296-115-603	Sequence 603, App	C 859	62.5	13.5	609	15	US-10-027-632-33271	Sequence 33271, A
787	63.5	13.7	1931	9	US-09-935-986A-5	Sequence 5, Appli	C 860	62.5	13.5	619	18	US-10-425-115-145167	Sequence 145167, A
788	63.5	13.7	2042	15	US-10-104-047-1396	Sequence 1396, Ap	C 861	62.5	13.5	633	18	US-10-653-047-1476	Sequence 1476, Ap
789	63.5	13.7	2118	15	US-10-369-493-25551	Sequence 25551, A	C 862	62.5	13.5	984	16	US-10-320-797-1044	Sequence 1044, Ap
790	63.5	13.7	2286	16	US-10-282-122A-23690	Sequence 23690, A	C 863	62.5	13.5	1140	13	US-10-047-260-11	Sequence 11, Appl
791	63.5	13.7	2476	17	US-10-363-829-146	Sequence 146, App	C 864	62.5	13.5	1140	13	US-10-027-632-118036	Sequence 118036, A
792	63.5	13.7	2601	15	US-10-221-097-6	Sequence 6, Appli	C 865	62.5	13.5	1140	13	US-10-027-632-118037	Sequence 118037, A
793	63.5	13.7	2631	9	US-09-949-192-24	Sequence 24, Appli	C 866	62.5	13.5	1140	13	US-10-027-632-118038	Sequence 118038, A
794	63.5	13.7	2631	15	US-10-190-115-5	Sequence 5, Appli	C 867	62.5	13.5	1140	15	US-10-027-632-118036	Sequence 118036, A
795	63.5	13.7	2631	16	US-10-369-072-5	Sequence 5, Appli	C 868	62.5	13.5	1140	15	US-10-027-632-118037	Sequence 118037, A
796	63.5	13.7	3072	15	US-10-104-047-837	Sequence 837, App	C 869	62.5	13.5	1140	15	US-10-027-632-118038	Sequence 118038, A
797	63.5	13.7	3197	16	US-10-332-426-14	Sequence 14, Appl	C 870	62.5	13.5	1182	17	US-10-437-963-54956	Sequence 54956, A
798	63.5	13.7	3231	13	US-10-027-632-113493	Sequence 113493, A	C 871	62.5	13.5	1197	17	US-10-437-963-88477	Sequence 88477, A
799	63.5	13.7	3231	15	US-10-027-632-113493	Sequence 113493, A	C 872	62.5	13.5	1593	17	US-10-437-963-49151	Sequence 49151, A
800	63.5	13.7	3545	18	US-10-425-115-51504	Sequence 51504, A	C 873	62.5	13.5	1599	9	US-09-841-132-414	Sequence 414, App
801	63.5	13.7	3777	9	US-09-954-456-505	Sequence 505, App	C 874	62.5	13.5	1599	18	US-10-872-155-414	Sequence 414, App
802	63.5	13.7	4450	18	US-10-425-115-123190	Sequence 123190, A	C 875	62.5	13.5	1599	17	US-10-437-963-46545	Sequence 46545, A
803	63.5	13.7	35143	13	US-10-087-192-1894	Sequence 1894, Ap	C 876	62.5	13.5	2279	15	US-10-094-749-529	Sequence 529, App
804	63.5	13.7	52354	9	US-09-742-311-3	Sequence 3, Appli	C 877	62.5	13.5	2454	17	US-10-437-963-49173	Sequence 49173, A

C 878	62.5	13.5	2612	15	US-10-104-047-1151	Sequence 1151, Ap	C 951	62	13.4	209612	17	US-10-322-696-31	Sequence 31, Appl
C 879	62.5	13.5	2984	16	US-10-320-797-44	Sequence 44, Appl	C 952	62	13.4	653122	13	US-10-087-192-226	Sequence 226, App
C 880	62.5	13.5	3039	17	US-10-437-963-33155	Sequence 33155, A	C 953	62	13.4	653122	13	US-10-087-192-226	Sequence 226, App
C 881	62.5	13.5	3147	16	US-10-320-797-81	Sequence 81, Appl	C 954	61.5	13.3	472	10	US-09-918-395-33091	Sequence 33091, A
C 882	62.5	13.5	3229	18	US-10-425-115-72516	Sequence 72516, A	C 955	61.5	13.3	554	13	US-10-027-632-54270	Sequence 54270, A
C 883	62.5	13.5	7809	10	US-09-764-891-60954	Sequence 6094, Ap	C 956	61.5	13.3	554	13	US-10-027-632-77826	Sequence 77826, A
C 884	62.5	13.5	15514	10	US-09-764-891-8621	Sequence 8621, Ap	C 957	61.5	13.3	554	13	US-10-027-632-77827	Sequence 77827, A
C 885	62.5	13.5	15517	10	US-09-764-891-8622	Sequence 8622, Ap	C 958	61.5	13.3	554	13	US-10-027-632-322498	Sequence 322498, A
C 886	62.5	13.5	15518	10	US-09-764-891-8623	Sequence 8623, Ap	C 959	61.5	13.3	554	15	US-10-027-632-54270	Sequence 54270, A
C 887	62.5	13.5	21833	9	US-09-764-877-2275	Sequence 2275, Ap	C 960	61.5	13.3	554	15	US-10-027-632-77826	Sequence 77826, A
C 888	62.5	13.5	21833	16	US-10-242-515-2275	Sequence 2275, Ap	C 961	61.5	13.3	554	15	US-10-027-632-77827	Sequence 77827, A
C 889	62.5	13.5	27204	13	US-10-087-192-1528	Sequence 1528, Ap	C 962	61.5	13.3	554	15	US-10-027-632-322498	Sequence 322498, A
C 890	62.5	13.5	32586	13	US-10-087-192-7	Sequence 7, Appl	C 963	61.5	13.3	570	15	US-10-029-386-12718	Sequence 12718, A
C 891	62.5	13.5	33769	15	US-10-374-979-8	Sequence 8, Appl	C 964	61.5	13.3	619	18	US-10-425-115-57806	Sequence 57806, A
C 892	62.5	13.5	33769	16	US-10-182-936A-8	Sequence 8, Appl	C 965	61.5	13.3	619	17	US-10-767-701-6406	Sequence 6406, Ap
C 893	62.5	13.5	33769	17	US-10-731-739-8	Sequence 8, Appl	C 966	61.5	13.3	645	13	US-10-027-632-141637	Sequence 141637, A
C 894	62.5	13.5	33769	18	US-10-477-238A-8	Sequence 8, Appl	C 967	61.5	13.3	645	15	US-10-027-632-141637	Sequence 141637, A
C 895	62.5	13.5	35403	15	US-10-085-117-85	Sequence 85, Appl	C 968	61.5	13.3	704	13	US-10-027-632-25262	Sequence 25262, A
C 896	62.5	13.5	35421	13	US-10-087-192-1534	Sequence 1534, Ap	C 969	61.5	13.3	704	13	US-10-027-632-25262	Sequence 25262, A
C 897	62.5	13.5	65464	9	US-09-859-888-3	Sequence 3, Appl	C 970	61.5	13.3	704	15	US-10-027-632-25262	Sequence 25262, A
C 898	62.5	13.5	95846	13	US-10-087-192-1414	Sequence 1414, Ap	C 971	61.5	13.3	741	15	US-10-027-632-25263	Sequence 25263, A
C 899	62.5	13.5	156843	13	US-10-087-192-1408	Sequence 1408, Ap	C 972	61.5	13.3	741	17	US-10-027-632-8485	Sequence 8485, A
C 900	62.5	13.5	1503841	9	US-09-795-668-1	Sequence 1, Appl	C 973	61.5	13.3	766	13	US-10-027-632-158597	Sequence 158597, A
C 901	62.5	13.5	1503841	9	US-09-795-668-1	Sequence 1, Appl	C 974	61.5	13.3	766	15	US-10-027-632-158597	Sequence 158597, A
C 902	62.5	13.5	1503841	9	US-09-946-807-1	Sequence 1, Appl	C 975	61.5	13.3	803	13	US-10-027-632-135379	Sequence 135379, A
C 903	62.5	13.5	2731748	17	US-10-297-465A-1	Sequence 1, Appl	C 976	61.5	13.3	803	15	US-10-027-632-135379	Sequence 135379, A
C 904	62	13.4	277	18	US-10-425-115-133608	Sequence 133608, A	C 977	61.5	13.3	871	16	US-10-424-599-59943	Sequence 59943, A
C 905	62	13.4	280	9	US-09-294-033B-590	Sequence 590, App	C 978	61.5	13.3	875	9	US-08-897-231-1	Sequence 1, Appl
C 906	62	13.4	294	11	US-09-922-293-1453	Sequence 1453, Ap	C 979	61.5	13.3	875	9	US-09-897-231-3	Sequence 3, Appl
C 907	62	13.4	851	13	US-10-027-632-28853	Sequence 28853, A	C 980	61.5	13.3	896	18	US-10-425-115-132904	Sequence 132904, A
C 908	62	13.4	851	15	US-10-027-632-28853	Sequence 28853, A	C 981	61.5	13.3	903	17	US-10-437-963-38106	Sequence 38106, A
C 909	62	13.4	854	18	US-10-425-115-14222	Sequence 14222, A	C 982	61.5	13.3	966	17	US-10-802-441-3	Sequence 3, Appl
C 910	62	13.4	889	9	US-09-764-864-466	Sequence 466, App	C 983	61.5	13.3	1220	18	US-10-802-441-1	Sequence 1, Appl
C 911	62	13.4	932	13	US-10-027-632-122298	Sequence 122298, A	C 984	61.5	13.3	1269	17	US-10-425-115-100962	Sequence 100962, A
C 912	62	13.4	932	15	US-10-027-632-122298	Sequence 122298, A	C 985	61.5	13.3	1314	16	US-10-425-114-27613	Sequence 27613, A
C 913	62	13.4	951	17	US-10-802-441-23	Sequence 23, Appl	C 986	61.5	13.3	1587	17	US-10-437-963-35751	Sequence 35751, A
C 914	62	13.4	992	16	US-10-424-599-112249	Sequence 112249, A	C 987	61.5	13.3	1685	18	US-10-425-115-137733	Sequence 137733, A
C 915	62	13.4	1082	18	US-10-363-345A-1555	Sequence 1555, Ap	C 988	61.5	13.3	2061	9	US-09-962-832-239	Sequence 239, App
C 916	62	13.4	1082	18	US-10-363-345A-1555	Sequence 1555, Ap	C 989	61.5	13.3	2061	9	US-09-954-456-1593	Sequence 1593, App
C 917	62	13.4	1205	17	US-10-802-441-21	Sequence 21, Appl	C 990	61.5	13.3	2175	16	US-10-108-260A-559	Sequence 559, App
C 918	62	13.4	1403	17	US-10-437-963-83768	Sequence 83768, A	C 991	61.5	13.3	2367	15	US-10-099-285-91	Sequence 91, Appl
C 919	62	13.4	1470	18	US-10-425-115-50142	Sequence 50142, A	C 992	61.5	13.3	2370	17	US-09-850-351A-5	Sequence 5, Appl
C 920	62	13.4	1675	16	US-10-424-599-129128	Sequence 129128, A	C 993	61.5	13.3	2370	17	US-10-698-096-5	Sequence 5, Appl
C 921	62	13.4	1762	16	US-10-425-114-8659	Sequence 8659, Ap	C 994	61.5	13.3	2547	15	US-10-104-047-819	Sequence 819, App
C 922	62	13.4	1798	17	US-10-437-963-34224	Sequence 34224, A	C 995	61.5	13.3	2562	18	US-10-425-115-1320	Sequence 1320, Ap
C 923	62	13.4	1850	18	US-10-425-115-14200	Sequence 14200, A	C 996	61.5	13.3	2703	15	US-10-155-895-3	Sequence 3, Appl
C 924	62	13.4	1961	16	US-10-424-599-30233	Sequence 30233, A	C 997	61.5	13.3	2774	15	US-10-459-970-1	Sequence 1, Appl
C 925	62	13.4	1980	15	US-10-369-493-46591	Sequence 46591, A	C 998	61.5	13.3	2883	18	US-10-793-639-371	Sequence 371, App
C 926	62	13.4	2197	16	US-10-387-937A-1	Sequence 1, Appl	C 999	61.5	13.3	3651	16	US-10-320-797-197	Sequence 197, App
C 927	62	13.4	2198	18	US-10-817-483-5	Sequence 5, Appl	C 1000	61.5	13.3	4665	17	US-10-437-963-5425	Sequence 5425, Ap
C 928	62	13.4	2474	18	US-10-425-115-51927	Sequence 51927, A	C 1001	61.5	13.3	9319	18	US-09-956-004-85	Sequence 85, Appl
C 929	62	13.4	2628	17	US-10-437-963-9790	Sequence 9790, Ap	C 1002	61.5	13.3	9319	16	US-10-415-058-4	Sequence 4, Appl
C 930	62	13.4	3036	17	US-10-437-963-37943	Sequence 37943, A	C 1003	61.5	13.3	17953	16	US-10-820-002-3	Sequence 3, Appl
C 931	62	13.4	3054	16	US-10-654-416-11	Sequence 11, Appl	C 1004	61.5	13.3	21784	9	US-09-820-002-3	Sequence 3, Appl
C 932	62	13.4	3072	16	US-10-654-416-13	Sequence 13, Appl	C 1005	61.5	13.3	21784	15	US-10-274-031-3	Sequence 3, Appl
C 933	62	13.4	3084	16	US-10-654-416-7	Sequence 7, Appl	C 1006	61.5	13.3	31994	9	US-09-764-860-599	Sequence 599, App
C 934	62	13.4	3129	15	US-10-369-493-42336	Sequence 42336, A	C 1007	61.5	13.3	31994	9	US-09-764-904-71	Sequence 71, Appl
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C 936	62	13.4	4322	18	US-10-425-115-15092	Sequence 15092, A	C 1009	61.5	13.3	31994	14	US-10-074-095-599	Sequence 599, App
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C 938	62	13.4	9232	15	US-10-279-992A-2	Sequence 2, Appl	C 1011	61.5	13.3	32874	16	US-10-052-482-154	Sequence 154, App
C 939	62	13.4	9715	15	US-10-279-992A-6	Sequence 6, Appl	C 1012	61.5	13.3	41522	13	US-10-087-192-1741	Sequence 1741, Ap
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C 943	62	13.4	10274	10	US-09-827-688-5	Sequence 5, Appl	C 1016	61.5	13.3	61791	17	US-10-322-281-645	Sequence 645, App
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c1221	60.5	13.1	2724	18	US-10-425-115-146438	Sequence 146438, A
1222	60.5	13.1	2824	16	US-10-424-599-60402	Sequence 60402, A
1223	60.5	13.1	3025	9	US-09-947-199-1	Sequence 1, Appl
1224	60.5	13.1	3025	17	US-10-626-173-1	Sequence 1, Appl
1225	60.5	13.1	3061	16	US-10-425-114-6150	Sequence 6150, Ap
1226	60.5	13.1	3124	16	US-10-424-599-45543	Sequence 45543, A
1227	60.5	13.1	3341	15	US-10-144-194A-77	Sequence 77, Appl
1228	60.5	13.1	3598	15	US-10-144-194A-75	Sequence 75, Appl
1229	60.5	13.1	3664	15	US-10-144-194A-73	Sequence 73, Appl
c1230	60.5	13.1	3898	10	US-09-764-891-8570	Sequence 8570, Ap
c1231	60.5	13.1	3899	10	US-09-764-891-8571	Sequence 8571, Ap
c1232	60.5	13.1	3899	10	US-09-764-891-8572	Sequence 8572, Ap

Search completed: December 2, 2004, 05:51:01
Job time : 2806 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2004, 04:13:23 : Search time 2373 seconds
(without alignments)
1382.038 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

Sequence: 1 MTFFLSLLLVCEAIWRSN.....DSRGLILGAEANGRVKKNT 90

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+pn.model -DRV=xlh
-Q/cgn2_1/USPTO.spool/US09989293/runat_01122004_102145_13789/app_query.fasta_1.263
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09989293@cgn_1_1_3437@runat_01122004_102145_13789 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gss1:.*
9: gb_gss2:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	365.5	79.1	663	1	AU185777
C 2	306	66.2	800	6	CB958894
C 3	247.5	53.6	659	4	BI018962
C 4	209	45.2	663	8	AZ121459
C 5	206	44.6	673	1	AV721179
C 6	174	37.7	582	6	CB420818
C 7	138.5	30.0	855	4	BI107684
C 8	89	19.3	621	4	BJ675325
C 9	84	18.2	531	9	CL005921

10	82	17.7	833	2	BE865626
C 11	82	17.7	924	4	BG165693
C 12	81	17.5	1121	9	CNS04H30
C 13	80.5	17.4	683	4	BI914658
C 14	79	17.1	391	8	BH354332
C 15	79	17.1	504	8	BH354326
C 16	79	17.1	536	4	BJ193507
C 17	79	17.1	644	5	BQ406117
C 18	79	17.1	645	7	CF735257
C 19	78.5	17.0	884	9	CG183911
C 20	78.5	17.0	929	9	CG457562
C 21	78	16.9	473	7	CF899500
C 22	78	16.9	649	9	CC701258
C 23	78	16.9	653	8	CC171703
C 24	78	16.9	679	9	CG591911
C 25	78	16.9	723	9	AG009588
C 26	78	16.9	752	9	AG399913
C 27	78	16.9	819	9	CC616498
C 28	77.5	16.8	754	5	BP673082
C 29	77	16.7	477	4	BG276251
C 30	77	16.7	626	8	AZ822524
C 31	77	16.7	943	5	BQ920084
C 32	77	16.7	967	8	B08136
C 33	77	16.7	1383	2	BF238075
C 34	76.5	16.6	483	2	BE723365
C 35	76.5	16.6	551	4	BI898668
C 36	76.5	16.6	601	6	CB457947
C 37	76.5	16.6	867	2	BF214995
C 38	76	16.5	320	8	BH198757
C 39	76	16.5	596	7	CO819409
C 40	76	16.5	781	5	BU596994
C 41	76	16.5	968	8	BH135384
C 42	76	16.5	1007	9	CNS021NF
C 43	75.5	16.3	404	8	BH123205
C 44	75.5	16.3	504	1	AA614424
C 45	75.5	16.3	774	5	BI553528
C 46	75.5	16.3	879	5	BX346820
C 47	75.5	16.3	1006	5	BQ721671
C 48	75.5	16.3	1148	9	CG753752
C 49	75.5	16.3	1194	9	AG288428
C 50	75	16.2	533	7	CO699008
C 51	75	16.2	608	1	AV827009
C 52	75	16.2	672	9	CC615145
C 53	75	16.2	717	7	CF433331
C 54	75	16.2	733	8	AZ599571
C 55	75	16.2	989	2	BF970572
C 56	74.5	16.1	363	4	BI799496
C 57	74.5	16.1	416	8	BZ701258
C 58	74.5	16.1	439	9	CL242558
C 59	74.5	16.1	454	8	AZ646965
C 60	74.5	16.1	513	9	CL242205
C 61	74.5	16.1	515	9	CC785997
C 62	74.5	16.1	518	4	BG867189
C 63	74.5	16.1	529	5	BQ620088
C 64	74.5	16.1	534	2	AW421219
C 65	74.5	16.1	635	9	CC937887
C 66	74.5	16.1	648	9	CG412189
C 67	74.5	16.1	665	7	CK349913
C 68	74.5	16.1	713	5	BU719824
C 69	74.5	16.1	714	7	CN066491
C 70	74.5	16.1	747	9	CG357201
C 71	74.5	16.1	788	5	BU271319
C 72	74.5	16.1	804	7	CF948874
C 73	74.5	16.1	834	7	CN067940
C 74	74.5	16.1	908	9	CG357210
C 75	74.5	16.1	920	5	BU901423
C 76	74.5	16.1	921	9	CC987850
C 77	74.5	16.1	3143	9	AY407051
C 78	74	16.0	363	5	BY547544
C 79	74	16.0	419	5	BY536686
C 80	74	16.0	495	9	CG761866
C 81	74	16.0	523	9	CG848025
C 82	74	16.0	577	8	AZ614165

83	74	16.0	718	8	BH942690	odi31a05.	156	71.5	15.5	705	7	CK841550	UI-R-BJ0P
84	74	16.0	773	9	CC827780	ZMPPBb017	157	71.5	15.5	733	8	AQ864248	nbe00022D
85	74	16.0	831	9	CQ227326	OGYAR87TV	c 158	71.5	15.5	786	9	CG809293	FSAAH277F
86	74	16.0	853	5	BX898738	BX898738	c 159	71.5	15.5	863	9	CR069477	Forward s
87	74	16.0	928	6	CB237690	AGENCOURT	c 160	71.5	15.5	920	5	BUS59239	AGENCOURT
88	73.5	15.9	272	6	CA779994	MPL384_3	c 161	71.5	15.5	1021	4	BG117244	602346529
89	73.5	15.9	413	4	B1528576	102409IG1	c 162	71	15.4	442	5	BY007753	BY007753
90	73.5	15.9	482	8	AZ355372	1M0095G03	c 163	71	15.4	469	1	AL830619	AL830619
91	73.5	15.9	511	4	BJ165112	BJ165112	c 164	71	15.4	479	6	CF190483	k8107J2.f
92	73.5	15.9	521	9	CG469914	ZMPPBb026	c 165	71	15.4	485	8	AZ411824	1M0185J02
93	73.5	15.9	531	4	BJ157136	BJ157136	c 166	71	15.4	486	5	BQ039779	gd03a07.Y
94	73.5	15.9	603	4	BJ219257	BJ219257	c 167	71	15.4	486	8	B59572	CIT-HSP-342
95	73.5	15.9	748	4	BJ349579	BJ349579	c 168	71	15.4	506	8	B2891662	CH240_246
96	73.5	15.9	786	8	BH207342	BH207342	c 169	71	15.4	516	6	CD138103	MGL-0051T
97	73.5	15.9	934	2	BF203185	BF203185	c 170	71	15.4	530	6	CF189873	ksh20J2.r
98	73.5	15.9	1020	4	B1852456	B1852456	c 171	71	15.4	568	4	BI477033	dal129a10.
99	73	15.8	289	2	AW781028	s188a09.Y	c 172	71	15.4	593	2	BE284040	601102754
100	73	15.8	389	9	CE000745	t1gr-g8s-	c 173	71	15.4	624	7	CO150738	EST825791
101	73	15.8	422	7	F22961	SSC17F05_Po	c 174	71	15.4	625	5	BQ109837	VD0100841
102	73	15.8	450	1	AA735021	EST00001	c 175	71	15.4	641	9	CE391323	t1gr-g8s-
103	73	15.8	615	8	AZ629426	1M0482H20	c 176	71	15.4	722	4	BI824863	BI824863
104	73	15.8	674	5	BQ543460	BQ543460	c 177	71	15.4	728	9	AG504661	Mus_muscu
105	73	15.8	674	6	BY747794	BY747794	c 178	71	15.4	851	5	BU200911	6031101634
106	73	15.8	728	5	BU342242	603519895	c 179	71	15.4	880	7	CO116228	GR_Eb018
107	73	15.8	875	7	CN178168	AGENCOURT	c 180	71	15.4	902	4	BG323884	602422913
108	73	15.8	903	9	CG388854	CG388854	c 181	71	15.4	999	9	CL055391	CH216-81B
109	73	15.8	1064	4	BN906989	AGENCOURT	c 182	70.5	15.3	301	2	BB128571	BB128571
110	73	15.8	1143	4	BG846739	BG846739	c 183	70.5	15.3	319	2	BB095250	BB095250
111	73	15.8	1572	4	BN809808	AGENCOURT	c 184	70.5	15.3	354	4	BJ074656	BJ074656
112	72.5	15.7	378	5	BQ040452	gdl5h07.Y	c 185	70.5	15.3	408	1	AW005459	wz86G05.X
113	72.5	15.7	438	4	BJ181703	BJ181703	c 186	70.5	15.3	478	8	AQ933716	RPCL-23-2
114	72.5	15.7	457	5	BQ041627	BQ041627	c 187	70.5	15.3	502	8	A2178275	SP_0160.B
115	72.5	15.7	467	8	B33873	HS-1023-A2-	c 188	70.5	15.3	515	4	BJ614777	BJ614777
116	72.5	15.7	487	4	BJ610341	BJ610341	c 189	70.5	15.3	567	9	CL757675	OR_BBA012
117	72.5	15.7	487	8	BZ709370	OGDAJ45TM	c 190	70.5	15.3	633	9	CL726495	OR_BBA005
118	72.5	15.7	491	4	BJ173003	BJ173003	c 191	70.5	15.3	639	9	CL775593	OR_BBA008
119	72.5	15.7	491	4	BJ597166	BJ597166	c 192	70.5	15.3	644	4	BG469723	602534082
120	72.5	15.7	506	4	BJ586627	BJ586627	c 193	70.5	15.3	660	5	BU027664	QHG7A04.Y
121	72.5	15.7	520	6	CD924818	CD924818	c 194	70.5	15.3	749	7	CK844155	UI-R-BJ1-
122	72.5	15.7	525	4	BJ204417	BJ204417	c 195	70.5	15.3	750	5	EX718654	EX718654
123	72.5	15.7	534	8	AZ120193	RPCL-23-1	c 196	70.5	15.3	753	7	CN060991	A22_Ag2_P
124	72.5	15.7	549	4	BJ163632	BJ163632	c 197	70.5	15.3	781	4	BI544428	603241940
125	72.5	15.7	578	5	BJ170664	BJ170664	c 198	70.5	15.3	909	2	BF166515	601776614
126	72.5	15.7	594	4	BJ167135	BJ167135	c 199	70.5	15.3	1053	9	CNS02902	Tetraodon
127	72.5	15.7	600	9	CG770244	CH240_4L2	c 200	70	15.2	212	2	BB323124	BB323124
128	72.5	15.7	622	9	CE770244	CE770244	c 201	70	15.2	234	8	AQ080974	CIT-HSP-2
129	72.5	15.7	674	9	CE285411	t1gr-g8s-	c 202	70	15.2	298	2	BB027757	BB027757
130	72.5	15.7	800	7	CR569078	CR569078	c 203	70	15.2	419	2	BF716011	saa13b03.
131	72.5	15.7	840	7	CR569078	CR569078	c 204	70	15.2	453	9	CG916863	ZMPPBb038
132	72.5	15.7	844	5	BJ754561	BJ754561	c 205	70	15.2	517	9	CL806427	OR_CBA002
133	72.5	15.7	852	5	BU718783	BU718783	c 206	70	15.2	527	4	BJ319386	BJ319386
134	72.5	15.7	874	5	BJ710524	BJ710524	c 207	70	15.2	528	8	AZ436677	1M0224G06
135	72.5	15.7	906	1	CF216888	AGENCOURT	c 208	70	15.2	529	6	CD808875	LCA01G20C
136	72	15.6	407	6	AL664342	ue84h04.r	c 209	70	15.2	544	8	AQ619932	HS_5186_A
137	72	15.6	461	9	CNS03V0Z	AL261836	c 210	70	15.2	559	6	CD877569	AZ04_100JF
138	72	15.6	501	8	AZ772952	1M0584O09	c 211	70	15.2	581	6	CD920487	G608.117F
139	72	15.6	634	6	CD228090	CCCL_5_CO	c 212	70	15.2	620	9	CG792844	ZMPPBb030
140	72	15.6	642	6	CB690059	CEST-54_D	c 213	70	15.2	626	4	BJ321535	BJ321535
141	72	15.6	643	8	AZ635537	1M0491L19	c 214	70	15.2	637	1	AJ790118	AJ790118
142	72	15.6	649	6	CD228757	CCCL_9_G1	c 215	70	15.2	638	6	CA441667	UI-H-DP0-
143	72	15.6	669	6	CB690313	CEST-56-C	c 216	70	15.2	649	9	CL805736	OR_CBA001
144	72	15.6	796	5	BU255765	BU255765	c 217	70	15.2	653	8	AQ160730	nbx0005L
145	72	15.6	846	6	CD793931	EST665292	c 218	70	15.2	655	8	AZ646231	1M0512101
146	72	15.6	876	5	BU366421	603584630	c 219	70	15.2	660	6	CB687781	CEST-18-B
147	71.5	15.5	283	1	AL382560	qz03e09.x	c 220	70	15.2	672	1	AL886592	AL886592
148	71.5	15.5	325	2	BB315456	BB315456	c 221	70	15.2	674	4	BI459648	BI459648
149	71.5	15.5	403	8	AQ211245	HS_3239_B	c 222	70	15.2	680	7	CK605220	UT01767.3
150	71.5	15.5	505	9	CG914309	ZMPPBb037	c 223	70	15.2	691	6	CA190542	SCCORT1C0
151	71.5	15.5	520	4	BI528577	102409IG1	c 224	70	15.2	699	6	CA132838	SCBORT102
152	71.5	15.5	555	6	CA707355	wk2c_pk0	c 225	70	15.2	743	8	AF010910	AF010910
153	71.5	15.5	613	7	CN652654	EG_PSSLS	c 226	70	15.2	765	9	CL819548	OR_CBA003
154	71.5	15.5	626	8	AQ801692	HS_5397_A	c 227	70	15.2	769	6	CD101380	AGENCOURT
155	71.5	15.5	669	8	AZ793957	2M0047D05	c 228	70	15.2	786	8	AQ741688	HS_5566_B

229	70	15.2	786	9	CC934591	CC934591	ZMMBC054	C 302	69.5	15.0	827	8	BH717713	BH717713	BOMPT59TF
230	70	15.2	789	4	CC529707	CC529707	CH240_405	C 303	69.5	15.0	836	5	EX750394	EX750394	EX750394
231	70	15.2	792	7	CN758662	CN758662	I00AA22D	C 304	69.5	15.0	841	7	CG442769	CG442769	OGVOO07TH
232	70	15.2	970	4	BG569030	BG569030	602588250	C 305	69.5	15.0	851	9	CK598755	CK598755	AGENCOURT
233	70	15.2	1050	9	CNS05911	CNS05911	Tetraodon	C 306	69.5	15.0	856	9	CNS07970	CNS07970	AL434944 T3 end of
234	70	15.2	1062	9	CNS06R9A	CNS06R9A	AL411668 T7 end of	C 307	69.5	15.0	858	9	CR145372	CR145372	Reverse s
235	69.5	15.0	294	2	B332601	B332601	B3332601	C 308	69.5	15.0	869	8	BZ993799	BZ993799	PUGJ2P7TD
236	69.5	15.0	339	1	AI058567	AI058567	UI-R-C1-k	C 309	69.5	15.0	878	5	BQ218575	BQ218575	AGENCOURT
237	69.5	15.0	347	2	AW481245	AW481245	35119 MAR	C 310	69.5	15.0	889	4	BI601034	BI601034	603249514
238	69.5	15.0	388	5	EX475320	EX475320	DFZP6861	C 311	69.5	15.0	899	5	BQ887552	BQ887552	AGENCOURT
239	69.5	15.0	414	4	BG199055	BG199055	RST18333	C 312	69.5	15.0	901	5	EX429925	EX429925	AGENCOURT
240	69.5	15.0	433	1	AL711082	AL711082	DFZP686M	C 313	69.5	15.0	906	9	CG097139	CG097139	PURFP49TD
241	69.5	15.0	456	1	AJ673455	AJ673455	DFZP686M	C 314	69.5	15.0	910	9	CG651268	CG651268	OGLIB180TH
242	69.5	15.0	467	8	AO106699	AO106699	HS_3083_A	C 315	69.5	15.0	923	9	CG442774	CG442774	OGVOO07TV
243	69.5	15.0	468	9	CG468826	CG468826	0350703-0	C 316	69.5	15.0	943	9	CG366515	CG366515	OG2AX74TV
244	69.5	15.0	470	5	EX956127	EX956127	DFZP781E	C 317	69.5	15.0	946	4	BI551040	BI551040	603195783
245	69.5	15.0	473	2	BE322863	BE322863	NF048F101	C 318	69.5	15.0	1031	6	CB960785	CB960785	AGENCOURT
246	69.5	15.0	481	1	AA858672	AA858672	UI-R-A0-b	C 319	69.5	15.0	1093	9	CNS05P18	CNS05P18	Tetraodon
247	69.5	15.0	483	6	CD686907	CD686907	EST3428 h	C 320	69.5	15.0	1098	5	EX425511	EX425511	AGENCOURT
248	69.5	15.0	489	5	EX475734	EX475734	DFZP6860	C 321	69.5	15.0	1122	2	BE746555	BE746555	601580122
249	69.5	15.0	503	5	BQ907097	BQ907097	N003A03_0	C 322	69.5	15.0	1257	8	CC227275	CC227275	CH261-44D
250	69.5	15.0	514	5	BQ140635	BQ140635	NF038D03P	C 323	69.5	15.0	1280	4	BM011096	BM011096	603634793
251	69.5	15.0	516	4	BI594193	BI594193	As nc_07D	C 324	69.5	15.0	1889	3	AK037589	AK037589	Mus muscu
252	69.5	15.0	518	8	BZ419784	BZ419784	if59d11.b	C 325	69	14.9	343	1	AL773904	AL773904	AL773904
253	69.5	15.0	531	1	AL709797	AL709797	DFZP686N	C 326	69	14.9	384	9	CC890977	CC890977	ZMMBC051
254	69.5	15.0	535	2	BF597446	BF597446	su97h09_Y	C 327	69	14.9	406	3	AY431886	AY431886	Ades aeg
255	69.5	15.0	536	4	BI495228	BI495228	df116a09	C 328	69	14.9	408	8	AO81642	AO81642	RPCL11-55
256	69.5	15.0	547	5	EX495014	EX495014	DFZP7790	C 329	69	14.9	413	2	BB688023	BB688023	BB688023
257	69.5	15.0	548	1	AL696403	AL696403	DFZP686E	C 330	69	14.9	438	4	BM040589	BM040589	TJESTZya6
258	69.5	15.0	553	4	BG840686	BG840686	MEST10-F0	C 331	69	14.9	473	1	AJ797266	AJ797266	AJ797266
259	69.5	15.0	554	4	BG840498	BG840498	MEST10-F0	C 332	69	14.9	484	2	BE142365	BE142365	CM0-HT014
260	69.5	15.0	555	1	AA963978	AA963978	UI-R-C0-g	C 333	69	14.9	498	9	CG472463	CG472463	ZMMBC028
261	69.5	15.0	571	5	EX476208	EX476208	DFZP686N	C 334	69	14.9	520	9	CE095266	CE095266	tigr-gss-
262	69.5	15.0	579	1	AL711159	AL711159	DFZP686G	C 335	69	14.9	534	1	AJ790888	AJ790888	AGENCOURT
263	69.5	15.0	586	1	AL711109	AL711109	DFZP686G	C 336	69	14.9	549	5	B930612	B930612	AGENCOURT
264	69.5	15.0	586	1	AL711109	AL711109	DFZP686P	C 337	69	14.9	562	8	AZ615309	AZ615309	1M044A04
265	69.5	15.0	588	5	EX471177	EX471177	DFZP686P	C 338	69	14.9	562	8	AZ711889	AZ711889	RPCL-24-1
266	69.5	15.0	590	5	BQ599155	BQ599155	MI-P-B4-a	C 339	69	14.9	599	7	CN744222	CN744222	SAL_US027
267	69.5	15.0	590	5	EX489566	EX489566	DFZP686N	C 340	69	14.9	599	8	AZ358525	AZ358525	1M010E07
268	69.5	15.0	615	6	CD695832	CD695832	EST12355	C 341	69	14.9	609	9	CE373824	CE373824	tigr-gss-
269	69.5	15.0	620	7	CN428766	CN428766	170005325	C 342	69	14.9	620	9	CL721772	CL721772	OR_BBA005
270	69.5	15.0	623	6	CD687111	CD687111	EST3632 h	C 343	69	14.9	621	1	AA046826	AA046826	zf12g12-r
271	69.5	15.0	630	4	BJ245296	BJ245296	AL895054	C 344	69	14.9	627	9	CC498089	CC498089	CH240_335
272	69.5	15.0	631	1	AL895054	AL895054	AL895054	C 345	69	14.9	678	9	CG178952	CG178952	1119055C0
273	69.5	15.0	637	1	AL036875	AL036875	DFZP686P	C 346	69	14.9	687	9	CL773274	CL773274	OR_BBA008
274	69.5	15.0	645	7	CA428769	CA428769	170005313	C 347	69	14.9	703	9	CL743462	CL743462	OR_BBA007
275	69.5	15.0	652	1	AV645564	AV645564	AV645564	C 348	69	14.9	714	9	CE135655	CE135655	tigr-gss-
276	69.5	15.0	653	5	EX750916	EX750916	EX750916	C 349	69	14.9	724	6	CB600172	CB600172	AGENCOURT
277	69.5	15.0	660	5	EX956313	EX956313	DFZP781M	C 350	69	14.9	728	1	AV653772	AV653772	AV653772
278	69.5	15.0	664	1	AL897227	AL897227	AL897227	C 351	69	14.9	751	9	AG082016	AG082016	Par tlogl
279	69.5	15.0	664	4	BJ244343	BJ244343	BU244343	C 352	69	14.9	761	2	BF529283	BF529283	602041742
280	69.5	15.0	665	2	BE439753	BE439753	HMI-611F	C 353	69	14.9	792	7	CR281411	CR281411	CR281411
281	69.5	15.0	667	4	BG720289	BG720289	602692352	C 354	69	14.9	803	9	CL619181	CL619181	OR_BBA001
282	69.5	15.0	690	8	BH958147	BH958147	odf85h09	C 355	69	14.9	810	4	BI147396	BI147396	602913845
283	69.5	15.0	707	7	CN428762	CN428762	170005328	C 356	69	14.9	812	9	CL831338	CL831338	OR_CBA005
284	69.5	15.0	710	5	EX781858	EX781858	EX781858	C 357	69	14.9	847	7	CF595957	CF595957	AGENCOURT
285	69.5	15.0	712	5	BU622977	BU622977	UI-H-FL1-	C 358	69	14.9	860	9	CL763143	CL763143	OR_BBA013
286	69.5	15.0	714	4	BI548683	BI548683	603196856	C 359	69	14.9	864	4	BI260085	BI260085	602971843
287	69.5	15.0	714	6	CF342879	CF342879	AGENCOURT	C 360	69	14.9	937	9	CNS038BK	CNS038BK	AL232409 Tetraodon
288	69.5	15.0	723	7	CK840134	CK840134	UI-R-C0-g	C 361	69	14.9	948	5	BQ935476	BQ935476	AGENCOURT
289	69.5	15.0	742	5	BU219137	BU219137	603105953	C 362	69	14.9	955	9	CL469743	CL469743	SAIL_133
290	69.5	15.0	752	1	CC651278	CC651278	OGLIB180TV	C 363	69	14.9	959	5	BQ943515	BQ943515	AGENCOURT
291	69.5	15.0	781	9	AJ395101	AJ395101	AJ395101	C 364	69	14.9	981	5	BU174126	BU174126	AGENCOURT
292	69.5	15.0	786	6	CB961098	CB961098	AGENCOURT	C 365	69	14.9	981	8	CC225443	CC225443	CH261-174
293	69.5	15.0	791	6	CB961182	CB961182	AGENCOURT	C 366	69	14.9	1063	9	AG539137	AG539137	Mus muscu
294	69.5	15.0	792	1	AJ392832	AJ392832	AJ392832	C 367	69	14.9	1142	8	CC290837	CC290837	CH261-172
295	69.5	15.0	792	6	CB989256	CB989256	AGENCOURT	C 368	69	14.9	1191	5	BQ953934	BQ953934	AGENCOURT
296	69.5	15.0	794	5	EX346825	EX346825	EX346825	C 369	69	14.9	1237	8	BH860551	BH860551	ORNL022_P
297	69.5	15.0	795	5	BU180033	BU180033	603143967	C 370	69	14.9	1716	2	BF036853	BF036853	601460329
298	69.5	15.0	808	6	CB961104	CB961104	AGENCOURT	C 371	68.5	14.8	227	2	BE012135	BE012135	945013E02
299	69.5	15.0	813	9	CG156714	CG156714	PUFZ94TD	C 372	68.5	14.8	312	2	BE012135	BE012135	945013E02
300	69.5	15.0	822	8	BZ640571	BZ640571	OGCAL68TM	C 373	68.5	14.8	393	1	AL711222	AL711222	DFZP686A
301	69.5	15.0	823	8	BZ815470	BZ815470	PURFCR69TB	C 374	68.5	14.8	456	6	CF193065	CF193065	15k16j2.f

C 375	375	68.5	14.8	477	8	A2620793	1M0453109	A2620793	1M0453109	C 448	68.5	14.8	2483	3	CNSLTLIAF	BX161398	human full
C 376	376	68.5	14.8	480	1	AU077781	AU077781	AU077781	AU077781	C 449	68.5	14.8	2512	3	CR622268	full-leng	
C 377	377	68.5	14.8	500	4	B1808273	C05G05 O	B1808273	C05G05 O	C 450	68.5	14.8	2514	3	CR605233	full-leng	
C 378	378	68.5	14.8	504	8	AQ430821	HS_5103_A	AQ430821	HS_5103_A	C 451	68	14.7	296	2	BB156194	BB156194	
C 379	379	68.5	14.8	507	8	A2340358	1M0072119	A2340358	1M0072119	C 452	68	14.7	336	5	BY332423	BY332423	
C 380	380	68.5	14.8	511	4	BG325857	602424592	BG325857	602424592	C 453	68	14.7	369	8	CC462009	ZMMBB035	
C 381	381	68.5	14.8	514	1	AJ805303	AJ805303	AJ805303	AJ805303	C 454	68	14.7	441	8	BZ492491	BONTQ30TR	
C 382	382	68.5	14.8	519	2	BF013957	to18d09.Y	BF013957	to18d09.Y	C 455	68	14.7	463	9	CG778453	1123028G1	
C 383	383	68.5	14.8	520	9	CL202774	ZMREBB056	CL202774	ZMREBB056	C 456	68	14.7	472	1	AV741413	AV741413	
C 384	384	68.5	14.8	524	6	CB279853	ru8bc07.Y	CB279853	ru8bc07.Y	C 457	68	14.7	473	9	CG779150	1123031H1	
C 385	385	68.5	14.8	524	6	CB825564	rqj5b02.Y	CB825564	rqj5b02.Y	C 458	68	14.7	481	5	EX675612	EX675612	
C 386	386	68.5	14.8	525	6	CB376012	tw18d03.Y	CB376012	tw18d03.Y	C 459	68	14.7	493	8	AZ645823	1M0511B01	
C 387	387	68.5	14.8	550	6	B0672907	AGENCOURT	B0672907	AGENCOURT	C 460	68	14.7	503	2	BE370817	601219008	
C 388	388	68.5	14.8	552	6	CD748261	rw34h03.Y	CD748261	rw34h03.Y	C 461	68	14.7	506	9	CG912858	ZMMBB037	
C 389	389	68.5	14.8	554	5	BQ031122	UI-1-CF0-	BQ031122	UI-1-CF0-	C 462	68	14.7	506	4	BG977571	PM4-CI008	
C 390	390	68.5	14.8	555	9	CE300600	tiGr-988-	CE300600	tiGr-988-	C 463	68	14.7	506	5	BF101855	BP101855	
C 391	391	68.5	14.8	573	5	BQ097771	FO18B11 O	BQ097771	FO18B11 O	C 464	68	14.7	516	4	BQ206080	BQ206080	
C 392	392	68.5	14.8	580	6	CB280350	ru4eall.Y	CB280350	ru4eall.Y	C 465	68	14.7	518	8	AZ312197	1M0027J19	
C 393	393	68.5	14.8	606	6	CB378449	rq12e01.Y	CB378449	rq12e01.Y	C 466	68	14.7	521	6	CD291788	StrPu538.	
C 394	394	68.5	14.8	624	1	AL037950	KDFP564N	AL037950	KDFP564N	C 467	68	14.7	522	4	BJ197266	BJ197266	
C 395	395	68.5	14.8	628	6	CB375609	rw13a12.Y	CB375609	rw13a12.Y	C 468	68	14.7	534	6	CA041331	ssalmg400	
C 396	396	68.5	14.8	629	6	CB374909	ru66d09.Y	CB374909	ru66d09.Y	C 469	68	14.7	537	9	CG779054	1123031D1	
C 397	397	68.5	14.8	638	1	A1648276	AEMTAA70	A1648276	AEMTAA70	C 470	68	14.7	539	1	AJ397988	AJ397988	
C 398	398	68.5	14.8	643	6	CB374879	ru6ea07.Y	CB374879	ru6ea07.Y	C 471	68	14.7	544	8	AZ387390	1M0146C17	
C 399	399	68.5	14.8	668	8	AZ642143	1M0505102	AZ642143	1M0505102	C 472	68	14.7	553	5	BQ080568	san35b11.	
C 400	400	68.5	14.8	670	8	BZ409803	OGAAQ94TC	BZ409803	OGAAQ94TC	C 473	68	14.7	554	4	BM522312	essu0850	
C 401	401	68.5	14.8	678	7	KX521345	rswea0.00	KX521345	rswea0.00	C 474	68	14.7	555	5	BQ080504	san34b11.	
C 402	402	68.5	14.8	686	9	AG064679	Pan trogl	AG064679	Pan trogl	C 475	68	14.7	558	4	BI681498	460909 MA	
C 403	403	68.5	14.8	703	5	BX508840	KDFP686A	BX508840	KDFP686A	C 476	68	14.7	560	2	BF607013	MY2.00007	
C 404	404	68.5	14.8	704	6	CB526294	UI-M-FY0-	CB526294	UI-M-FY0-	C 477	68	14.7	560	9	CG778421	1123028F0	
C 405	405	68.5	14.8	709	4	BG720914	602692164	BG720914	602692164	C 478	68	14.7	564	8	BH597917	BOGHR63TF	
C 406	406	68.5	14.8	721	5	BX347315	BX347315	BX347315	BX347315	C 479	68	14.7	569	7	KX583403	IST.W15.4	
C 407	407	68.5	14.8	730	9	CG170127	PUPQF94TB	CG170127	PUPQF94TB	C 480	68	14.7	585	6	CB503448	ssalmgd50	
C 408	408	68.5	14.8	741	1	AJ795262	AJ795262	AJ795262	AJ795262	C 481	68	14.7	589	6	CA044397	ssalplnb5	
C 409	409	68.5	14.8	747	9	CL177029	104.383.1	CL177029	104.383.1	C 482	68	14.7	597	8	AZ435944	1M0223013	
C 410	410	68.5	14.8	753	1	AJ787129	AJ787129	AJ787129	AJ787129	C 483	68	14.7	608	9	CG778953	1123031A0	
C 411	411	68.5	14.8	759	8	BZ409754	OGAAR66TC	BZ409754	OGAAR66TC	C 484	68	14.7	618	9	CG779007	1123031C0	
C 412	412	68.5	14.8	760	9	AG446840	Mus muscu	AG446840	Mus muscu	C 485	68	14.7	619	9	FR0018535	AL011430 F.rubripe	
C 413	413	68.5	14.8	791	8	BZ409810	OGAAQ94TM	BZ409810	OGAAQ94TM	C 486	68	14.7	623	9	CC470702	CH240.145	
C 414	414	68.5	14.8	791	9	AG587594	Mus muscu	AG587594	Mus muscu	C 487	68	14.7	626	2	AM694618	NF078B10S	
C 415	415	68.5	14.8	794	9	CL173883	104.377.1	CL173883	104.377.1	C 488	68	14.7	628	8	AZ348899	1M0085J09	
C 416	416	68.5	14.8	795	8	BZ409760	OGAAR66TM	BZ409760	OGAAR66TM	C 489	68	14.7	629	5	BQ038217	pgmic.BK0	
C 417	417	68.5	14.8	841	6	CB628419	OSIIEB03P	CB628419	OSIIEB03P	C 490	68	14.7	630	4	BJ804047	BJ804047	
C 418	418	68.5	14.8	846	8	BZ173401	CH230-505	BZ173401	CH230-505	C 491	68	14.7	636	6	CD729890	CD729890	
C 419	419	68.5	14.8	858	8	BZ640565	OGCAL68TC	BZ640565	OGCAL68TC	C 492	68	14.7	645	8	CC157417	ig19e05.b	
C 420	420	68.5	14.8	861	8	AZ183776	SP.1001.B	AZ183776	SP.1001.B	C 493	68	14.7	657	2	BF645128	NF028E11E	
C 421	421	68.5	14.8	863	5	B0214670	603750129	B0214670	603750129	C 494	68	14.7	658	9	CE460363	tiGr-988-	
C 422	422	68.5	14.8	874	9	CL484223	SAIL.393-	CL484223	SAIL.393-	C 495	68	14.7	662	4	BM486199	BM486199	
C 423	423	68.5	14.8	876	8	CC086576	CSU-K33r-	CC086576	CSU-K33r-	C 496	68	14.7	671	9	CG402916	ZMMBB024	
C 424	424	68.5	14.8	888	5	BX347451	BX347451	BX347451	BX347451	C 497	68	14.7	678	8	AZ652320	1M0525E10	
C 425	425	68.5	14.8	893	5	BX742802	BM742802	BX742802	BM742802	C 498	68	14.7	690	6	CA759555	BR060007B	
C 426	426	68.5	14.8	900	5	BX388530	BX388530	BX388530	BX388530	C 499	68	14.7	698	2	BE651121	BB651121	
C 427	427	68.5	14.8	902	2	BF620503	HVMECC002	BF620503	HVMECC002	C 500	68	14.7	716	4	BU789022	BU789022	
C 428	428	68.5	14.8	921	5	BQ676414	AGENCOURT	BQ676414	AGENCOURT	C 501	68	14.7	719	4	CK775602	966732.MA	
C 429	429	68.5	14.8	925	9	AG073642	Pan trogl	AG073642	Pan trogl	C 502	68	14.7	747	4	BJ147887	BJ147887	
C 430	430	68.5	14.8	927	5	BX391032	BX391032	BX391032	BX391032	C 503	68	14.7	749	4	BJ778679	BJ778679	
C 431	431	68.5	14.8	936	2	BE959892	601654624	BE959892	601654624	C 504	68	14.7	750	9	CG029377	CHGAA80TR	
C 432	432	68.5	14.8	942	6	CF216565	AGENCOURT	CF216565	AGENCOURT	C 505	68	14.7	763	1	A1829107	wj38q06.x	
C 433	433	68.5	14.8	951	2	BF238272	601811630	BF238272	601811630	C 506	68	14.7	765	4	AI8277206	BU777206	
C 434	434	68.5	14.8	1041	9	AY412740	Homo sapi	AY412740	Homo sapi	C 507	68	14.7	765	4	BU815016	BU815016	
C 435	435	68.5	14.8	1055	3	CR664351	Tetraodon	CR664351	Tetraodon	C 508	68	14.7	772	5	BM382889	BM382889	
C 436	436	68.5	14.8	1084	4	BM562864	AGENCOURT	BM562864	AGENCOURT	C 509	68	14.7	773	4	BJ793397	BJ793397	
C 437	437	68.5	14.8	1114	2	BE791299	601582855	BE791299	601582855	C 510	68	14.7	777	8	BH595798	BOGXX43TF	
C 438	438	68.5	14.8	1118	7	CR284553	CR284553	CR284553	CR284553	C 511	68	14.7	779	1	AU217459	AU217459	
C 439	439	68.5	14.8	1166	5	BQ896595	AGENCOURT	BQ896595	AGENCOURT	C 512	68	14.7	788	8	BZ462718	BONOV92TR	
C 440	440	68.5	14.8	1176	2	BE961364	601655389	BE961364	601655389	C 513	68	14.7	790	4	BF408515	602964924	
C 441	441	68.5	14.8	1312	5	BF663171	602145095	BF663171	602145095	C 514	68	14.7	801	2	BE053950	GA_Ea003	
C 442	442	68.5	14.8	1369	5	BQ682884	AGENCOURT	BQ682884	AGENCOURT	C 515	68	14.7	814	8	CC138668	NDL.37M7.	
C 443	443	68.5	14.8	1405	2	BE898599	601681534	BE898599	601681534	C 516	68	14.7	814	9	CNS06V6N	CC006774	
C 444	444	68.5	14.8	1470	2	BF302634	602032490	BF302634	602032490	C 517	68	14.7	817	8	CC006774	PUEAH45TD	
C 445	445	68.5	14.8	1765	2	BF980840	602304038	BF980840	602304038	C 518	68	14.7	841	8	BZ528888	OGARD93TC	
C 446	446	68.5	14.8	2439	3	CR613005	full-leng	CR613005	full-leng	C 519	68	14.7	873	8	BZ960822	PUDFC65TD	
C 447	447	68.5	14.8	2450	3	CR603680	full-leng	CR603680	full-leng	C 520	68	14.7	874	8	CC377517	PURKG28TB	

521	68	14.7	907	5	BU3151177	603488575	594	67.5	14.6	764	9	AG521422	Mus muscu
522	68	14.7	911	6	CA195688	SCRZAD107	595	67.5	14.6	759	5	AX870084	AX870084
523	68	14.7	912	8	CC377519	PURCG28TD	596	67.5	14.6	778	6	CF203283	RR890315N
524	68	14.7	918	5	BQ220555	AGENCOURT	597	67.5	14.6	778	7	CK305827	SB02031A2
525	68	14.7	942	3	CNS08NRK	Single re	598	67.5	14.6	786	6	CD779144	EST650505
526	68	14.7	964	9	CL317303	ZMMBB003	599	67.5	14.6	793	6	CD781458	EST652819
527	68	14.7	990	9	CG229545	OG2BR91TV	600	67.5	14.6	806	6	CD779145	EST650506
528	68	14.7	1011	9	CNS06CW3	T7 end of	601	67.5	14.6	812	5	BU109604	603002244
529	68	14.7	1050	1	AL517161	AL517161	602	67.5	14.6	815	5	BU231050	603400378
530	68	14.7	1063	1	AL575154	AL575154	603	67.5	14.6	815	6	CD788530	CH2630-437
531	68	14.7	1089	4	BM552997	AGENCOURT	604	67.5	14.6	827	8	BZ208609	EST659891
532	68	14.7	1245	5	BQ072304	AGENCOURT	605	67.5	14.6	831	7	CO566206	AGENCOURT
533	68	14.7	1522	3	AK050682	Mus muscu	606	67.5	14.6	859	2	BF120949	601757760
534	68	14.7	1550	3	CNS0A5K8	Arabidops	607	67.5	14.6	865	2	BP675153	602136563
535	68	14.7	1621	3	CNS0AARN	Arabidops	608	67.5	14.6	872	5	EX395727	BP395727
536	68	14.7	3891	3	AK031526	Mus muscu	609	67.5	14.6	876	8	CC409984	PURHNA9TD
537	67.5	14.6	259	9	CG651031	OST411103	610	67.5	14.6	879	4	CC730312	OGAD39TH
538	67.5	14.6	349	9	CG125574	PURF214TD	611	67.5	14.6	883	4	BI088008	602852480
539	67.5	14.6	365	9	CG471916	ZMMBB027	612	67.5	14.6	891	9	CG289557	OGKDL12TH
540	67.5	14.6	369	1	AF063558	AF063558	613	67.5	14.6	907	4	BI246957	602960443
541	67.5	14.6	417	8	B52071	CIT-HSP-386	614	67.5	14.6	910	7	CF408386	CH3#054 C
542	67.5	14.6	429	9	CG628221	CG628221	615	67.5	14.6	913	9	CG125572	PURF214TB
543	67.5	14.6	444	6	CF193393	16D1912.F	616	67.5	14.6	918	5	EX453712	EX453712
544	67.5	14.6	449	5	BY277314	BY277314	617	67.5	14.6	922	6	CA234093	SCRZAM225
545	67.5	14.6	466	6	CB714859	CB714859	618	67.5	14.6	936	9	CG282134	OGWIA88TV
546	67.5	14.6	478	4	BM088800	502343 MA	619	67.5	14.6	943	7	CK017712	AGENCOURT
547	67.5	14.6	487	6	CA185451	SCSFS307	620	67.5	14.6	945	5	BU504726	AGENCOURT
548	67.5	14.6	491	2	BE644797	BE644797	621	67.5	14.6	947	4	BG288937	602383887
549	67.5	14.6	492	9	CL245451	ZMMBB039	622	67.5	14.6	951	5	BU183985	AGENCOURT
550	67.5	14.6	518	2	AW566507	660075G10	623	67.5	14.6	992	4	BI950736	HVSMEL1002
551	67.5	14.6	518	8	AQ456378	HS 5114.A	624	67.5	14.6	1041	9	CNS03SV6	AL259143
552	67.5	14.6	533	6	CD780587	EST651948	625	67.5	14.6	1067	1	AL542211	Tetraodon
553	67.5	14.6	538	9	CL237985	ZMMBB057	626	67.5	14.6	1089	1	AL520511	AL520511
554	67.5	14.6	544	6	CB270142	1009049.H	627	67.5	14.6	1094	5	EX354974	EX354974
555	67.5	14.6	550	9	CG865499	ZMMBB033	628	67.5	14.6	1096	2	BE788012	601482614
556	67.5	14.6	565	8	BH620447	1007065H1	629	67.5	14.6	1101	9	CNS05030	AL515045
557	67.5	14.6	566	8	CC313811	TAM32-412	630	67.5	14.6	1142	1	AL556982	Tetraodon
558	67.5	14.6	583	1	AI110684	HA0116.Hu	631	67.5	14.6	1212	3	CR659705	Tetraodon
559	67.5	14.6	584	2	BE769825	RC2-F7004	632	67.5	14.6	1225	4	BI198293	602760135
560	67.5	14.6	585	7	CN938494	010615AVB	633	67.5	14.6	1257	5	BU846131	AGENCOURT
561	67.5	14.6	585	7	CK304699	SB02025B1	634	67.5	14.6	1563	3	CR626791	full-leng
562	67.5	14.6	595	8	BH093894	RFC1-24-3	635	67.5	14.6	1585	3	CR609231	full-leng
563	67.5	14.6	604	6	CD747844	rw28f04.Y	636	67.5	14.6	1623	3	CR624161	full-leng
564	67.5	14.6	607	6	CA082717	SCBFAW202	637	67.5	14.6	1638	3	CR604339	full-leng
565	67.5	14.6	607	8	BH377267	AG-ND-173	638	67.5	14.6	1646	3	CR605829	full-leng
566	67.5	14.6	608	7	CK955330	4095203.B	639	67.5	14.6	1651	3	CR624583	full-leng
567	67.5	14.6	610	8	AZ425537	1M0205K10	640	67.5	14.6	1673	3	CR599167	full-leng
568	67.5	14.6	613	6	CB376225	rw02b08.Y	641	67.5	14.6	1686	3	CR591618	full-leng
569	67.5	14.6	615	4	BJ361809	BJ361809	642	67.5	14.6	301	1	AA885838	OJ36a10.s
570	67.5	14.6	615	6	CB426255	601421.MA	643	67.5	14.5	304	7	CN589500	TT0000041
571	67.5	14.6	616	2	BB618973	BB618973	644	67.5	14.5	341	7	CN589500	TT0000041
572	67.5	14.6	616	3	CB426255	601421.MA	645	67.5	14.5	342	6	CB693752	AMGNNUC:N
573	67.5	14.6	648	9	CC938453	ZMMBB023	646	67.5	14.5	356	2	BF351412	CMO-HT050
574	67.5	14.6	650	8	BH263129	CH230-43C	647	67.5	14.5	374	9	CE701036	Ugr-ges-
575	67.5	14.6	652	9	AG565031	Mus muscu	648	67.5	14.5	398	4	BM073211	MEST62-F0
576	67.5	14.6	655	8	AZ981122	2M0258M22	649	67.5	14.5	409	2	BE243059	TCAAP2E22
577	67.5	14.6	656	8	CL798234	OR.CBa000	650	67.5	14.5	414	5	BQ604824	MT-P-CF1-
578	67.5	14.6	662	9	CG406178	ZMMBB026	651	67.5	14.5	422	6	CB763861	AMGNNUC:S
579	67.5	14.6	669	6	CD218175	gpr1n.pk0	652	67.5	14.5	438	2	BB821085	BB821085
580	67.5	14.6	672	6	CA132639	SCEQRT102	653	67.5	14.5	440	4	BI029834	MR4-MT025
581	67.5	14.6	673	6	CD786014	EST657375	654	67.5	14.5	441	1	AA175430	ms84c04.r
582	67.5	14.6	686	8	BH093891	RFC1-24-3	655	67.5	14.5	445	1	AI156215	ud95901.x
583	67.5	14.6	692	6	CB052365	NISC-gl07	656	67.5	14.5	447	2	BE927292	RC1-C7028
584	67.5	14.6	694	6	CA147130	SCCRL100	657	67.5	14.5	464	2	BE784671	601473530
585	67.5	14.6	701	6	CA188969	SCCCL4C0	658	67.5	14.5	465	6	CD852967	DHOAMW112
586	67.5	14.6	705	5	BX316562	BX316562	659	67.5	14.5	466	6	CD855552	DHOAMW92C
587	67.5	14.6	702	1	AJ393703	AJ393703	660	67.5	14.5	467	8	BH266145	CH230-55L
588	67.5	14.6	705	8	CC153539	CSU-K34-1	661	67.5	14.5	471	1	AI156211	ud95901.x
589	67.5	14.6	715	5	BU290764	60416412	662	67.5	14.5	474	2	AW989210	ug13408.y
590	67.5	14.6	732	9	EX181453	Danio rer	663	67.5	14.5	478	8	AQ617096	HS 5158.A
591	67.5	14.6	739	1	AJ396130	AJ396130	664	67.5	14.5	479	2	BB860690	BB860690
592	67.5	14.6	753	9	CC760739	ZMMBB015	665	67.5	14.5	488	6	CD852153	DHOALL25Z
593	67.5	14.6	763	2	BE916907	601666448	666	67.5	14.5	512	7	CN457318	UT-M-HN0-

667	67	14.5	515	1	AA797644	AA797644 vw26dl1.r	C 740	67	14.5	811	7	CN593371	CN593371 TTE000135
668	67	14.5	515	7	CN244198	CN244198 ES010075	C 741	67	14.5	814	7	CN593579	CN593579 TTE000137
669	67	14.5	531	1	AA867153	AA867153 vx24a02.r	C 742	67	14.5	816	7	AL523541	AL523541
C 670	67	14.5	535	8	AZ612124	AZ612124 IM0438F21	C 743	67	14.5	836	7	CN594924	CN594924 TTE000140
671	67	14.5	537	8	AZ335051	AZ335051 IM0064P09	C 744	67	14.5	838	7	CN595086	CN595086 TTE000150
672	67	14.5	543	1	AA396321	AA396321 vb46d01.r	C 745	67	14.5	845	5	BU291930	BU291930 603605G23
673	67	14.5	543	6	CD450982	CD450982 USDA-EP.1	C 746	67	14.5	854	7	CN596130	CN596130 TTE000114
674	67	14.5	549	2	B8484758	B8484758 232868 BA	C 747	67	14.5	856	7	CN596273	CN596273 TTE000102
C 675	67	14.5	553	4	BG143501	BG143501 mab57a09.	C 748	67	14.5	857	7	CN596345	CN596345 TTE000152
676	67	14.5	555	6	CD571840	CD571840 k065hl2.y	C 749	67	14.5	858	7	CN596382	CN596382 TTE000134
C 677	67	14.5	558	4	BG803560	BG803560 0233-96 M	C 750	67	14.5	863	7	CN596692	CN596692 TTE000151
678	67	14.5	568	4	BG277199	BG277199 ux40g04.y	C 751	67	14.5	863	7	CN596724	CN596724 TTE000077
C 679	67	14.5	571	7	CN590448	CN590448 TTE000064	C 752	67	14.5	869	7	CN597063	CN597063 TTE000110
680	67	14.5	572	8	BH392683	BH392683 AG-ND-137	C 753	67	14.5	871	7	CN597175	CN597175 TTE000094
C 681	67	14.5	573	3	AK008492	AK008492 Mus muscu	C 754	67	14.5	874	3	BC048759	BC048759 Mus muscu
682	67	14.5	578	8	AZ362611	AZ362611 IM0107H17	C 755	67	14.5	876	7	CN597509	CN597509 TTE000067
683	67	14.5	579	6	CD833555	CD833555 BN40.067L	C 756	67	14.5	877	7	CN597518	CN597518 TTE000097
684	67	14.5	582	6	BY708383	BY708383 BY708383	C 757	67	14.5	877	7	CN597556	CN597556 TTE000136
685	67	14.5	583	5	BP873076	BP873076 BP873076	C 758	67	14.5	877	7	CN597558	CN597558 TTE000139
686	67	14.5	587	8	AZ951175	AZ951175 2M0215H04	C 759	67	14.5	878	7	CN597667	CN597667 TTE000150
C 687	67	14.5	589	7	CN590480	CN590480 TTE000084	C 760	67	14.5	878	7	CN597671	CN597671 TTE000150
C 688	67	14.5	591	6	CA022702	CA022702 HZ44B21r	C 761	67	14.5	881	7	CN597865	CN597865 TTE000090
689	67	14.5	597	6	CB493854	CB493854 omykrb1b0	C 762	67	14.5	881	7	CN597871	CN597871 TTE000095
C 690	67	14.5	600	4	BI988498	BI988498 4011-86 M	C 763	67	14.5	882	7	CN597907	CN597907 TTE000076
C 691	67	14.5	602	8	AZ506016	AZ506016 IM0347A23	C 764	67	14.5	882	7	CN597922	CN597922 TTE000068
C 692	67	14.5	613	4	BG560095	BG560095 RHI22.69	C 765	67	14.5	882	7	CN597967	CN597967 TTE000112
693	67	14.5	617	5	BU042000	BU042000 PP_LEA001	C 766	67	14.5	884	6	CB236635	CB236635 AGENCOURT
694	67	14.5	625	6	CG492917	CG492917 omykrbna0	C 767	67	14.5	884	7	CN598059	CN598059 TTE000106
C 695	67	14.5	628	9	CG986914	CG986914 CH240.158	C 768	67	14.5	885	7	CN598092	CN598092 TTE000125
C 696	67	14.5	635	8	BM392808	BM392808 50071-2-2	C 769	67	14.5	885	7	CN598103	CN598103 TTE000134
C 697	67	14.5	641	4	BM394117	BM394117 50072-2-2	C 770	67	14.5	885	7	CN598104	CN598104 TTE000134
C 698	67	14.5	641	4	BM394117	BM394117 UI-M-HB0-	C 771	67	14.5	885	9	CC761296	CC761296 ZMMEB020
C 699	67	14.5	643	7	CF727944	CF727944 UI-M-HB0-	C 772	67	14.5	886	7	CN598187	CN598187 TTE000140
700	67	14.5	647	8	AZ509950	AZ509950 IM0354E09	C 773	67	14.5	887	7	CN598245	CN598245 TTE000080
C 701	67	14.5	653	2	BE294330	BE294330 601172840	C 774	67	14.5	887	7	CN598250	CN598250 TTE000121
C 702	67	14.5	653	8	BZ430792	BZ430792 BONKJ25TF	C 775	67	14.5	891	8	BZ130579	BZ130579 ZM230-298
C 703	67	14.5	658	8	CC148548	CC148548 ZMMEB001	C 776	67	14.5	891	9	CC933471	CC933471 ZM230-298
704	67	14.5	659	6	CA905132	CA905132 PCSC16904	C 777	67	14.5	896	9	CNS01DYF	AL139864 Anophel
C 705	67	14.5	662	7	CN703501	CN703501 E0476D07-	C 778	67	14.5	897	4	BF982223	BF982223 602306274
706	67	14.5	668	5	BU204865	BU204865 604156162	C 779	67	14.5	903	5	BQ888749	BQ888749 AGENCOURT
707	67	14.5	669	6	CB493958	CB493958 omykrbna0	C 780	67	14.5	904	5	CN598904	CN598904 TTE000123
708	67	14.5	669	8	BH004544	BH004544 BMBAC08C0	C 781	67	14.5	905	7	CN598933	CN598933 TTE000078
709	67	14.5	673	2	BB004080	BB004080 BU004080	C 782	67	14.5	906	7	CN598951	CN598951 TTE000107
710	67	14.5	676	7	CK780445	CK780445 UI-M-GV0-	C 783	67	14.5	907	4	BG166416	BG166416 602339470
711	67	14.5	678	5	BU609318	BU609318 UI-M-DJ2-	C 784	67	14.5	924	7	CN599252	CN599252 TTE000139
C 712	67	14.5	679	6	BY727234	BY727234 BY727234	C 785	67	14.5	925	7	CN599255	CN599255 TTE000108
C 713	67	14.5	681	8	AZ584129	AZ584129 IM0388N20	C 786	67	14.5	934	7	CK414345	CK414345 AUF_IPG11
714	67	14.5	687	6	BY763336	BY763336 BY763336	C 787	67	14.5	938	9	AG136236	AG136236 Pan trogl
C 715	67	14.5	689	9	AG098389	AG098389 Pan trogl	C 788	67	14.5	946	6	CA581619	CA581619 EST001294
C 716	67	14.5	690	6	BY709407	BY709407 IM0086B01	C 789	67	14.5	953	5	BQ931310	BQ931310 AGENCOURT
717	67	14.5	695	8	AZ349126	AZ349126 IM0086B01	C 790	67	14.5	1018	4	BQ561385	BQ561385 AGENCOURT
718	67	14.5	702	8	BH401395	BH401395 AG-ND-106	C 791	67	14.5	1053	4	BG416372	BG416372 HVSMBK001
719	67	14.5	708	2	BF720650	BF720650 mab57a09.	C 792	67	14.5	1156	9	CL462537	CL462537 SAIL_1167
C 720	67	14.5	710	8	BZ128566	BZ128566 CH230-394	C 793	67	14.5	1181	3	AK088941	AK088941 Mus muscu
721	67	14.5	711	5	BQ183129	BQ183129 UI-H-EU0-	C 794	67	14.5	1212	3	CR673711	CR673711 Pan trogl
722	67	14.5	719	8	AZ058799	AZ058799 RPT-23-4	C 795	67	14.5	1435	4	BG497144	BG497144 602537640
723	67	14.5	719	8	BH114120	BH114120 RPT-24-3	C 796	67	14.5	1493	3	AX081629	AX081629 Mus muscu
724	67	14.5	722	6	BY715280	BY715280 BY715280	C 797	67	14.5	225	9	CG696436	CG696436 BARC BFGU
725	67	14.5	732	9	CR224044	CR224044 Forward s	C 798	67	14.5	279	1	AV210494	AV210494
726	67	14.5	732	1	AI056300	AI056300 0202h06.x	C 799	67	14.5	298	2	AW433952	AW433952 UI-R-BUOP
727	67	14.5	742	4	BI660575	BI660575 603303659	C 800	67	14.5	312	7	R24476	R24476 YH48e10.r1
C 728	67	14.5	742	5	BX084001	BX084001 BX084001	C 801	67	14.5	354	5	BY411560	BY411560
729	67	14.5	744	6	CA201275	CA201275 SCRFPL103	C 802	67	14.5	354	4	BI399612	BI399612 MI-P-AV1-
730	67	14.5	756	9	CR252686	CR252686 Reverse s	C 803	67	14.5	377	6	CA898029	CA898029
C 731	67	14.5	763	5	BU408210	BU408210 603483658	C 804	67	14.5	386	2	BE247262	BE247262 TCBAPIE40
732	67	14.5	770	8	BH375575	BH375575 AG-ND-137	C 805	67	14.5	391	5	BU584592	BU584592 564508686
733	67	14.5	782	9	CC702199	CC702199 OGDARF43TC	C 806	67	14.5	398	4	BH153728	BH153728 TCBAPE272
734	67	14.5	786	6	CB520517	CB520517 UI-M-GIO-	C 807	67	14.5	410	2	BH815772	BH815772 BB815772
C 735	67	14.5	793	8	CC067355	CC067355 CSU-K33r.	C 808	67	14.5	432	1	AU229864	AU229864
C 736	67	14.5	797	7	CN592602	CN592602 TTE000061	C 809	67	14.5	439	8	AQ014562	AQ014562 CIT-HSP-2
737	67	14.5	799	6	CB994696	CB994696 AGENCOURT	C 810	67	14.5	450	1	AA018305	AA018305 ze40d07.r
C 738	67	14.5	806	7	CN593042	CN593042 TTE000126	C 811	67	14.5	470	2	BE858246	BE858246 7g20h05.x
C 739	67	14.5	811	7	CN593324	CN593324 TTE000107	C 812	67	14.5	474	4	BI136771	BI136771 F073P56Y

813	66.5	14.4	476	8	AZ118627	RPCI-23-1	886	66	14.3	359	1	AJ433297	AJ433297
814	66.5	14.4	478	4	BM152485	TCBAP1E91	C 887	66	14.3	361	1	AA728067	AA728067
C 815	66.5	14.4	487	4	B1810428	J007910 O	888	66	14.3	365	9	CG418981	ZMMBB002
816	66.5	14.4	495	2	BF606302	273305 MA	C 889	66	14.3	387	4	BI002360	MR3-HN015
817	66.5	14.4	505	6	CA043599	scslp1a00	C 890	66	14.3	392	5	BY506013	BY506013
C 818	66.5	14.4	506	4	BI140963	IPI 41 EO	891	66	14.3	400	8	AZ047976	LMAJFV1_1
C 819	66.5	14.4	511	2	AW377245	MR2-CT022	C 892	66	14.3	405	1	AU092546	AU092546
C 820	66.5	14.4	514	6	CA898028	PCBP01559	C 893	66	14.3	412	4	BM094336	sa14c06
C 821	66.5	14.4	518	1	AL780542	AL780542	894	66	14.3	415	4	BM778646	fx52g07.Y
C 822	66.5	14.4	519	6	CD513873	AGENCOURT	895	66	14.3	416	8	AZ331922	IM0060F02
C 823	66.5	14.4	519	6	AZ980418	2M0257N24	896	66	14.3	432	8	AZ358121	IM0100116
824	66.5	14.4	522	6	CA905254	PCS05528	C 897	66	14.3	432	8	AZ358121	IM0100116
825	66.5	14.4	534	9	CE250385	tigr-gss-	898	66	14.3	440	8	CC176785	ZMMBB030
826	66.5	14.4	534	7	CO796854	AGENCOURT	899	66	14.3	481	1	AI539955	SMOV3MCM
C 827	66.5	14.4	557	8	AZ249214	RPCI-23-4	900	66	14.3	481	1	AI539955	SMOVAFCAP
C 828	66.5	14.4	557	8	AZ661306	IM0539N17	901	66	14.3	493	4	BI949280	HVSMEL001
829	66.5	14.4	566	8	BZ295460	CG1493.f1	C 901	66	14.3	495	6	CA599960	wawic.pk0
830	66.5	14.4	579	9	CG900311	ZMMBB023	C 902	66	14.3	497	8	AZ342620	IM0075G17
831	66.5	14.4	581	1	AU020988	AU020988	C 903	66	14.3	500	1	AL584436	AL584436
832	66.5	14.4	585	8	BZ295738	CG1649.r1	C 904	66	14.3	501	1	AI026841	ow02h05.X
C 833	66.5	14.4	587	7	CK563317	rswpb0_00	C 905	66	14.3	507	8	AZ369965	IM0120113
C 834	66.5	14.4	589	5	BQ566746	GI68C11.Y	C 906	66	14.3	508	5	EX886097	EX886097
835	66.5	14.4	591	9	CG045329	PUMCS6TD	C 907	66	14.3	508	5	EX888863	EX888863
836	66.5	14.4	592	8	BZ293311	CG0261.f1	908	66	14.3	510	6	CB030403	TgESTxyd6
837	66.5	14.4	596	2	BF508852	UI-H-BI4-	C 909	66	14.3	518	7	AN878502	020910B09
C 838	66.5	14.4	598	1	AL869928	AL869928	C 910	66	14.3	518	7	AN878502	020910B09
C 839	66.5	14.4	621	8	AZ780960	AL869928	911	66	14.3	518	8	AQ844540	an32h09.J
840	66.5	14.4	623	2	BF178347	601808586	C 912	66	14.3	526	8	AQ430889	HS_5137.A
C 841	66.5	14.4	624	7	CG652548	Eg_PSSLS	913	66	14.3	535	4	BM660782	95204JH06
842	66.5	14.4	627	7	CF350702	r154b12.Y	914	66	14.3	539	1	AA546833	vk67a05.8
843	66.5	14.4	627	9	CG830297	ZMMBB017	915	66	14.3	543	8	AZ325600	IM0048K05
C 844	66.5	14.4	631	1	AL861326	AL861326	C 916	66	14.3	547	9	CG986335	ZUAF554TH
C 845	66.5	14.4	642	8	AZ833342	2M0115C21	917	66	14.3	556	6	CF326448	JMT1--06-
C 846	66.5	14.4	643	1	AL871050	AL871050	C 918	66	14.3	559	7	CF798181	NCST3C77
C 847	66.5	14.4	649	1	AL851911	AL851911	919	66	14.3	559	8	AZ359975	IM0103J06
C 848	66.5	14.4	672	9	CL734541	OR_BBA006	920	66	14.3	573	8	AZ363614	IM0109P10
C 849	66.5	14.4	680	4	BJ816990	BJ816990	921	66	14.3	577	6	CB424174	598411.MA
850	66.5	14.4	681	5	BQ447018	UI-H-EU1-	922	66	14.3	583	5	BQ695873	NXPV_033
C 851	66.5	14.4	706	7	CL817442	CL817442	923	66	14.3	584	9	CC560737	CH240_470
C 852	66.5	14.4	707	9	CL817442	CL817442	924	66	14.3	585	6	CB502156	ssalmge50
853	66.5	14.4	709	4	BF723531	602694235	C 925	66	14.3	586	8	AZ403378	IM0171M02
C 854	66.5	14.4	710	7	CF542729	S014677w-	C 926	66	14.3	593	7	CF536200	UI-M-GIO-
C 855	66.5	14.4	715	4	BJ715392	BJ715392	C 927	66	14.3	594	6	CA824333	RAOC01.tw
856	66.5	14.4	716	4	BG069857	H3080405-	C 928	66	14.3	595	2	AW623262	EST321207
857	66.5	14.4	722	7	CR442494	CR442494	929	66	14.3	597	6	CB510992	ssalmwh50
C 858	66.5	14.4	735	7	CK862356	33510.In	C 930	66	14.3	598	9	CE561999	tigr-gss-
C 859	66.5	14.4	766	8	BH247576	BOGAP14TR	931	66	14.3	600	8	BZ313028	id32h10.b
C 860	66.5	14.4	771	4	BJ721129	BJ721129	C 932	66	14.3	605	7	CK637554	UI-M-HOO-
861	66.5	14.4	821	5	BP707793	BP707793	C 933	66	14.3	610	1	AU023490	AU023490
C 862	66.5	14.4	827	9	CG069452	PUPPX08TB	C 934	66	14.3	618	9	CC714389	OGUCW50TV
C 863	66.5	14.4	844	7	CK197013	FGAS00548	935	66	14.3	622	8	AZ624801	IM0463P14
C 864	66.5	14.4	846	5	EX400005	EX400005	C 936	66	14.3	634	1	AL784209	AL784209
865	66.5	14.4	856	5	BU764148	BU764148	C 937	66	14.3	636	8	AZ959699	AZ959699
866	66.5	14.4	868	5	BU459905	60366795	938	66	14.3	637	2	BF599140	SMOV3MCM
867	66.5	14.4	870	2	BF027903	601764224	939	66	14.3	637	9	CG027501	CHGAJ51TR
C 868	66.5	14.4	871	2	BE745211	601733961	940	66	14.3	640	8	AZ704524	RBC1-23-2
869	66.5	14.4	891	9	CG069455	PUPPX08TD	941	66	14.3	641	4	BJ754873	BJ754873
C 870	66.5	14.4	902	6	CF206674	RR8909151	942	66	14.3	643	8	AZ607375	IM0429J17
C 871	66.5	14.4	914	5	EX759853	EX759853	943	66	14.3	644	2	AW562298	SMOVAFCAP
C 872	66.5	14.4	936	2	BF739880	601593168	944	66	14.3	644	8	AZ330132	IM0050L11
873	66.5	14.4	945	9	CNS01QNU	Asopheles	C 945	66	14.3	651	9	CC852117	NDL_44D6
C 874	66.5	14.4	947	6	CA983324	AGENCOURT	C 946	66	14.3	652	6	CA244244	CA244244
C 875	66.5	14.4	948	2	BF125220	601762239	C 947	66	14.3	653	8	BZ921414	BZ921414
C 876	66.5	14.4	980	9	CNS06E8U	601762239	C 948	66	14.3	661	9	AZ611148	IM0436G03
C 877	66.5	14.4	1013	6	CA280742	SCVPFL4C0	949	66	14.3	662	9	CC507035	CC507035
C 878	66.5	14.4	1041	9	AY412741	Pan trolg	950	66	14.3	663	4	BG113922	602284386
879	66.5	14.4	1116	9	AG314193	Mus muscu	C 951	66	14.3	663	8	AZ503157	IM0342M15
C 880	66.5	14.4	1274	4	BM807404	AGENCOURT	C 952	66	14.3	666	9	CG028022	CHGAC69TF
881	66.5	14.4	1305	9	CG746758	P040-1-D1	C 953	66	14.3	669	9	CA491388	CA491388
C 882	66.5	14.4	1394	3	CNS0A6LS	Arabidops	C 954	66	14.3	671	8	AZ653045	IM0526H06
C 883	66	14.3	186	2	BF819958	MR1-RT002	955	66	14.3	673	5	EX780226	EX780226
884	66	14.3	194	2	BE068154	CM2-BT036	C 956	66	14.3	675	1	AJ800622	AJ800622
C 885	66	14.3	297	9	CG688979	ZMMBB012	957	66	14.3	682	6	CA449012	UI-H-EIO-
							958	66	14.3	687	1	AJ635722	AJ635722

c 959	66	14.3	690	7	CN876869	020814AAR	1032	65.5	14.2	292	1	AA280017	zs93a04.s
960	66	14.3	693	8	AZ633172	1M0488G15	1033	65.5	14.2	292	2	BB341197	BB341197
961	66	14.3	698	8	CC084766	CSU-K33r	1034	65.5	14.2	294	1	AA860877	AA860877
c 962	66	14.3	704	8	AZ614549	1M0443J21	1035	65.5	14.2	294	1	AI079152	AI079152
963	66	14.3	713	1	AI818341	WK59E02.x	1036	65.5	14.2	295	1	AI350635	AI350635
964	66	14.3	713	5	BQ182647	UI-H-EU0-	c1037	65.5	14.2	296	7	CN621111	CN621111
965	66	14.3	717	9	AG318885	Mus muscu	1038	65.5	14.2	297	1	AI435326	AI435326
c 966	66	14.3	724	9	CG220684	OGXAN24TV	1039	65.5	14.2	308	2	AW296694	AW296694
967	66	14.3	734	8	AQ274235	nbxb0034G	1040	65.5	14.2	313	1	AI582739	AI582739
968	66	14.3	737	9	CU564731	OB_Ba003	c1041	65.5	14.2	318	1	AV701228	AV701228
969	66	14.3	738	5	BW041402	BW041402	c1042	65.5	14.2	326	1	AA483997	AA483997
c 970	66	14.3	742	8	CG333595	OGUCB66TH	1043	65.5	14.2	333	1	AA255455	AA255455
971	66	14.3	744	9	CC640472	OGVCD91TH	1044	65.5	14.2	333	8	BH434445	BH434445
c 972	66	14.3	753	9	CG202979	CG247402	1045	65.5	14.2	334	1	AA665063	AA665063
973	66	14.3	754	5	BU231913	CHGAC31TR	c1046	65.5	14.2	334	7	CN621109	CN621109
c 974	66	14.3	755	7	CF407798	CH3H050_F	1047	65.5	14.2	337	9	CE182470	CE182470
975	66	14.3	758	1	AJ797695	AJ797695	1048	65.5	14.2	338	2	AW008787	AW008787
c 976	66	14.3	758	1	BG975661	602845373	c1049	65.5	14.2	343	6	CD061013	CD061013
977	66	14.3	765	9	AG405628	Mus muscu	1050	65.5	14.2	346	1	AA737959	AA737959
978	66	14.3	766	9	CG247402	OGXCR67TH	1051	65.5	14.2	346	1	AA988111	AA988111
979	66	14.3	774	8	BH712029	BOMNS59TF	1052	65.5	14.2	358	1	AA235287	AA235287
980	66	14.3	780	8	BZ741746	OGEDJ10TC	1053	65.5	14.2	358	2	BF447463	BF447463
c 981	66	14.3	781	5	BU243943	603593540	1054	65.5	14.2	367	2	BE116463	BE116463
982	66	14.3	788	5	BQ015344	UI-H-ED1-	c1055	65.5	14.2	367	7	CK144951	CK144951
c 983	66	14.3	790	6	CB943808	AGENCOURT	1056	65.5	14.2	368	1	AI025858	AI025858
c 984	66	14.3	790	9	AG560399	Mus muscu	c1057	65.5	14.2	368	7	F34646	F34646
985	66	14.3	794	5	BQ617371	UI-H-DF0-	1058	65.5	14.2	371	1	AA242829	AA242829
986	66	14.3	804	2	BF918209	SNOW3MCAM	c1059	65.5	14.2	374	4	EM451907	EM451907
c 987	66	14.3	806	5	BU594374	AGENCOURT	1060	65.5	14.2	375	1	AA706689	AA706689
c 988	66	14.3	814	7	CO099601	GR_Ea24J	1061	65.5	14.2	377	1	AA694424	AA694424
c 989	66	14.3	817	7	CO557312	AGENCOURT	1062	65.5	14.2	377	2	BB802457	BB802457
c 990	66	14.3	837	7	CK298081	EST760795	c1063	65.5	14.2	377	2	BF119128	BF119128
c 991	66	14.3	838	8	BH265545	CH230-121	1064	65.5	14.2	378	1	AI122572	AI122572
c 992	66	14.3	845	7	CO117799	GR_Eb01N	1065	65.5	14.2	379	1	W95169	W95169
993	66	14.3	854	9	CC516641	CH240_362	1066	65.5	14.2	385	1	AI769255	AI769255
c 994	66	14.3	859	9	CG367950	OGYCO08TH	c1067	65.5	14.2	386	1	AI193789	AI193789
c 995	66	14.3	874	4	BI661557	603305873	c1068	65.5	14.2	386	1	AJ572056	AJ572056
996	66	14.3	877	9	CG824755	SOYAC15TV	1069	65.5	14.2	387	2	BF405235	BF405235
c 997	66	14.3	878	9	CNS09A71	Single re	1070	65.5	14.2	390	1	AA242808	AA242808
c 998	66	14.3	883	9	CL428670	ZMBB044	1071	65.5	14.2	392	1	AA658557	AA658557
c 999	66	14.3	895	7	CK292528	EST755242	1072	65.5	14.2	392	1	AI333959	AI333959
c1000	66	14.3	899	9	CG696261	OGUH062TH	1073	65.5	14.2	394	1	AA588269	AA588269
c1001	66	14.3	901	9	CG378328	OG18C57TH	1074	65.5	14.2	397	1	AI494381	AI494381
c1002	66	14.3	910	9	CNS01XA7	Tetraodon	1075	65.5	14.2	397	2	AW265213	AW265213
1003	66	14.3	913	8	CG363693	PUHU41TB	1076	65.5	14.2	398	2	AW183620	AW183620
1004	66	14.3	920	8	CC001619	PUGJU79TD	1077	65.5	14.2	400	1	AA515424	AA515424
c1005	66	14.3	921	7	CO770149	testis_ES	1078	65.5	14.2	401	1	AI004938	AI004938
1006	66	14.3	922	9	CG315108	OG3AT64TV	1079	65.5	14.2	404	1	AI223243	AI223243
1007	66	14.3	931	9	CG30613G	T7 end of	c1080	65.5	14.2	404	1	AI223243	AI223243
1008	66	14.3	932	2	BF580422	602097181	c1081	65.5	14.2	407	1	AJ573623	AJ573623
c1009	66	14.3	933	4	BI691870	603307594	c1082	65.5	14.2	407	7	F36871	F36871
1010	66	14.3	943	9	CG378340	OG18C57TV	1083	65.5	14.2	408	1	AA778139	AA778139
1011	66	14.3	955	9	CG385627V	OGUH062TV	1084	65.5	14.2	408	4	EM667896	EM667896
1012	66	14.3	967	9	CG385738	OGUH062TV	c1085	65.5	14.2	413	4	BG193491	BG193491
1013	66	14.3	979	9	CG199853	PURQ90TD	1086	65.5	14.2	416	4	BM355906	BM355906
1014	66	14.3	984	4	BG530481	602559046	1087	65.5	14.2	417	1	AI022251	AI022251
1015	66	14.3	1028	5	BQ050496	AGENCOURT	1088	65.5	14.2	422	1	AA961762	AA961762
c1016	66	14.3	1029	9	AG366507	Mus muscu	1089	65.5	14.2	422	1	AI219023	AI219023
1017	66	14.3	1034	4	BM450683	AGENCOURT	1090	65.5	14.2	422	5	BQ013064	BQ013064
1018	66	14.3	1078	4	BI253085	602953165	1091	65.5	14.2	422	6	CB099518	CB099518
c1019	66	14.3	1202	3	CR667434	Tetraodon	1092	65.5	14.2	424	1	AA031356	AA031356
1020	66	14.3	1223	9	CL649740	CH213-249	1093	65.5	14.2	424	1	AA723621	AA723621
1021	66	14.3	1336	5	BQ899897	AGENCOURT	1094	65.5	14.2	424	1	AI359616	AI359616
c1022	66	14.3	1343	4	BM809720	AGENCOURT	1095	65.5	14.2	425	1	AA908659	AA908659
1023	66	14.3	1405	2	BE965531	601659462	1096	65.5	14.2	426	1	AA244165	AA244165
c1024	65.5	14.2	205	1	AA973367	oo43c11.s	c1097	65.5	14.2	428	7	W63551	W63551
1025	65.5	14.2	235	1	AA491729	ne96d08.s	1098	65.5	14.2	431	1	AI041609	AI041609
1026	65.5	14.2	243	1	AA705997	ah25f05.s	1099	65.5	14.2	431	1	AI091063	AI091063
1027	65.5	14.2	262	9	CL227797	ZMBBc002	1100	65.5	14.2	432	1	AA057167	AA057167
1028	65.5	14.2	267	1	AI208662	CG34e05.x	1101	65.5	14.2	432	8	AQ001088	AQ001088
1029	65.5	14.2	280	1	AA879084	o118d12.s	1102	65.5	14.2	436	5	BY018900	BY018900
1030	65.5	14.2	283	1	AA815469	ai65f05.s	c1103	65.5	14.2	439	9	AY405586	AY405586
c1031	65.5	14.2	290	2	BF216025	601881585	c1104	65.5	14.2	444	1	AA313833	AA313833

1105	14.2	65.5	14.2	446	1	AI088743	AI088743 qal6904.x	cl1178	65.5	14.2	571	1	AV717534	AV717534	AV717534	AV717534
1106	14.2	65.5	14.2	446	1	AI198896	AI198896 qf55a08.x	1179	65.5	14.2	580	7	CF914441	CF914441	B0964A12-	CF914441
1107	14.2	65.5	14.2	447	1	AI1859174	AI1859174 w166f11.x	1180	65.5	14.2	582	6	CB095552	CB095552	py14a03.y	CB095552
cl1108	65.5	14.2	65.5	447	1	AU090073	AU090073 AU090073	1181	65.5	14.2	583	6	CB186895	CB186895	TG8STzyf3	CB186895
11109	65.5	14.2	65.5	448	1	AA789242	AA789242 aj27f08.s	cl1182	65.5	14.2	584	6	CO404806	CO404806	AGENCOURT	CO404806
11110	65.5	14.2	65.5	449	1	AA551358	AA551358 nk72e01.s	cl1183	65.5	14.2	586	6	CF246301	CF246301	TG8STzyv6	CF246301
11111	65.5	14.2	65.5	450	1	AI571201	AI571201 tq43d01.x	1184	65.5	14.2	593	4	BG831805	BG831805	602765433	BG831805
11112	65.5	14.2	65.5	451	1	AI335114	AI335114 qn85d01.x	cl1185	65.5	14.2	594	6	CF246666	CF246666	TG8STzyi7	CF246666
11113	65.5	14.2	65.5	451	4	BM659420	BM659420 SGD603702	cl1186	65.5	14.2	595	4	BJ477821	BJ477821	BJ477821	BJ477821
11114	65.5	14.2	65.5	453	1	AI224530	AI224530 q134a03.x	1187	65.5	14.2	599	6	CA732981	CA732981	w1pic.pk0	CA732981
11115	65.5	14.2	65.5	453	1	AI301947	AI301947 qn57b12.x	1188	65.5	14.2	600	4	BI508920	BI508920	BI508920	BI508920
11116	65.5	14.2	65.5	456	7	BE15811	BE15811 ya46d07.s2	cl1189	65.5	14.2	604	1	AV710037	AV710037	AV710037	AV710037
11117	65.5	14.2	65.5	456	2	BE785072	BE785072 601478331	1190	65.5	14.2	609	6	CB938876	CB938876	IPCGJX13	CB938876
11118	65.5	14.2	65.5	459	1	AA280088	AA280088 zs93a04.r	1191	65.5	14.2	614	7	CK952594	CK952594	4091991.B	CK952594
11119	65.5	14.2	65.5	460	7	W46182	W46182 zc31s08.s1	1192	65.5	14.2	614	7	CK952594	CK952594	4091991.B	CK952594
11120	65.5	14.2	65.5	462	4	BI006883	BI006883 QV3-R1007	1193	65.5	14.2	617	7	CK952594	CK952594	4091991.B	CK952594
11121	65.5	14.2	65.5	463	2	BE685567	BE685567 187925.MA	1194	65.5	14.2	618	4	BI957297	BI957297	HVSMER000	BI957297
11122	65.5	14.2	65.5	464	4	BG032957	BG032957 602300350	cl1195	65.5	14.2	620	4	AV734952	AV734952	AV734952	AV734952
11123	65.5	14.2	65.5	470	5	BM993558	BM993558 UI-H-DT0-	1196	65.5	14.2	627	5	BM277715	BM277715	BM277715	BM277715
11124	65.5	14.2	65.5	471	5	BU162058	BU162058 AGENCOURT	cl1197	65.5	14.2	635	9	CE388480	CE388480	tigr-g8s-	CE388480
11125	65.5	14.2	65.5	471	6	CD251491	CD251491 AGENCOURT	1198	65.5	14.2	636	7	CO532443	CO532443	3530.1.21	CO532443
11126	65.5	14.2	65.5	471	8	BH170175	BH170175 SALK_0024	1199	65.5	14.2	647	6	CB456748	CB456748	714038.MA	CB456748
11127	65.5	14.2	65.5	474	6	CB857967	CB857967 NISC_hall1	1200	65.5	14.2	654	1	AA519499	AA519499	TG8STzz56	AA519499
11128	65.5	14.2	65.5	475	2	BE622098	BE622098 601440962	cl1201	65.5	14.2	654	4	BI088409	BI088409	602852904	BI088409
11129	65.5	14.2	65.5	476	1	AA838682	AA838682 ai86h05.s	1202	65.5	14.2	655	6	CD479934	CD479934	eca01-14m	CD479934
11130	65.5	14.2	65.5	476	6	AJ709787	AJ709787 AJ709787	cl1203	65.5	14.2	660	1	AV718251	AV718251	4066409.B	AV718251
11131	65.5	14.2	65.5	476	6	CD520862	CD520862 AGENCOURT	1204	65.5	14.2	661	4	BG890457	BG890457	ESTV16308	BG890457
11132	65.5	14.2	65.5	479	6	CB050872	CB050872 NISC_gj20	1205	65.5	14.2	661	8	AZ131601	AZ131601	ESUNB0011	AZ131601
11133	65.5	14.2	65.5	480	1	AI150241	AI150241 qf34e06.x	1206	65.5	14.2	662	6	CB420281	CB420281	593219.MA	CB420281
11134	65.5	14.2	65.5	482	6	CB050873	CB050873 NISC_gj20	cl1207	65.5	14.2	664	7	CO435349	CO435349	10b3-L3.M	CO435349
11135	65.5	14.2	65.5	482	8	AZ616448	AZ616448 1M0446H14	1208	65.5	14.2	666	5	BU731504	BU731504	UI-E-C11-	BU731504
11136	65.5	14.2	65.5	486	1	AA757125	AA757125 ah54901.s	cl1209	65.5	14.2	666	8	CC329682	CC329682	OGQAM67TH	CC329682
11137	65.5	14.2	65.5	487	5	BX094121	BX094121 BX094121	cl1210	65.5	14.2	671	4	BM607536	BM607536	170000870	BM607536
11138	65.5	14.2	65.5	489	4	BG716062	BG716062 602677478	1211	65.5	14.2	671	8	CB012306	CB012306	He_ad.37C	CB012306
11139	65.5	14.2	65.5	495	6	CD106922	CD106922 AGENCOURT	1212	65.5	14.2	673	6	BH876132	BH876132	hr29b11.g	BH876132
11140	65.5	14.2	65.5	496	2	BF937965	BF937965 fm70g10.y	1213	65.5	14.2	673	9	EX176378	EX176378	Danio rer	EX176378
11141	65.5	14.2	65.5	497	2	BE719498	BE719498 RCO-HT085	1214	65.5	14.2	679	6	CD478066	CD478066	eca01-30m	CD478066
11142	65.5	14.2	65.5	497	5	BQ920060	BQ920060 AGENCOURT	cl1215	65.5	14.2	679	9	CG097325	CG097325	PUPFN06TD	CG097325
11143	65.5	14.2	65.5	498	4	BM048375	BM048375 603625619	1216	65.5	14.2	679	9	CG097324	CG097324	PUPFN06TD	CG097324
11144	65.5	14.2	65.5	500	8	CF196778	CF196778 7n05f09.x	1217	65.5	14.2	680	6	CB923770	CB923770	TAmapi103	CB923770
11145	65.5	14.2	65.5	500	8	CC095755	CC095755 CSU-K34.1	cl1218	65.5	14.2	693	8	BZ017983	BZ017983	oe108f01.	BZ017983
11146	65.5	14.2	65.5	501	4	BM664548	BM664548 UI-E-CL1-	cl1219	65.5	14.2	696	2	BE255897	BE255897	601109853	BE255897
11147	65.5	14.2	65.5	502	6	BM696033	BM696033 UI-E-CL1-	cl1220	65.5	14.2	699	4	BG829783	BG829783	602764263	BG829783
11148	65.5	14.2	65.5	503	6	CD673146	CD673146 fg21d03.y	cl1221	65.5	14.2	701	2	BB246398	BB246398	BB246398	BB246398
11149	65.5	14.2	65.5	503	6	CD699252	CD699252 ESTV15755	1222	65.5	14.2	703	7	CF922765	CF922765	gmchrw24	CF922765
11150	65.5	14.2	65.5	504	4	BG282226	BG282226 602403384	cl1223	65.5	14.2	705	9	CG140938	CG140938	FUIGZ87TB	CG140938
11151	65.5	14.2	65.5	507	2	AW424739	AW424739 707064B04	cl1224	65.5	14.2	708	4	BI668359	BI668359	603292628	BI668359
11152	65.5	14.2	65.5	509	2	BF687139	BF687139 602102948	cl1225	65.5	14.2	710	4	BG723516	BG723516	602694219	BG723516
11153	65.5	14.2	65.5	509	4	GD533575	GD533575 602562206	1226	65.5	14.2	711	2	AW085732	AW085732	xb43e09.x	AW085732
11154	65.5	14.2	65.5	511	6	CD748067	CD748067 rx32b07.y	cl1227	65.5	14.2	711	4	BM920325	BM920325	AGENCOURT	BM920325
11155	65.5	14.2	65.5	511	7	CN366741	CN366741 170006000	1228	65.5	14.2	713	9	EX129373	EX129373	Danio rer	EX129373
11156	65.5	14.2	65.5	514	5	BQ673276	BQ673276 AGENCOURT	cl1229	65.5	14.2	720	8	BZ892620	BZ892620	Hm6.0139.	BZ892620
11157	65.5	14.2	65.5	521	5	BU960237	BU960237 AGENCOURT	1230	65.5	14.2	730	9	CL767997	CL767997	OR_BBA014	CL767997
11158	65.5	14.2	65.5	525	8	AZ315850	AZ315850 1M0033D17	cl1231	65.5	14.2	734	8	BH420108	BH420108	BOGYQ02TF	BH420108
11159	65.5	14.2	65.5	532	9	CE175913	CE175913 tigr-g8s-	1232	65.5	14.2	737	9	AG453128	AG453128	Mus muscu	AG453128
11160	65.5	14.2	65.5	532	9	CG996078	CG996078 ZMMBB038	cl1233	65.5	14.2	741	9	CC560884	CC560884	CH240.471	CC560884
11161	65.5	14.2	65.5	535	1	AA180788	AA180788 zp44c05.s	cl1234	65.5	14.2	744	4	BI834244	BI834244	603084151	BI834244
11162	65.5	14.2	65.5	538	6	CB135858	CB135858 K-EST0188	1235	65.5	14.2	753	8	BH481550	BH481550	BOGPF46TF	BH481550
11163	65.5	14.2	65.5	539	5	BU698069	BU698069 Lu2in1251	1236	65.5	14.2	762	8	BH648568	BH648568	BOMGF21TF	BH648568
11164	65.5	14.2	65.5	539	7	CO791355	CO791355 NT012A.G1	cl1237	65.5	14.2	771	6	CB026001	CB026001	TG8STzyd3	CB026001
11165	65.5	14.2	65.5	544	1	AV749144	AV749144 AV749144	1238	65.5	14.2	781	9	CG270866	CG270866	OGVF004TV	CG270866
11166	65.5	14.2	65.5	546	8	BQ216276	BQ216276 AGENCOURT	1239	65.5	14.2	786	9	CG414397	CG414397	ZMMBB0208	CG414397
11167	65.5	14.2	65.5	550	5	BZ616245	BZ616245 i958a11.b	1240	65.5	14.2	793	9	EX1716342	EX1716342	BX716342	EX1716342
11168	65.5	14.2	65.5	551	5	BU590248	BU590248 AGENCOURT	1241	65.5	14.2	794	5	BN238535	BN238535	EST004388	BN238535
11169	65.5	14.2	65.5	554	4	BG702905	BG702905 602684846	1242	65.5	14.2	798	8	CN238535	CN238535	EST004388	CN238535
11170	65.5	14.2	65.5	556	4	BM189844	BM189844 TG8STzyb4	1243	65.5	14.2	804	8	BZ612249	BZ612249	WHADP51TF	BZ612249
11171	65.5	14.2	65.5	556	9	TA80B10Q	TA80B10Q T. brucei	cl1244	65.5	14.2	806	8	BH391853	BH391853	AG-ND-142	BH391853
11172	65.5	14.2	65.5	562	4	BG703314	BG703314 602685246	1245	65.5	14.2	807	1	AJ513783	AJ513783	EX735313	AJ513783
11173	65.5	14.2	65.5	563	1	AA388107	AA388107 v-88h07.r	1246	65.5	14.2	807	5	BX735313	BX735313	EX735313	BX735313
11174	65.5	14.2	65.5	563	4	BG721783	BG721783 602695959	1247	65.5	14.2	815	9	CG012763	CG01		

1251	65.5	14.2	847	2	BF257282	HVSMef001	BF257282	1324	65	14.1	508	4	BM839829	BM839829	K-EST0116
1252	65.5	14.2	868	2	BF381752	601815979	BF381752	1325	65	14.1	512	2	AW099682	sd29g03.Y	AW099682
1253	65.5	14.2	868	7	CR589674	CR589674	CR589674	1326	65	14.1	513	4	BM755722	K-EST0033	BM755722
1254	65.5	14.2	874	7	CR265254	EST711332	CR265254	1327	65	14.1	513	6	CA045327	ssalpla00	CA045327
1255	65.5	14.2	877	8	BZ841409	CH240_205	BZ841409	1328	65	14.1	513	8	AZ489867	LM0322104	AZ489867
1256	65.5	14.2	895	2	BF248328	601821369	BF248328	1329	65	14.1	514	6	CA905264	PCSC14129	CA905264
1257	65.5	14.2	895	7	CR294407	EST757121	CR294407	1330	65	14.1	514	8	AZ758287	LM0550A13	AZ758287
1258	65.5	14.2	896	5	BQ688958	AGENCOURT	BQ688958	1331	65	14.1	515	8	BU972824	HB22N07r	BU972824
1259	65.5	14.2	897	5	BU464732	603366232	BU464732	1332	65	14.1	515	8	AZ458689	LM0263E03	AZ458689
1260	65.5	14.2	900	9	CNS0481A	Tetraodon	AL278695	1333	65	14.1	515	9	CC861891	NBL72481	CC861891
1261	65.5	14.2	933	8	CC383141	PURPE45TB	CC383141	1334	65	14.1	517	2	BB772481	BD772481	BB772481
1262	65.5	14.2	945	5	BU522215	AGENCOURT	BU522215	1335	65	14.1	530	2	BF292424	IL2-NT020	BF292424
1263	65.5	14.2	958	8	CC358586	PUNL51TD	CC358586	1336	65	14.1	530	8	AZ460536	LM0265119	AZ460536
1264	65.5	14.2	963	5	BQ678483	AGENCOURT	BQ678483	1337	65	14.1	531	6	CB113770	K-EST0157	CB113770
1265	65.5	14.2	966	5	BU953192	AGENCOURT	BU953192	1338	65	14.1	531	6	BM848300	K-EST0128	BM848300
1266	65.5	14.2	967	7	CK293111	EST755825	CK293111	1339	65	14.1	532	7	CN430730	170006008	CN430730
1267	65.5	14.2	988	4	BG337964	602435672	BG337964	1340	65	14.1	534	6	CA768010	ssalmgf00	CA768010
1268	65.5	14.2	990	9	CC889900	ZMBBCC050	CC889900	1341	65	14.1	535	8	AZ644712	LM0508H14	AZ644712
1269	65.5	14.2	1030	7	CN802046	ILLUWIGN	CN802046	1342	65	14.1	536	4	BM711990	UI-E-EJO-	BM711990
1270	65.5	14.2	1050	4	B1116796	602868495	B1116796	1343	65	14.1	536	4	BO661358	HM03C10u	BO661358
1271	65.5	14.2	1052	4	BG292052	602386333	BG292052	1344	65	14.1	543	8	AZ497799	LM0334J14	AZ497799
1272	65.5	14.2	1101	9	CNS008EW	Drosophil	AL056989	1345	65	14.1	544	8	AZ428028	LM0210018	AZ428028
1273	65.5	14.2	1101	9	CNS008LO	AL057310	AL057310	1346	65	14.1	545	5	BU879647	V062G03 P	BU879647
1274	65.5	14.2	1135	4	BM908095	AGENCOURT	BM908095	1347	65	14.1	546	4	BM709550	UI-E-CQI-	BM709550
1275	65.5	14.2	1170	8	CC290384	CH261-550	CC290384	1348	65	14.1	546	9	CG318030	OGXCA44TH	CG318030
1276	65.5	14.2	1199	8	CC256807	CH261-50F	CC256807	1349	65	14.1	555	8	AZ597180	LM0410F21	AZ597180
1277	65.5	14.2	1217	4	BM804261	AGENCOURT	BM804261	1350	65	14.1	564	5	BU877285	NCW13GBT3	BU877285
1278	65.5	14.2	1297	9	AG551145	Mus muscu	AG551145	1351	65	14.1	560	9	CG018300	ZUADOBBTV	CG018300
1279	65.5	14.2	1279	9	AG551145	Mus muscu	AG551145	1352	65	14.1	562	5	BU875536	HM03C10r	BU875536
1280	65.5	14.2	1597	3	AK042669	Zea mays	AK042669	1353	65	14.1	562	8	AZ622376	LM0459G10	AZ622376
1281	65	14.1	267	2	BF603332	268923 MA	BF603332	1354	65	14.1	564	5	BU877285	V032C02 P	BU877285
1282	65	14.1	277	7	R34348	Yh85b06.sl	R34348	1355	65	14.1	565	1	AI397530	V040D03 P	AI397530
1283	65	14.1	279	2	BB163043	BB163043	BB163043	1356	65	14.1	565	5	BU877875	BM755259	BU877875
1284	65	14.1	290	2	BB564585	BB564585	BB564585	1357	65	14.1	565	5	BU875536	V010D12 P	BU875536
1285	65	14.1	295	4	BM798639	K-EST0082	BM798639	1358	65	14.1	566	5	BU875536	V032C02 P	BU875536
1286	65	14.1	315	9	CE373562	tigr-g88-	CE373562	1359	65	14.1	567	5	BU877285	NCW13GBT3	BU877285
1287	65	14.1	318	2	BB320192	BB320192	BB320192	1360	65	14.1	568	4	B1858485	603391717	B1858485
1288	65	14.1	328	8	AZ619259	LM0451F06	AZ619259	1361	65	14.1	571	8	AZ821129	2M0093F14	AZ821129
1289	65	14.1	341	4	BM097470	EBR005 SQ	BM097470	1362	65	14.1	573	6	CB505358	ssalmgd50	CB505358
1290	65	14.1	344	4	BM050046	QV1-UM009	BM050046	1363	65	14.1	575	2	BE395052	601309455	BE395052
1291	65	14.1	349	5	BY185467	BY185467	BY185467	1364	65	14.1	576	8	AZ505928	LM0346P17	AZ505928
1292	65	14.1	369	1	AJ433441	AJ433441	AJ433441	1365	65	14.1	579	6	CA044504	ssalmgd00	CA044504
1293	65	14.1	373	8	BF158664	LM0452B17	BF158664	1366	65	14.1	580	4	BM876348	1j61f01.X	BM876348
1294	65	14.1	402	2	BF158664	601766777	BF158664	1367	65	14.1	582	6	CD392970	Gm_ck1226	CD392970
1295	65	14.1	428	2	BF420722	UI-R-BJ2-	BF420722	1368	65	14.1	584	8	AZ398043	LM0163118	AZ398043
1296	65	14.1	430	5	BM387810	BM387810	BM387810	1369	65	14.1	584	8	AZ454658	LM0256N11	AZ454658
1297	65	14.1	430	8	AQ145961	BW2224 B	AQ145961	1370	65	14.1	586	6	CB503010	ssalmg50	CB503010
1298	65	14.1	438	5	BP653704	BP653704	BP653704	1371	65	14.1	589	6	CA599105	ssalmg50	CA599105
1299	65	14.1	442	1	AA226710	AA226710	AA226710	1372	65	14.1	589	6	CB506405	wyric.pk0	CB506405
1300	65	14.1	442	1	AA226710	AA226710	AA226710	1373	65	14.1	594	4	BM707975	UI-E-C11-	BM707975
1301	65	14.1	445	5	BU878416	V047A02 P	BU878416	1374	65	14.1	594	6	CA767971	ssalplnb5	CA767971
1302	65	14.1	447	8	CC076018	CC076018	CC076018	1375	65	14.1	599	7	CN751506	ApHL3SD-V	CN751506
1303	65	14.1	450	8	AZ632427	LM0487K04	AZ632427	1376	65	14.1	602	4	BM355722	tigr2g05.Y	BM355722
1304	65	14.1	458	5	BM333693	BM333693	BM333693	1377	65	14.1	603	5	BU877753	V038G011	BU877753
1305	65	14.1	459	6	C26059	Rice	C26059	1378	65	14.1	604	8	AZ323550	LM0045H03	AZ323550
1306	65	14.1	466	1	AA808309	oc41g05.s	AA808309	1379	65	14.1	607	4	BG638901	LD38661.5	BG638901
1307	65	14.1	468	5	BQ453252	sa098c04.	BQ453252	1380	65	14.1	611	2	BE898642	LM0246A04	BE898642
1308	65	14.1	469	1	CB016640	sg09g02.s	CB016640	1381	65	14.1	611	5	BU877895	V062G04 P	BU877895
1309	65	14.1	471	6	ABT26891	TgEstrizyc7	ABT26891	1382	65	14.1	612	1	AJ436476	BJ436476	AJ436476
1310	65	14.1	472	1	BM150213	TCAAP6Q11	BM150213	1383	65	14.1	614	5	BM372888	BM372888	BM372888
1311	65	14.1	473	1	AA043632	AA043632	AA043632	1384	65	14.1	614	5	BM386780	BM386780	BM386780
1312	65	14.1	473	1	AA043632	AA043632	AA043632	1385	65	14.1	616	5	BU877895	V040F04 P	BU877895
1313	65	14.1	475	8	AZ493933	LM0328E24	AZ493933	1386	65	14.1	618	5	BU877386	V033D09 P	BU877386
1314	65	14.1	482	1	BM739076	K-EST0008	BM739076	1387	65	14.1	619	8	AZ486559	LM0246A04	AZ486559
1315	65	14.1	485	1	AJ503619	AJ503619	AJ503619	1388	65	14.1	621	5	BU875789	V011E03 P	BU875789
1316	65	14.1	486	2	AW881107	QV0-OT003	AW881107	1389	65	14.1	622	8	AZ338360	LM0069H21	AZ338360
1317	65	14.1	487	5	BQ162650	WHE0445 G	BQ162650	1390	65	14.1	622	8	AZ374217	LM0126M17	AZ374217
1318	65	14.1	490	9	CE773559	tigr-g88-	CE773559	1391	65	14.1	624	4	BM330110	PIC1_47 C	BM330110
1319	65	14.1	496	6	CA045331	ssalpla00	CA045331	1392	65	14.1	624	5	BM767879	EBR008 SQ	BM767879
1320	65	14.1	497	7	CN452582	B05_MU-L1	CN452582	1393	65	14.1	625	4	BM747365	K-EST0021	BM747365
1321	65	14.1	497	8	AQ702987	HS_E443 B	AQ702987	1394	65	14.1	625	5	BM389271	BM389271	BM389271
1322	65	14.1	501	7	CC605829	SmrRnw6-	CC605829	1395	65	14.1	628	5	BM332664	BM332664	BM332664
1323	65	14.1	502	9	CK630334	OGWDU58TH	CK630334	1396	65	14.1	628	5	BM389296	BM389296	BM389296

C1397	65	14.1	629	2	BE391298	601284217	BE391298	601284217	C1470	65	14.1	733	5	BW424941	BW424941
C1398	65	14.1	631	6	CB026031	TGEST2YC6	CB026031	TGEST2YC6	C1471	65	14.1	733	5	BW501315	BW501315
C1399	65	14.1	632	5	BW878462	V047E11 P	BW878462	V047E11 P	1472	65	14.1	733	8	CC089987	CC089987
1400	65	14.1	636	1	AJ635863	AJ635863	AJ635863	AJ635863	1473	65	14.1	735	6	CA306522	UI-H-F31r
1401	65	14.1	637	7	CK824079	IJ61F01.X	CK824079	IJ61F01.X	1474	65	14.1	736	6	CB502554	ssalimgd50
C1402	65	14.1	637	5	BM979505	UI-CF-DU1	BM979505	UI-CF-DU1	1475	65	14.1	737	6	CB505729	ssalimgd50
C1403	65	14.1	637	8	BW388829	BW388829	BW388829	BW388829	1476	65	14.1	737	7	CF871405	tric027xe
C1404	65	14.1	638	5	CB361925	IM0106M18	CB361925	IM0106M18	1477	65	14.1	738	8	AZ759177	IM0551H03
1405	65	14.1	639	6	CD818775	BN20.046K	CD818775	BN20.046K	1478	65	14.1	739	5	BW418912	BW418912
C1406	65	14.1	640	9	CB925079	ABAL_29_A	CB925079	ABAL_29_A	1479	65	14.1	740	5	BQ181835	BQ181835
C1407	65	14.1	642	9	CL153408	104_337_1	CL153408	104_337_1	1480	65	14.1	740	5	BW419989	BW419989
C1408	65	14.1	643	6	CB840395	M15E-0674	CB840395	M15E-0674	1481	65	14.1	741	5	BW382352	BW382352
1409	65	14.1	643	8	CB2340641	IM0072B13	CB2340641	IM0072B13	1482	65	14.1	741	5	BW411225	BW411225
1410	65	14.1	644	9	CG215792	OGYAM30TH	CG215792	OGYAM30TH	1483	65	14.1	742	5	BW381629	BW381629
C1411	65	14.1	645	5	BW487903	CG487903	BW487903	CG487903	1484	65	14.1	743	5	BW419182	BW419182
1412	65	14.1	646	4	BI729522	603349155	BI729522	603349155	1485	65	14.1	743	8	AZ405615	AZ405615
C1413	65	14.1	648	5	BW877844	U039H09 P	BW877844	U039H09 P	1486	65	14.1	744	5	BW501293	BW501293
1414	65	14.1	648	8	AZ324778	IM0046D21	AZ324778	IM0046D21	1487	65	14.1	746	5	BW379361	BW379361
C1415	65	14.1	651	4	BW609994	K-EST0041	BW609994	K-EST0041	1488	65	14.1	747	5	BW383230	BW383230
1416	65	14.1	655	1	AU171939	AU171939	AU171939	AU171939	1489	65	14.1	748	9	CL783957	CL783957
C1417	65	14.1	655	1	CB242899	UI-CF-PN0	CB242899	UI-CF-PN0	1490	65	14.1	749	9	CR103925	Reverse S
C1418	65	14.1	661	4	BJ443092	BJ443092	BJ443092	BJ443092	1491	65	14.1	750	5	BW387493	BW387493
C1419	65	14.1	661	7	CK114177	V038G11 P	CK114177	V038G11 P	1492	65	14.1	752	5	BW376698	BW376698
1420	65	14.1	666	6	CA768289	ssalplnb5	CA768289	ssalplnb5	1493	65	14.1	752	5	BW382001	BW382001
1421	65	14.1	667	4	BI370842	RE57608.5	BI370842	RE57608.5	1494	65	14.1	755	4	BG768506	BG768506
1422	65	14.1	669	9	AG122885	Pan.trog1	AG122885	Pan.trog1	1495	65	14.1	756	7	CN216530	CN216530
1423	65	14.1	670	2	BE308453	601090276	BE308453	601090276	1496	65	14.1	757	7	CK939736	CK939736
1424	65	14.1	671	6	CD055373	MO09A21S	CD055373	MO09A21S	1497	65	14.1	757	9	AG399129	AG399129
1425	65	14.1	673	6	CA041413	ssalplnb5	CA041413	ssalplnb5	1498	65	14.1	758	5	BW379850	BW379850
1426	65	14.1	673	6	CB503358	ssalimgd50	CB503358	ssalimgd50	1499	65	14.1	762	5	BW500252	BW500252
1427	65	14.1	673	6	CB503636	ssalimgd50	CB503636	ssalimgd50	1499	65	14.1	762	5	BW500252	BW500252
1428	65	14.1	673	6	CB505728	ssalimgd50	CB505728	ssalimgd50	1500	65	14.1	763	1	AU056259	AU056259
1429	65	14.1	673	6	CB509449	ssalnhw50	CB509449	ssalnhw50							
1430	65	14.1	675	6	CB505293	ssalimgd50	CB505293	ssalimgd50							
C1431	65	14.1	677	5	BW384670	BW384670	BW384670	BW384670							
1432	65	14.1	677	8	AZ374836	IM0127J21	AZ374836	IM0127J21							
1433	65	14.1	678	5	BW616441	UI-H-DF0-	BW616441	UI-H-DF0-							
C1434	65	14.1	679	5	BW877474	V034F05 P	BW877474	V034F05 P							
1435	65	14.1	679	7	CR572714	CR572714	CR572714	CR572714							
C1436	65	14.1	680	5	BW384449	BW384449	BW384449	BW384449							
C1437	65	14.1	681	5	BW414692	BW414692	BW414692	BW414692							
C1438	65	14.1	681	5	BW493351	BW493351	BW493351	BW493351							
C1439	65	14.1	683	5	BW389902	BW389902	BW389902	BW389902							
C1440	65	14.1	685	8	AZ614465	IM0443J17	AZ614465	IM0443J17							
C1441	65	14.1	687	5	BW375168	BW375168	BW375168	BW375168							
C1442	65	14.1	689	4	BI799123	HI25D09 E	BI799123	HI25D09 E							
C1443	65	14.1	691	5	BW385809	BW385809	BW385809	BW385809							
C1444	65	14.1	694	9	AG074816	Pan.trog1	AG074816	Pan.trog1							
C1445	65	14.1	698	5	BW488717	BW488717	BW488717	BW488717							
C1446	65	14.1	698	5	BW414125	BW414125	BW414125	BW414125							
C1447	65	14.1	702	4	BG678532	602624211	BG678532	602624211							
1448	65	14.1	703	4	BM838229	K-EST0114	BM838229	K-EST0114							
C1449	65	14.1	706	8	BH955129	od166a09.	BH955129	od166a09.							
1450	65	14.1	706	9	CR087762	Forward S	CR087762	Forward S							
1451	65	14.1	707	5	BQ114114	EST599690	BQ114114	EST599690							
C1452	65	14.1	707	6	CF130324	UI-HF-ES0	CF130324	UI-HF-ES0							
C1453	65	14.1	710	5	BW493764	BW493764	BW493764	BW493764							
C1454	65	14.1	711	2	BE281321	601155252	BE281321	601155252							
1455	65	14.1	715	5	BW730435	UI-E-C11-	BW730435	UI-E-C11-							
1456	65	14.1	717	5	BQ182041	UI-H-EU0-	BQ182041	UI-H-EU0-							
C1457	65	14.1	717	5	BW385799	BW385799	BW385799	BW385799							
1458	65	14.1	718	5	BW482880	BW482880	BW482880	BW482880							
C1459	65	14.1	719	7	CK969267	4084682 B	CK969267	4084682 B							
1460	65	14.1	719	7	AG013808	Homo sapi	AG013808	Homo sapi							
C1461	65	14.1	721	5	BW415688	BW415688	BW415688	BW415688							
C1463	65	14.1	721	5	BW491621	BW491621	BW491621	BW491621							
C1464	65	14.1	724	9	CC821374	MBSP1G5 U	CC821374	MBSP1G5 U							
C1465	65	14.1	727	8	AZ877093	2M0192K10	AZ877093	2M0192K10							
C1466	65	14.1	728	5	BW387360	BW387360	BW387360	BW387360							
1467	65	14.1	730	5	BW422552	BW422552	BW422552	BW422552							
C1468	65	14.1	732	5	BW382853	BW382853	BW382853	BW382853							
1469	65	14.1	733	2	BF701572	602129007	BF701572	602129007							

ALIGNMENTS

RESULT 1

AU185777/c

LOCUS

AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens

DEFINITION

cDNA clone B02302-019, mRNA sequence.

ACCESSION

AU185777

VERSION

AU185777.1 GI:14623690

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 663)

AUTHORS

Sugita,Y., Oshida,T. and Oya,Y.

TITLE

Human cDNA sequencing

JOURNAL

Unpublished (2001)

COMMENT

Contact: Yuji Sugita
Genex Research, Inc.
907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan
Tel: 81-44-797-2281
Fax: 81-44-797-2622
Email: syuji@genex.co.jp, URL: http://www.genex.co.jp.

FEATURES

Location/Qualifiers

source

1..663

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="B02302-019"

/cell_type="Mast cell"

/clone_lib="Homo sapiens Mast cell library (Sugita Y)"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

5.05e-34

365.50

89.01%

89.01%

79.11%

Length:

Matches:

Conservative:

Mismatches:

Indels:

663

81

0

8

3

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DB:      1      1      Gaps:      1
US-09-989-293A-377 (1-90) x AU185777 (1-663)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTrrArgSerAs 20
    |||||
Db 507 ATGACATTTTTCGGTCAACATTTATNATGTTGGTATGTGAAGCTATTGTGGNAGATCCAA 448
    |||||

Qy 20 nSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSe 40
    |||||
Db 447 TTCAGNAAGC---ACATTTGNAGAAATGGCTACTTTCTATCAAGAAATAAAGAGAACCCACAG 391
    |||||

Qy 40 rGlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThrTh 60
    |||||
Db 390 TCACCCACACATTCATCTTTAGAGACAGTGG-ACTCTACCAAGCTGTCAAAACCAC 332
    |||||

Qy 60 rGlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGl 80
    |||||
Db 331 AGGCAAGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAAATCTTGGTGCTGA 272
    |||||

Qy 80 uAlaTrrpGlyArgGlyValLysLysAsnThr 90
    |||||
Db 271 AGCCTGGGGCAGGGGTGTAAGAAACACT 241
    |||||

RESULT 2
CB958894      800 bp      mRNA      linear      EST 29-APR-2003
LOCUS      AGENCOURT_13785021 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION      IMAGE:30352338 5', mRNA sequence.
ACCESSION      CB958894
VERSION
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abbs-remail.nih.gov
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDQM151 row: e column: 19
High quality sequence stop: 488.
Location/Qualifiers
1..800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352338"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Stfl (ggccattatggcc); Site_2: Sfil (ggccgcctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTTAGGCC-3' and 3' adaptor sequence:
5'-ATTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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Alignment Scores:      1.15e-26      Length:      800
Score:      306.00      Matches:      70
Percent Similarity:      66.38%      Conservative:      7
Best Local Similarity:      60.34%      Mismatches:      10
Query Match:      66.23%      Indels:      29
DB:      6      Gaps:      3
US-09-989-293A-377 (1-90) x CB958894 (1-800)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTrrArgSerAsn 20
    |||||
Db 342 ATGACATTTTTCGTCACTATTATTATTGTTGGTATGTGAAGCTATTGTGAGATCCAAT 401
    |||||

Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSe 40
    |||||
Db 402 TCAGGAAGCAACACATTCGGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCCACAGT 461
    |||||

Qy 41 GlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaVal-LysThrTh 60
    |||||
Db 462 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACAAC 521
    |||||

Qy 60 rGly-----LysGlyIleValLys-----GlyArgAsnLeuAspSerArgGl 74
    |||||
Db 522 GGGGGTCTTTTCCAGCCCTTGTCTCCCAATTGGAATTATATATATGAGAGAAAGC 581
    |||||

Qy 74 yLeuIle----- 76
    |||||
Db 582 TGTATTATCTTATTCAGCAATTGTCCTCAATAAATTTCCCTGGGGATTGGGAAGATAAAA 641
    |||||

Qy 77 -----LeuGlyAlaGluAlaTrrpGlyArgGlyValLys 87
    |||||
Db 642 AAGACAATTGGCTTGGGGCCAAACCTTGGGGGCTTCCCTATAAA 687
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RESULT 3
BI018962/c
LOCUS      BI018962
DEFINITION      IL3-MT0267-050101-437-A02 MT0267 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BI018962
VERSION      BI018962.1 GI:14425592
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 659)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-MT0267-
050101-437-A02&t3=2001-01-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 639.
Location/Qualifiers

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source
1. .659
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0267"
/notes="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1.2e-19 Length: 659
Score: 247.50 Matches: 50
Percent Similarity: 87.10% Conservative: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 4 Gaps: 1

US-09-989-293A-377 (1-90) x BI018962 (1-659)

QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTTPArgSer 19
Db 617 CTATGTTGGTATACCTGGGTAGTCTGGTCTGGTACCATGGCTATTTGGAGTCC 558
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 557 AATTCAAGGAGCAACATTTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCC 498
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 497 AGTCAACCCACACAATCATCTTTAGAGACAGTGTGACTCTCAACAAAGCTGTCAAAACC 438
QY 60 ThrGly 61
Db 437 ACAGGG 432

RESULT 4
AZ121459/c
LOCUS
DEFINITION
RPCI-23-30A15-TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,
genomic survey sequence.
ACCESSION
AZ121459
VERSION
AZ121459.1 GI:7788387
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 663)
Akinret B., Levins M., Feldhlyum, T., Malek, J., Shatsman, S.,
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSs: RPCI-23-30A15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

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Plate: 30 row: A column: 15
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .663
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-30A15"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methyase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
Alignment Scores:
Pred. No.: 5.94e-15 Length: 663
Score: 209.00 Matches: 50
Percent Similarity: 69.51% Conservative: 7
Best Local Similarity: 60.98% Mismatches: 22
Query Match: 45.24% Indels: 4
DB: 8 Gaps: 2

US-09-989-293A-377 (1-90) x AZ121459 (1-663)

QY 4 PheLeuSerLeuLeuLeuValCysGluAlaIleTTPArgSerAsnSerGlySer 23
Db 248 TTTCTGTGTCATTTGCTGTGTTGTCAGCATTTTGGTACACAATTCAGGGAGA 189
QY 24 AsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThr 43
Db 188 AATCCAGAGAGAAAACAACACTTCTCTATCAAGAAATAAGAGAACCCAC---AGCCCCACA 132
QY 44 GlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGly 63
Db 131 GAATCATCTTTAGTAGAGAGGTGGTCTCCCTCAAGGCATCCCAAACTACAGCAAGGGC 72
QY 64 IleValLysGlyArgAsn-----LeuAspSerArgGlyLeuLeuLeuGlyAlaGluAla 81
Db 71 AGCACGAAGAGGAGC-AATGGGATCCCGGATTCAGAGGTTTCATTTCTGCTGTGAGGCC 13
QY 82 TrpGly 83
Db 12 TGGGGT 7

RESULT 5
AV7211179
LOCUS
DEFINITION
AV7211179 HTB Homo sapiens cDNA clone HTBAK11 5', mRNA sequence.
ACCESSION
AV7211179
VERSION
AV7211179.1 GI:10818331
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 673)
Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

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QY 37 Glu-----AsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro 53
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 Db 357 CCAAGACTATGACCATGTACAA-----CAGTCTTCAACCCCAAGATCACCAGCAT 410
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 QY 54 ThrLysAlaValLysThrThrGlyLysGlyLeValLysGlyArgAsnLeuAspSerArg 73
 |||||
 Db 410 ----- 410

QY 74 GlyLeuLeuLeuGlyAlaGluAlaTrpGlyArgGlyValLysLysAsn 89
 |||||
 Db 411 ---GTGATCTTAGGGCGGAGCGGTGGGAAATGAGTTCCTTGCAAT 455
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RESULT 10
 BE865626
 LOCUS 601677978F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960715 5',
 mRNA sequence.
 DEFINITION
 BE865626
 ACCESSION
 BE865626
 VERSION
 BE865626.1 GI:10314402
 KEYWORDS
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 833)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LCGW843 row: k column: 20
 High quality sequence stop: 571.
 Location/Qualifiers

FEATURES

1..833
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3960715"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 53"
 /note="Organ: bladder; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgcc); site 2: SfiI
 (ggcgattatgcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CAGCGCCATTATGCC-3' and
 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGGCACATG-DT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.55
 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Alignment Scores:
 Pred. No.: 24 Length: 833
 Score: 82.00 Matches: 24
 Percent Similarity: 50.91% Conservative: 4
 Best Local Similarity: 43.64% Mismatches: 21
 Query Match: 17.75% Indels: 6
 DB: 2 Gaps: 1

US-09-989-293A-377 (1-90) x BE865626 (1-833)

QY 36 LysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLys 55

Db 657 AAAGAGAATTCAGCAAGCAAAATGCGAAGTCATCATGATGAAGATTCAAGCTCGTCTACAGAT 716
 |||||
 QY 56 -----AlaValLysThrThrGlyLysGlyLeValLysGlyArgAsn 59
 |||||
 Db 717 AGAAGATCTTGAAGGGGAAATTTAAACAAGGCGCATTTGGAATCTAGAAGGGTTTAAAG 776
 |||||

QY 70 LeuAspSerArgGlyLeuLeuGlyAlaGluAlaTrpGlyArg 84
 |||||

Db 777 GGGGCTCCAGGGGAGCTTGATTGGGGCAGGTAATTGGGGCGGA 821
 |||||

RESULT 11
 BE165693
 LOCUS 602344512F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4454450 5',
 mRNA sequence.
 DEFINITION
 BE165693
 ACCESSION
 BE165693.1 GI:12672396
 VERSION
 BE165693.1
 KEYWORDS
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 924)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10246 row: h column: 03
 High quality sequence stop: 703.
 Location/Qualifiers

FEATURES

1..924
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4454450"
 /tissue_type="hypernephroma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 89"
 /note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 27.4 Length: 924
 Score: 82.00 Matches: 30
 Percent Similarity: 40.00% Conservative: 14
 Best Local Similarity: 27.2% Mismatches: 22
 Query Match: 17.75% Indels: 44
 DB: 4 Gaps: 5

US-09-989-293A-377 (1-90) x BE165693 (1-924)

QY 4 PheLeuSerLeuLeuLeuLeuVal-----CysGluAlaIle 16
 |||||
 Db 534 TTCCTCAGCCTCTTCCTCTCGCATCTGCTGCCACCATCGTCCATTCCTAGTATC 475
 |||||
 QY 17 TrpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLys 36
 |||||
 Db 474 CTCACATTCCTTCCTTCATCAGATCAATA----- 445
 |||||

QY 37 GluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerVal----- 51

this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 28.2 Length: 683
 Score: 80.50 Matches: 25
 Percent Similarity: 54.72% Conservative: 4
 Best Local Similarity: 47.17% Mismatches: 15
 Query Match: 17.42% Indels: 9
 DB: 4 Gaps: 5

US-09-989-293A-377 (1-90) x BI914658 (1-683)

QY 39 HisSerGlnProThrGlnSer-----SerLeuGluAspSerValThrProThr 54
 DB 515 CACCAGCACCACCAATGCGCGGCATCAAGGCTCAGTCTGGGACAGCTGTACCTAGC 456
 QY 55 LysAlaValLysThrThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg--- 73
 DB 455 TCTGCTTC--TGTACCAAGCTCTGGCATAGTTGGGGTAAACACATAGATAGTAGGCAG 399
 QY 74 GlyLeuIleGluGlyAlaGluAlaTrp---GlyArgGly 85
 DB 398 GGC-----CTCGGGTTTCAGGGGCTGGCAGGGGCGGGG 366

RESULT 14

BH354332/c

LOCUS

DEFINITION BH354332 391 bp DNA linear GSS 03-DEC-2001
 CH230-163F16, genomic survey sequence.

ACCESSION

BH354332

VERSION

BH354332.1

KEYWORDS

GSS.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

1 (bases 1 to 391)

AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
 Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, F., de Jong, P. and Fraser, C.M.

TITLE

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL

Unpublished (1999)

COMMENT

Other_GSSs: CH230-163F16.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

plate: 163 row: F column: 16

Seq primer: SP6

Class: BAC ends.

FEATURES

Source

1..391

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/strain="BN/SeNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-163F16"

/sex="Female"

/cell_type="Brain"

/clone_lib="CHORI-230 Segment 1"

/note="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CHORI-230 Rat (BN/SeNHsd/MCW) BAC library produced by

ORIGIN

Alignment Scores:

Pred. No.: 20.7 Length: 391
 Score: 79.00 Matches: 22
 Percent Similarity: 46.38% Conservative: 10
 Best Local Similarity: 31.88% Mismatches: 23
 Query Match: 17.10% Indels: 14
 DB: 8 Gaps: 1

US-09-989-293A-377 (1-90) x BH354332 (1-391)

QY 34 ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro 53
 DB 334 AGGGGTCTCTGTAATTTCTTTTCACATCTCAGTCTCATGCTCGACATATCACTATT 275
 QY 54 ThrLysAlaValLysThrThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg 73
 DB 274 TCTAAGTTAAACAAAAGTCCGGGCTGCTAGTACTGATAGTGAACAGAGGAATCTAAC 215
 QY 74 Gly-----LeuIleLeuGlyAla 79
 DB 214 GGGAGAACTAATGCTTCCACACAGACCATCAGTGGAAAAGTCTTATGTGCGAGCAGA 155

QY 80 GluAlaTrpGlyArgGlyValLysLys 88

DB 154 GAGGTCTTTGGAGAGGGGGGGGAAG 128

RESULT 15

BH354326/c

LOCUS

DEFINITION

BH354326

ACCESSION

BH354326

VERSION

BH354326.1

KEYWORDS

GSS.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

1 (bases 1 to 504)

AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
 Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, F., de Jong, P. and Fraser, C.M.

TITLE

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL

Unpublished (1999)

COMMENT

Other_GSSs: CH230-163F15.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

plate: 163 row: F column: 15

Seq primer: SP6

Class: BAC ends.

FEATURES

Source

1..504

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/strain="BN/SeNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-163F15"

/sex="Female"

/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Alignment Scores:

Pred. No.:	28.9	Length:	504
Score:	79.00	Matches:	22
Percent Similarity:	46.38%	Conservative:	10
Best Local Similarity:	31.88%	Mismatches:	23
Query Match:	17.10%	Indels:	14
DB:	8	Gaps:	1

US-09-989-293A-377 (1-90) x BH354326 (1-504)

QY	34	ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro	53
Db	334	AGGGGTTCTCTGTAATTCTCTTTTCATCTCAGTCCTCATGCTGCTGCAATATCACTATT	275
QY	54	ThrLysAlaValLysThrThrGlyLysGlylleValLysGlyArgAsnLeuAspSerArg	73
Db	274	TCTAAGTTAAACAAAGATCCGGGTCGTGGGCTACTGATAGTGAGAACAGAGGAATCTAAC	215
QY	74	Gly-----LeuIleLeuGlyAla	79
Db	214	GGGAGAACTAATGCTTCCACACAGACCCCTCAGTGGAAACTGCTTATGTGCAGGCAAA	155
QY	80	GluAlaTrpGlyArgGlyValLysLys	88
Db	154	GAGGTGTTTGGAAAGAGGGCGGGGAAG	128

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Job time : 2580 secs

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